

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 2, 2006, 06:47:12 ; Search time 199 Seconds
(without alignments)
2242.428 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043

Sequence: 1 MAFRIYVLLGLFCLSLVA.....SASDAQPLRFQGVISONSE 976

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_8: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5043	100.0	976	2	AAW13408 Arabidops
2	5043	100.0	976	5	ABB91884 Arabidops
3	5043	100.0	976	8	AD132614 Thale cre
4	5043	100.0	976	9	AED28149 Arabidops
5	3602.5	71.4	838	8	ADX95769 plant ful
6	3372.5	66.9	921	8	AD132618 sorghum t
7	3372.5	66.9	921	8	AD132618 sorghum t
8	3167	62.8	614	9	AED28151 Arabidops
9	3113	61.7	999	8	AD132616 Rice tran
10	3091.5	61.3	966	5	ABB93915 Herbicida
11	3091.5	61.3	966	8	AD132622 Thale cre
12	3089.5	61.3	967	9	AED28155 Arabidops
13	3079.5	61.1	966	9	AED28153 Arabidops
14	3059	60.7	932	5	ABB93386 Herbicida
15	3059	60.7	932	8	AD132620 Thale cre
16	2791	55.3	764	8	ADX95784 plant ful
17	2482	49.2	675	8	AD132657 Maize tra
18	2384.5	47.3	578	8	AD132617 plant ful
19	2322.5	46.1	611	9	AED28234 Rice ERBC
20	2259.5	44.8	613	9	AED28233 Rice ERBC
21	2236.5	44.3	541	8	AD132616 plant ful
22	2215	43.9	713	8	ADX95337 plant ful
23	2010	39.9	621	9	AED28235 Rice ERBC

24	1968.5	39.0	619	9	AED28159 Arabidops
25	1956.5	38.8	616	9	AED28157 Arabidops
26	1596	31.6	458	8	AD132614 plant ful
27	1568	31.1	502	3	ABB25570 Pinus rad
28	1543	30.6	426	8	AD132617 plant ful
29	1504.5	29.8	1124	5	ABB91986 Herbicida
30	1489	29.5	1102	5	ABB93939 Herbicida
31	1480.5	29.4	1109	7	ABM6574 Rice abio
32	1446	28.7	1109	8	AD132617 plant ful
33	1442	28.6	1109	5	ABB93705 Arabidops
34	1441	28.6	1109	8	AD132617 plant ful
35	1432.5	28.4	998	3	ABB25556 Pinus rad
36	1417.5	28.1	448	8	AD132632 Bread whe
37	1412.5	28.0	1133	4	ABB91038 Herbicida
38	1410.5	28.0	1003	4	AAW52369 Receptor
39	1410.5	28.0	1003	5	ABB93956 Herbicida
40	1404.5	27.9	998	3	ABB25520 Pinus rad
41	1397	27.7	1123	3	AAW52369 Receptor
42	1393.5	27.6	370	3	AAW52369 Receptor
43	1373.5	27.2	1192	6	ABB25564 Arabidops
44	1368.5	27.1	1002	3	AAW52369 Receptor
45	1368.5	27.1	1002	5	ABB92602 Herbicida

ALIGNMENTS

RESULT 1
AAW13408 standard; protein; 976 AA.
ID AAW13408

AC AAW13408;

DT 10-JUN-1997 (first entry)

DE Arabidopsis thaliana plant morphogenesis regulatory protein.

KW plant, morphogenesis; regulation; short; stem; alteration; inflorescence;

KW extraneous; gene; expression; transformation; increase; control; form;

KW length.

OS Arabidopsis thaliana.

PN JP09056382-A.

PF 24-AUG-1995; 95JP-00216187.

PR 24-AUG-1995; 95JP-00216187.

PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIITSU KENKYU.

PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

DR WPI; 1997-206629/19.

DR N-PSDB; AAT62124.

PT DNA encoding plant morphogenesis regulatory protein - useful to yield

PS plants with short stems or altered inflorescence.

PS Claim 1; Page 6-10; 17pp; Japanese.

CC The present sequence is an Arabidopsis thaliana plant morphogenesis

CC regulatory protein (MRP), which can be used to yield a plant with, e.g.

CC short stems or altered inflorescence. The MRP acts on a plant at a

CC specific site for a specific period, and can therefore be used to

CC regulate extraneous gene expression in a plant. The MRP's cDNA or genomic

CC DNA can be used to transform a plant to increase its MRP expression, and

CC therefore control the form (particularly stem length) of the plant

XX Sequence 976 AA;

SQ Query Match 100.0%; Score 5043; DB 2; Length 976;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MALFRDVLVLLGFLFCLSLVATVTSEEGATLLEIKKSPFDVNNVLYDMTSSSSDYCWMRG 60
DB 1 MALFRDVLVLLGFLFCLSLVATVTSEEGATLLEIKKSPFDVNNVLYDMTSSSSDYCWMRG 60
QY VSCENVTFNNVALNLSDLNLDGEISPAIGDKLSLIDLRGNRLSGQIPDEIGCCSLON 120
DB 61 VSCENVTFNNVALNLSDLNLDGEISPAIGDKLSLIDLRGNRLSGQIPDEIGCCSLON 120
QY 121 LDISFNEISGDIPEISIKLQLEQILKNNQLIGPIBSTLSQIPNLKIIDLQNKLSGEI 180
DB 121 LDISFNEISGDIPEISIKLQLEQILKNNQLIGPIBSTLSQIPNLKIIDLQNKLSGEI 180
QY 181 PRLIYMEVQYIGLRGNLVGNISPDLCQLTGLWFDPVNNSLTGSIPETIGNCTAFQV 240
DB 181 PRLIYMEVQYIGLRGNLVGNISPDLCQLTGLWFDPVNNSLTGSIPETIGNCTAFQV 240
QY 241 LDISYNQLTGEIPEDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
DB 241 LDISYNQLTGEIPEDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
QY 301 PILGNLTFTEKLYLHSHNKLTSISIPPELGNNSKLHYLELNDNHLTGHIPEELGKLTDLFDL 360
DB 301 PILGNLTFTEKLYLHSHNKLTSISIPPELGNNSKLHYLELNDNHLTGHIPEELGKLTDLFDL 360
QY 361 NVANNDEGPIPDHLSCTNLNSLVHGNKFSGTIPPAFOKLEMTYLNLSNNIKGPIR 420
DB 361 NVANNDEGPIPDHLSCTNLNSLVHGNKFSGTIPPAFOKLEMTYLNLSNNIKGPIR 420
QY 421 VELSRIGNLDTLDSNNKINGIIPSSLGDEHLKNNLSRNHITGVVPGDFGNLSIMEI 480
DB 421 VELSRIGNLDTLDSNNKINGIIPSSLGDEHLKNNLSRNHITGVVPGDFGNLSIMEI 480
QY 481 DLSNNDISGPIPEELNQLONTILRLENNNTGVVSGLANCLSTVLNVSHNNLVGDIK 540
DB 481 DLSNNDISGPIPEELNQLONTILRLENNNTGVVSGLANCLSTVLNVSHNNLVGDIK 540
QY 541 NNNSRSRSPDSFGNPGICGSMWNSPCHDSRTVRVISRRAIIGIIGIVILMLVLA 600
DB 541 NNNSRSRSPDSFGNPGICGSMWNSPCHDSRTVRVISRRAIIGIIGIVILMLVLA 600
QY 601 ACRPHNPPLFDGSLDKPVYTSPEKLYLHNNMALHYEDIMRMTENLSEKXIIGHGASS 660
DB 601 ACRPHNPPLFDGSLDKPVYTSPEKLYLHNNMALHYEDIMRMTENLSEKXIIGHGASS 660
QY 661 TVYKCVLKNCKPVAIKRLYSHNPQSMKOFETELMSSIKARNLVSIQANSLSHLGSLF 720
DB 661 TVYKCVLKNCKPVAIKRLYSHNPQSMKOFETELMSSIKARNLVSIQANSLSHLGSLF 720
QY 721 YDYENGLSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHHDSPRIIHRDVKSSNLL 780
DB 721 YDYENGLSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHHDSPRIIHRDVKSSNLL 780
QY 781 LDKDLRLRLTDGFIAGSLCVSKSHTSYVMGTIYIDPEVARTSRLTEKSDVVSYGIVLL 840
DB 781 LDKDLRLRLTDGFIAGSLCVSKSHTSYVMGTIYIDPEVARTSRLTEKSDVVSYGIVLL 840
QY 841 ELLTRRAVAVDESLHLHILMSKTGNNEVEMADPDITSTCKDLGVKKVFOALALCTKRQ 900
DB 841 ELLTRRAVAVDESLHLHILMSKTGNNEVEMADPDITSTCKDLGVKKVFOALALCTKRQ 900
QY 901 PNDRPETHQVTRVYSGFMLSROPAPATDTSATLAGSCVDEYANLKTPHSVNGSSMSASD 960
DB 901 PNDRPETHQVTRVYSGFMLSROPAPATDTSATLAGSCVDEYANLKTPHSVNGSSMSASD 960
QY 961 AOLFLRFGQVISONSE 976
DB 961 AOLFLRFGQVISONSE 976
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RESULT 2

ABB91884
ID ABB91884 standard; protein; 976 AA.

AC ABB91884;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 1095.

KW Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN W0200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP009892.

PR 28-AUG-2001; 2001WO-EP009892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidner M;

DR WPI; 2002-269010/31.

XX

PT Identifying plant target proteins for herbicidally active compounds,

PT comprising aligning and comparing nucleic acid or amino acid sequences

PT from plant with nucleic acid or amino acid sequences from non-plant

PT organisms.

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Sequence 976 AA;

Query Match 100.0%; Score 5043; DB 5; Length 976;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MALFRDVLVLLGFLFCLSLVATVTSEEGATLLEIKKSPFDVNNVLYDMTSSSSDYCWMRG 60
DB 1 MALFRDVLVLLGFLFCLSLVATVTSEEGATLLEIKKSPFDVNNVLYDMTSSSSDYCWMRG 60
QY VSCENVTFNNVALNLSDLNLDGEISPAIGDKLSLIDLRGNRLSGQIPDEIGCCSLON 120
DB 61 VSCENVTFNNVALNLSDLNLDGEISPAIGDKLSLIDLRGNRLSGQIPDEIGCCSLON 120
QY 121 LDISFNEISGDIPEISIKLQLEQILKNNQLIGPIBSTLSQIPNLKIIDLQNKLSGEI 180
DB 121 LDISFNEISGDIPEISIKLQLEQILKNNQLIGPIBSTLSQIPNLKIIDLQNKLSGEI 180
QY 181 PRLIYMEVQYIGLRGNLVGNISPDLCQLTGLWFDPVNNSLTGSIPETIGNCTAFQV 240
DB 181 PRLIYMEVQYIGLRGNLVGNISPDLCQLTGLWFDPVNNSLTGSIPETIGNCTAFQV 240
QY 241 LDISYNQLTGEIPEDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
DB 241 LDISYNQLTGEIPEDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
QY 301 PILGNLTFTEKLYLHSHNKLTSISIPPELGNNSKLHYLELNDNHLTGHIPEELGKLTDLFDL 360
DB 301 PILGNLTFTEKLYLHSHNKLTSISIPPELGNNSKLHYLELNDNHLTGHIPEELGKLTDLFDL 360
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Db 601 ACRPHNPPEFLDGLDKPVTYSTPKLVILHMNALHVEDIMMTEENLSEKYLIIHGASS 660
QY 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720
Db 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720
QY 721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHDCSPRIIHRDVKSNI 780
Db 721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHDCSPRIIHRDVKSNI 780
QY 781 LDKDLEARLTDGFIASLCSVSKSHSTYVNGTIGYIDPEYARTSRRLTEKSDVSYGIVL 840
Db 781 LDKDLEARLTDGFIASLCSVSKSHSTYVNGTIGYIDPEYARTSRRLTEKSDVSYGIVL 840
QY 841 ELITRRKAVDSENLHLIMSKTGNNVEMADPDITSTCKDGVYKVFQALALCTKRQ 900
Db 841 ELITRRKAVDSENLHLIMSKTGNNVEMADPDITSTCKDGVYKVFQALALCTKRQ 900
QY 901 PNDPRTMHQVTRVLGFMLESEOPPAATDTSATLAGSCYVDEYANLKTPHSVNCSMSASD 960
Db 901 PNDPRTMHQVTRVLGFMLESEOPPAATDTSATLAGSCYVDEYANLKTPHSVNCSMSASD 960
QY 961 AOLFLRFGQVISONSE 976
Db 961 AOLFLRFGQVISONSE 976
RESULT 4
AED28149 standard; protein; 976 AA.
ID AED28149;
AC AED28149;
XX
XX 01-DEC-2005 (first entry)
DT
XX Arabidopsis thaliana ERECTA protein.
XX DE
XX Arabidopsis thaliana ERECTA protein.
XX KM
XX Plant growth regulation; transgenic plant; crop improvement; ERECTA.
XX OS
XX Arabidopsis thaliana.
XX PN
XX US2005223428-A1.
XX PD
XX 06-OCT-2005.
XX PF
XX 30-DEC-2004; 2004US-00027304.
XX PR
XX 01-APR-2004; 2004US-0558529P.
XX PA
XX (TORI/) TORII K U.
XX PA
XX (SHPA/) SHPAK E D.
XX PI
XX Torii KU, Shpak ED;
XX
XX WPI; 2005-675788/69.
XX DR
XX N-PSDB; AED28148.
XX
XX Modulating plant height and organ shape comprises expressing, in plants,
PT a transgene encoding an ERECTA-like protein lacking an active kinase
PT domain.
XX
XX Claim 3; SEQ ID NO 2; 722p; English.
XX
XX The present invention relates to a method for modulating plant height and
CC organ shape. The method involves expressing a transgene in a plant, where
CC the transgene encodes an ERECTA-like protein lacking an active kinase
CC domain and where expression of the transgene modulates plant height or
CC organ shape. ERECTA protein contains leucine-rich repeat receptor-like
CC kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and
CC function as a receptor-kinase activity. The invention is useful for producing
CC transgenic plant and for enhancing the yield of a crop plant. The present
CC sequence is the Arabidopsis thaliana ERECTA protein.
XX

SQ Sequence 976 AA:
Query Match 100.0%; Score 5043; DB 9; Length 976;
Best Local Similarity 100.0%; Pred. No.0;
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALFRDIVLGFPLCSLVATVTSSEGAATLLEIKSKFKDVNNVLYDMTSSPSDDCYWVG 60
Db 1 MALFRDIVLGFPLCSLVATVTSSEGAATLLEIKSKFKDVNNVLYDMTSSPSDDCYWVG 60
QY 61 VSCENVTFNVALNLSLMDGEISPAIGDKSLSDLRGNLSGQIPREIDCSSLON 120
Db 61 VSCENVTFNVALNLSLMDGEISPAIGDKSLSDLRGNLSGQIPREIDCSSLON 120
QY 121 LDISFNEISGDIPEFSISKQLEQLILKNNQLGPIPTLSQIPNLKILDLAONKLSGEI 180
Db 121 LDISFNEISGDIPEFSISKQLEQLILKNNQLGPIPTLSQIPNLKILDLAONKLSGEI 180
QY 181 PRLIYNNEVLQYLGKGNLVGNISPDLCQTLGWYFDVRNNSLTGSIPEITGNCTAFQV 240
Db 181 PRLIYNNEVLQYLGKGNLVGNISPDLCQTLGWYFDVRNNSLTGSIPEITGNCTAFQV 240
QY 241 LDISYNQLTGEIPFDIGFLOVATLSLQGNOLSGKISVIGMQLAVLDLSGNLSGSIP 300
Db 241 LDISYNQLTGEIPFDIGFLOVATLSLQGNOLSGKISVIGMQLAVLDLSGNLSGSIP 300
QY 301 PILGNLTFTFKLYLHNSKLTGSIPEELGNMSKLYLELNDNHLTGHIPPELAGKLTDFDL 360
Db 301 PILGNLTFTFKLYLHNSKLTGSIPEELGNMSKLYLELNDNHLTGHIPPELAGKLTDFDL 360
QY 361 NVANNDLEGP1PDHLSCTNLNSLVNHNKFSCTIPRAFOKLESMTYLNLSNNIKGPI 420
Db 361 NVANNDLEGP1PDHLSCTNLNSLVNHNKFSCTIPRAFOKLESMTYLNLSNNIKGPI 420
QY 421 VELSRIGNDLTDLNNKINGIIPSSLDGDEHLKXNLNHNITGVVPGDFGLRBSIMEI 480
Db 421 VELSRIGNDLTDLNNKINGIIPSSLDGDEHLKXNLNHNITGVVPGDFGLRBSIMEI 480
QY 481 DLSNNDISGP1PEELNQLQNIILRLNENNLGTGNVSLANCLSTVLVNSHNNLVGDIPK 540
Db 481 DLSNNDISGP1PEELNQLQNIILRLNENNLGTGNVSLANCLSTVLVNSHNNLVGDIPK 540
QY 541 NNNFSRSPDSFTGNPGLCGSWLNSPCHDSRRTRVVISRAAILGIALIGLVILLMVLIA 600
Db 541 NNNFSRSPDSFTGNPGLCGSWLNSPCHDSRRTRVVISRAAILGIALIGLVILLMVLIA 600
QY 601 ACRPHNPPEFLDGLDKPVTYSTPKLVILHMNALHVEDIMMTEENLSEKYLIIHGASS 660
Db 601 ACRPHNPPEFLDGLDKPVTYSTPKLVILHMNALHVEDIMMTEENLSEKYLIIHGASS 660
QY 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720
Db 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720
QY 721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHDCSPRIIHRDVKSNI 780
Db 721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHDCSPRIIHRDVKSNI 780
QY 781 LDKDLEARLTDGFIASLCSVSKSHSTYVNGTIGYIDPEYARTSRRLTEKSDVSYGIVL 840
Db 781 LDKDLEARLTDGFIASLCSVSKSHSTYVNGTIGYIDPEYARTSRRLTEKSDVSYGIVL 840
QY 841 ELITRRKAVDSENLHLIMSKTGNNVEMADPDITSTCKDGVYKVFQALALCTKRQ 900
Db 841 ELITRRKAVDSENLHLIMSKTGNNVEMADPDITSTCKDGVYKVFQALALCTKRQ 900
QY 901 PNDPRTMHQVTRVLGFMLESEOPPAATDTSATLAGSCYVDEYANLKTPHSVNCSMSASD 960
Db 901 PNDPRTMHQVTRVLGFMLESEOPPAATDTSATLAGSCYVDEYANLKTPHSVNCSMSASD 960
QY 961 AOLFLRFGQVISONSE 976
Db 961 AOLFLRFGQVISONSE 976

Query Match	Best Local Similarity	Score	DB	Length
71.4%	82.0%	3602.5	8	838
		4.1e-272		

Matches	688: Conservative	66: Mismatches	76: Indels	9: Gaps	2,
Qy	145 LILKNNQILGPIPBTTLSQIPFNLIKILDLIAQNKLSGEIPRLIYMEVLYQLGRNNLVGNI	204			
Db	2 LILKNNQILGPIPBTTLSQIPDLKLIDLAQNLSGEIPRLIYMEVLYQLGRNNLVGSL	61			
Qy	205 SPDLCOITGLMYPDVRRNSLTGSIPEITNGCTAFQVLDLSYNOUTGSIPEPDIGLOYATL	264			
Db	62 SPDMCOITGLMYPDVRRNSLTGSIPEINIGCTAFQVLDLSYNOUTGSIPEINIGLOYATL	121			
Qy	265 SLQGNQLSGKIPSYIGMQALAVLDLSGNLSGSIPEILGNLFTFEKLYLHNSKLTGSIP	324			
Db	122 SLQGNKLSGSHIPPIYIGMQALAVLDLSGNLSGSIPEILGNLFTFEKLYLHNSKLTGSIP	181			
Qy	325 PELGNMSKLYLELINDNHLTGHIPEELGKLTDLFDLVANNNDLGGPIPDHLSCTTNLSL	384			
Db	182 PELGNMSKLYLELINDNHLTGHIPEELGKLTDLFDLVANNNDLGGPIPSNLSCKNLSL	241			
Qy	385 NVHGNKSSGIIIPRAFQLESMTYLNLSNNIKGIPPELSRIGNLDPLDLSNNKINGIIP	444			
Db	242 NVHGNKNGSGIIPPELQLESMTYLNLSNNIQGAIPELSRIGNLDPLDLSNNLVGSIIP	301			
Qy	445 SSLGDLLEHLKMNLSRNHITGVVSGDEGNLSIMEIDLNNNDISGPIPEELNQONITLL	504			
Db	302 SSLGDLLEHLKMNLSRNHITGIIPEAFGNLSRWEIDLNNQNSGLPDELSQLONMISL	361			
Qy	505 RLENNNLTVNGVSLIANCLSLTVLNVSHNLVGDIPKNNNFSRFSDFSIGNPGLCGSMNL	564			
Db	362 RLENNKLTGDAVASLNSCISLTLNVSNYKLFVGVIPTSNNFTRFPDPSFGDKVNFSP	421			
Qy	565 SPCHDSRRYRVSISRAIILGIALGSLVILLMLVLIACRPNNRPPPLDGLSDKRVYVSTP	624			
Db	422 LPCHGAPRSEKRVTLSKAIIIGITLGAIVILLMLVLIACRPSPSPFPDGSFDKVNFSP	481			
Qy	625 KLVTLHNNMALHYVEDIMRMTENLSKEYIIGHGASSYVYKCVLKNCKPVAIKRLYSHNPQ	684			
Db	482 KLVTLHNNMALHYVEDIMRMTENLSKEYIIGHGASSYVYKCVLKNCKPVAIKRLYSHNPQ	541			
Qy	685 SMKPFETELELSSIKRNLVSLQAVSLSHLGSLLFYDYLENGSLMDLHGPTKKKTLDW	744			
Db	542 CIKFEFELELEVGSIIKRNLVSLQGYSLSPGHLLFYDYMGNSLMDLHGPTKKKTLDW	601			
Qy	745 DTRUKIAYGAAGCIATYIHHDCSPITIRHDVYKSSNILLDKULEANLTPPGIAKSLCVSKSH	804			
Db	602 ELRLKIALGAAGCIATYIHHDCSPRIIRHDVYKSSNILLDAFEPLTDFGIAKSLCPSKSH	661			
Qy	805 TSTVMTGITGIDEBYARTSRLETESDVSYSYGIVLLELTPRKAVDDESNLHLIMSKTG	864			
Db	662 TSTVMTGITGIDEBYARTSRLETESDVSYSYGIVLLELTPRKAVDDESNLHLILSKAA	721			
Qy	865 NNEVEMADPDITSTCKDLGVVKKVFOALALCTKROPNDRPTMQVTRVLGSPMLSEOP	923			
Db	722 TNAVMEVTPDITATCKDLGAVKKVYQDLALLCTKROPADRPTMEVTRVLGSLVSNTP	781			
Qy	924 -----PAIDTSTYTLAGSCYVDEYANLKTTPHASNCGSMASMDQLFLRQGVYQNSQE	976			
Db	782 KQLAALPPASNPASAKV--PCYVDEYANLKTTPHVLNCPMSMSTSDQLFLRQGEVISQNSE	838			
RESULT 6					
AD132618					
ID AD132618 standard; protein; 921 AA.					
XX AD132618;					
XX AC					
DT 22-APR-2004 (first entry)					
DE Sorghum transpiration efficiency-related ERECTA protein.					
XX KW plant; transpiration efficiency; ERECTA; breeding; genetic engineering;					
OS Sorghum bicolor.					

XX MO200400555-A1.
XX 15-JAN-2004.
PF 02-JUL-2003; 2003WO-AU000854.
XX 02-JUL-2002; 2002AU-00003339.
XX (AUSU) UNIV AUSTRALIAN NAT.
PI Maale J, Farquhar GD, Gilmore SR;
DR WPI; 2004-091390/09.
DR N-PSDB; AD132617.
PT Selecting plant having enhanced transpiration efficiency, useful for
PT producing plants with enhanced transpiration efficiency comprising
PT selecting plant expressing a genetic marker linked to the ERECTA locus in
PT the genome of the plant.
XX
XX
PS Claim 4; SEQ ID NO 6; 209pp; English.
XX
CC The invention relates to a novel method for selecting a plant having
CC enhanced transpiration efficiency comprising detecting a genetic marker
CC for transpiration efficiency, where the marker comprises a nucleotide
CC sequence linked genetically to an ERECTA locus in the genome of the plant
CC and selecting a plant that comprises or expresses the genetic marker. The
CC method of the invention may be useful for selecting a plant having
CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic
CC variant or protein-encoding region may be useful in the preparation of a
CC genetic construct for modulating the transpiration efficiency of a plant.
CC Furthermore, the ERECTA genes may be useful for producing plants having
CC enhanced transpiration efficiency by both traditional plant breeding and
CC genetic engineering approaches. The current sequence is that of the
CC borghum ERECTA protein of the invention.
XX
XX
SQ Sequence 921 AA;
Query Match 66.9%; Score 3372.5; DB 8; Length 921;
Best Local Similarity 68.4%; Pred. No. 4.5e-254;
Matches 666; Conservative 96; Mismatches 141; Indels 71; Gaps 8;
QY 13 LFCLSLVAATVTSRGATLLLEIKSKFDVNNVLYDMTTPSSSDYCVWRGVCENVTFNVA 72
DB 9 LVALLLVAVAADVADGATLVEIKSKFRNVGNVLYDMA---GDDYCSWNGVLCNDVTFAVAA 65
QY 73 LNISSLNLWDGEISPAIGDLKSLSIDLRGNRSLQIPDEIGDCSSLONLDSFNELSGDI 132
DB 66 LNISSLNLWDGEISPAIGDLKSLSIDLRGNRSLQIPDEIGDCSSLRTLPFSFNLLDGI 125
QY 133 PFSISKULKOLEQLLVKNNOLIGPISPTLSQIPNLIKILDLAONKLSGEIPRIYNEVLOY 192
DB 126 PFSISKULKLENLVLKNNOLIGALPSTLSQIPNLIKILDLAONKLSGEIPRIYNEVLOY 185
QY 193 LGLRGNNLVGNISPDQLTGLMYFDVNRNNSLTGSIPEITGNCTAFQVLDLSYNQLTGEI 252
DB 186 L-----DVKNNSLTGVIPDTIGNCTSFYLDLSYVRPFPI 221
QY 253 PFIDIGLQVATLSIQGNOLSGKIPSVIGLMQALAVLDLSGNLSGSIPIPIGNTTFBEKL 312
DB 222 PFNIGFLQVATLSIQGNKFTGPIPSVIGLMQALAVLDLSYNQLSGSIPIISGNTYTEKL 281
QY 313 YLSNKKLTGSPPELGMKSKLHYELNDNHLTGHIPPELIGKLTLPDLNVANNDLBGP 372
DB 282 YIQGNKLTGSPPELGMKSKLHYELNDNHLTGHIPPELIGKLTLPDLNVANNDLBGP 341
QY 373 DHSSTCTNLNLNHNKNGKFSGTIPRAFQKLESMYTLNLSNNIKGPIPVELSRIGNDTL 432
DB 342 DNLSSTCTNLNLNHNKNGKFSGTIPRAFQKLESMYTLNLSNNIKGPIPVELSRIGNDTL 401
QY 433 DLSNNKTINGIIPSSGLGLEHLKNNLSRNHITGVVPGDFGNLRIMEIDLSNNDISGP 492
DB 401 DLSNNKTINGIIPSSGLGLEHLKNNLSRNHITGVVPGDFGNLRIMEIDLSNNDISGP 492

DB 402 DLSNNMTGPIPPSSIGSLLEHLRLNLKNGLVGFIPAEFGNLSVMEIDLSYNHGLG 461
QY 493 BELNLQNIILRLRENNNLIGNVGSLANCLSTLVYANSHNNLVGDIKONNFSRFPDSF 552
DB 462 QELMLQNLML-----LNSYNNLGVVADNNFTFRSPDSF 498
QY 553 IGNPGLGSMNLNSPCHDSRRTRVVISRAAILGAIIGLVILMLVLIACRPHNPPFLD 612
DB 499 LGNPGGLGSMNLNSPCHDSRRTRVVISRAAILGAIIGLVILMLVLIACRPHNPPFLD 558
QY 613 GSLDKPYTSTPKVLIIHNNMALHYEDIMRMBENLSEKTIIGHGASTYKYKLNCKP 672
DB 559 VTWSKPYRNAAPPKVLIIHNNMALHYEDIMRMBENLSEKTIIGHGASTYKYKLNCKP 618
QY 673 VAIKRLYSHNPQSKOPETELEMLSIKHRLNLSLQAVSYSHLSGLSFLFYDLENGLMDL 732
DB 619 VAIKRLYSHNPQSKOPETELEMLSIKHRLNLSLQAVSYSHLSGLSFLFYDLENGLMDL 678
QY 733 LH-GPTKKTLMDWTRLKIAVGAAGLAVLHDCSPRIIHRDYKSNILLDKLEARLTD 791
DB 679 LHEGSSKKKKLDWETRLRIALGAAQGLAVLHDCSPRIIHRDYKSNILLDKLEARLTD 738
QY 792 FGLAKSLCVSKSHSTYVMGTIGYIDPEYARTSRITEKSVY-----SYGIVLLELTR 846
DB 739 FGLAKSLCVSKSHSTYVMGTIGYIDPEYARTSRITEKSVY-----SYGIVLLELTR 788
QY 847 KAVDDESNLHLNLSKTNENMEMADPDITSTCKDLGVVKKYFQALACTKROPNDRPT 906
DB 789 -ADWQASQSRILSKTASNEVDYDPDIDGTCKDLGSKVKKLPQALDLCTKROPNDRPT 847
QY 907 MHQVTRVLGSMLESEDP--AAITDSATLAGCYDEVANLKTPIHSVNC-SSMSASDAQ 962
DB 848 MHEVVRVLDCLVNPDPPEPKSAHQLPQSPAVPSYINEYVLSGTGALSCANSTSTSDAE 907
QY 963 LFLRFQGVISONSE 976
DB 908 LFLRFQGVISONSE 921
RESULT 7
ADJ49448
ID ADJ49448 standard; protein; 921 AA.
XX
XX ADJ49448;
AC
XX
DT 06-MAY-2004 (first entry)
XX
DB Oil-associated gene related protein #948.
XX
KM oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS unidentified.
XX
XX US2004025202-A1.
PN
XX
PD 05-FEB-2004.
PF
XX
PF 14-MAR-2003; 2003US-00389566.
XX
XX 15-MAR-2002; 2002US-0365301P.
PR 26-JUN-2002; 2002US-0391786P.
PR 26-JUN-2002; 2002US-0392018P.
XX
XX (LAUR/) LAURIE C. C.
PA (SAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J. R.
PA (ROGE/) ROGERS J. A.
PI
XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
DR

QY 1 MALFRDIIVLGFLFCLSLVATVTSEEGATLLEIKKSPKDVNNVLYDWTSSPSDYCWMG 60
DB 1 MALFRDIIVLGFLFCLSLVATVTSEEGATLLEIKKSPKDVNNVLYDWTSSPSDYCWMG 60
QY 61 VSCENVTNNVALNSDLNLDGEISPAIGDKSLSLDRLGNRLSGQIPPEIGDCSLON 120
DB 61 VSCENVTNNVALNSDLNLDGEISPAIGDKSLSLDRLGNRLSGQIPPEIGDCSLON 120
QY 121 LDISPNEISGDIPEPSISKLQLEOLILKNNOLIGPISSTISQIPNLTILLAONKLSGEI 180
DB 121 LDISPNEISGDIPEPSISKLQLEOLILKNNOLIGPISSTISQIPNLTILLAONKLSGEI 180
QY 181 PRLIYNEVQYIGLRGNLVGNISPDLCQTLGMYFDVNNSLTGSIPETIGCTAFQV 240
DB 181 PRLIYNEVQYIGLRGNLVGNISPDLCQTLGMYFDVNNSLTGSIPETIGCTAFQV 240
QY 241 LDISYNQLTGEIPPDIGFLOVATLSLOGNOLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
DB 241 LDISYNQLTGEIPPDIGFLOVATLSLOGNOLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
QY 301 PILGNLTFTFKLYHNSKLTGSIPEELGNMSKLTLYELNHNHLTGHTPEELGKLTDLFDL 360
DB 301 PILGNLTFTFKLYHNSKLTGSIPEELGNMSKLTLYELNHNHLTGHTPEELGKLTDLFDL 360
QY 361 NVANNDEGPIPHLSSTCTNLNSLVHGNKPSGTTIPPAFQKLEBSMTYLNLSNNIKGP 420
DB 361 NVANNDEGPIPHLSSTCTNLNSLVHGNKPSGTTIPPAFQKLEBSMTYLNLSNNIKGP 420
QY 421 VELSRIGNLDTLDSNNKINGIIPSSIGDLFHLKMLSRNHITGVPGPFGNLRSMET 480
DB 421 VELSRIGNLDTLDSNNKINGIIPSSIGDLFHLKMLSRNHITGVPGPFGNLRSMET 480
QY 481 DLSNNDISGPIPEELNOLONIILRLENNLTGVNGLANCLSTVTYVNSHNNLVGDI 540
DB 481 DLSNNDISGPIPEELNOLONIILRLENNLTGVNGLANCLSTVTYVNSHNNLVGDI 540
QY 541 NNNFSRSPDSFICGNPGLCGSWLNSPCHDSRRIVRSISRRAIIGIAGIIVILLMVLA 600
DB 541 NNNFSRSPDSFICGNPGLCGSWLNSPCHDSRRIVRSISRRAIIGIAGIIVILLMVLA 600
QY 601 ACRPHNPPLDGS 614
DB 601 ACRPHNPPLDGS 614

RESULT 9
AD132616 standard; protein; 999 AA.
AC AD132616;
XX
DT 22-APR-2004 (first entry)
DE Rice transpiration efficiency-related ERECTA protein.
XX
XX plant; transpiration efficiency; ERECTA; breeding; genetic engineering;
KM rice; chromosome 6.
XX
OS Oryza sativa.
XX
PN WO2004005555-A1.
PD 15-JAN-2004.
PF 02-JUL-2003; 2003WO-AU000854.
PR 02-JUL-2002; 2002AU-00003339.
PA (AUSU) UNIV AUSTRALIAN NAT.
PI Masle J, Farguhat GD, Gilmore SR;
XX
XX

DR WPI; 2004-091390/09.
DR N-PSDB; AD132615.
XX
PT Selecting plant having enhanced transpiration efficiency, useful for
PT selecting plant with enhanced transpiration efficiency comprising
PT selecting plant expressing a genetic marker linked to the ERECTA locus in
PT the genome of the plant.
XX
PS Claim 4; SEQ ID NO 4; 209pp; English.
XX
CC The invention relates to a novel method for selecting a plant having
CC enhanced transpiration efficiency comprising detecting a genetic marker
CC for transpiration efficiency, where the marker comprises a nucleotide
CC sequence linked genetically to an ERECTA locus in the genome of the plant
CC and selecting a plant that comprises or expresses the genetic marker. The
CC method of the invention may be useful for selecting a plant having
CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic
CC variant or protein-encoding region may be useful in the preparation of a
CC genetic construct for modulating the transpiration efficiency of a plant.
CC Furthermore, the ERECTA genes may be useful for producing plants having
CC enhanced transpiration efficiency by both traditional plant breeding and
CC genetic engineering approaches. The current sequence is that of the rice
CC ERECTA protein of the invention which is encoded by DNA located on
CC chromosome 6.
XX
SQ Sequence 999 AA;
XX
Query Match 61.7%; Score 313; DB 8; Length 999;
Best Local Similarity 63.1%; Pred. No. 9, 9e-234;
Matches 618; Conservative 135; Mismatches 182; Indels 44; Gaps 9;
QY 26 EGATLLEIKKSPKDVNNVLYDWTSSPSDYCWMGVCENVTNNVALNSDLNLDGEIS 85
DB 35 EGKALMGVXKAGFGANANALVDM--DGADHCAHRCVGTCDNASFAVALNLSNLTGGEIS 92
QY 86 PAIGDKSLSLDRLGNRLSGQIPPEIGDCSLONLDSFNEISGIPPSISKLQLEOL 145
DB 93 PAIGELKNLQFVLDKSNKLTGQIPDEIGDCISLKYVLDLGNLTYGQIPESISKLQLEOL 152
QY 146 ILKNNOLIGPISPTLSQIPNLKLTDLAONKLSGEIPRLIYNEVQYIGLRGNLVGNIS 205
DB 153 ILKNNOLIGPISPTLSQIPNLKLTDLAONKLTDLIRLIYNEVQYIGLRGNLSTGTL 212
QY 206 PDLCOLTGLMYFDVNNSLTGSIPETIGCTAFQVLDLSYNQLTGEIPPDIGFLOVATLS 265
DB 213 PDMCQLTGLMYFDVNNSLTGSIPETIGCTAFQVLDLSYNQLTGEIPPDIGFLOVATLS 272
QY 266 LOGNOLSGKIPSVIGLMQALAVLDLSGNLSSGIPILGNLTFTFKLYHNSKLTGSI 325
DB 273 LOGNRLTGKIPDIVIGLMQALAVLDLSGNLSSGIPILGNLTFTFKLYHNSKLTGSI 332
QY 326 ELGNMSKLTLYELNHNHLTGHTPEELGKLTDLFDLVANNDEGPIPHLSSTCTNLNSLN 385
DB 333 ELGNMSKLTLYELNHNHLTGHTPEELGKLTDLFDLVANNDEGPIPHLSSTCTNLNSLN 392
QY 386 VHGKPSGTTIPPAFQKLEBSMTYLNLSNNIKGPIPEELSRIGNLDTLDSNNKINGIIPS 445
DB 393 VHGKPSGTTIPPAFQKLEBSMTYLNLSNNIKGPIPEELSRIGNLDTLDSNNKINGIIPS 452
QY 446 SLGDLFHLKMLSRNHITGVNGLANCLSTVTYVNSHNNLVGDI 540
DB 453 SLGDLFHLKMLSRNHITGVNGLANCLSTVTYVNSHNNLVGDI 540
QY 541 LNNNNLTGNY-GSLANCLSTVTYVNSHNNLVGDI 550
DB 513 LNNNNLTGNY-GSLANCLSTVTYVNSHNNLVGDI 550
QY 551 -----SFIGNPGLCGSWLNSPCHDSRRIVRSISRRAIIGIAGIIVILLMVLA 598
DB 566 ISDCNQYINHKCSFLGNPLTHVYCODSCSHSGQ-RVNSKTAIACIIIGFIILCVLL 624
QY 599 IACRPHNPPLDGSIDKPVYSTFKLVILHNNMALHYVEDIMRTENISEKYYIIGGHA 658

Db	625	LAITYNDQPIVLKXS-DKPV-QGPEKLVVQLQMDAIIHTEYDLMRLTENISEKTIIGYCA	662
Qy	659	SSTVYKCVLKNCKPVAIKRLYSHNPQSMKOFETELEMLSIKRNLVSLQAVSLHLSGL	718
Db	663	SSTVYKCELSKSKRALAVKRLYSGYNHSLABEFETELTISIRHRNLVSLHGFSLSPGNL	742
Qy	719	LFYDYLENGSLMDLHGPTKKKTLMDWTFUKIAYGAAQGLAYVHHDCSPRIHRDYKSN	778
Db	743	LFYDYMENGSLMDLHGPEKKVYLMNDTRLRIAVGAAQGLAYVHHDCNPRIIHRDYKSN	802
Qy	779	ILLDNDLRLTLDFGLAKSLCVSKSHSTVYVWGTIGYIDPEVARTSLREKSNVSYGVY	838
Db	803	ILLDNFEPAHLSDFGLAKCVSPAKSHASTYVIGTIGYIDPEVARTSLREKSNVSYSGIV	862
Qy	839	LLELLTRRKAADVDESNLHMLIMSKGTNNNEMEAADPIDSTCDLGVVKKFPDALLCTK	898
Db	863	LLELLTGKKAVDNESNLHOLLISKADNNTVMEAVDESVYTCGDMGLVRRAPFDALLCTK	922
Qy	899	ROPNDRLPMHOVTRVLGSEFMISE--OPPATDTSATLACSCYVDEVANLTKPHSVNCSSM	956
Db	923	RHPSDRPTMHEVARVYLLSLPASAMTTPKVIVDSRLASTTTA--ADMKGHDVTIGDN	979
Qy	957	SASDAQFLRRGQVTSQNS 975	
Db	980	SSSDQWFRFGEVYSIKHT 998	

RESULT 10
ABB93915

ID ABB93915 standard; protein; 966 AA.

AC ABB93915;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 3126.

KW Herbicidal; plant; agriculture; herbicide.

OS *Arabidopsis thaliana*.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP009892.

PR 28-AUG-2001; 2001WO-EP009892.
XX

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

DR WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.

PS Claim 5; SEQ ID NO 3126; 261pp + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016)

CC amino acid sequences from non-plant organisms using suitable

CC parameters, where

CC The polypeptides

herbicides

XX Sequence 966 AA.

Query Match	61.3%;	Score 3091.5;	DB 5;	Length 966;
Best Local Similarity	62.9%;	Pred. No. 4.5e-232;		
Matches 610;	Conservative 139;	Mismatches 204;	Indels 17;	Gaps 6

[illegible]

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RESULT 11
AD132622
ID AD132622 standard; protein; 966 AA.
XX
AC AD132622;
XX
DT 22-APR-2004 (first entry)
XX
DE Thale cress ERECTA homologue protein - SEQ ID 10.
XX
KW plant; transpiration efficiency; ERECTA; breeding; genetic engineering;
XX thale cress.
XX
OS Arabidopsis thaliana.
XX
PN W02004005555-A1.
XX
PD 15-JAN-2004.
XX
PF 02-JUL-2003; 2003W0-AU000854.
XX
PR 02-JUL-2002; 2002AU-00003339.
XX
PA (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI Masle J, Farguhar GD, Gilmore SR;
XX
DR WPI, 2004-091390/09.
XX
DR N-PSDB; AD132621.
XX
PT Selecting plant having enhanced transpiration efficiency, useful for
XX producing plants with enhanced transcription efficiency comprising
XX selecting plant expressing a genetic marker linked to the ERECTA locus in
XX the genome of the plant.
XX
PS Claim 4; SEQ ID NO 10; 209pp; English.
XX
CC The invention relates to a novel method for selecting a plant having
XX enhanced transpiration efficiency comprising detecting a genetic marker
XX for transpiration efficiency, where the marker comprises a nucleotide
XX sequence linked genetically to an ERECTA locus in the genome of the plant
XX and selecting a plant that comprises or expresses the genetic marker. The
XX method of the invention may be useful for selecting a plant having
XX enhanced transpiration efficiency. The isolated ERECTA gene or allelic
XX variant or protein-encoding region may be useful in the preparation of a
XX genetic construct for modulating the transpiration efficiency of a plant.
XX Furthermore, the ERECTA genes may be useful for producing plants having
XX enhanced transcription efficiency by both traditional plant breeding and
XX genetic engineering approaches. The current sequence is that of the thale
XX cress ERECTA homologue protein of the invention.
XX
SQ Sequence 966 AA.

Query Match 61.3%; Score 3091.5; DB 8; Length 966;
Best Local Similarity 62.9%; Pred. No. 4.5e-232;
Matches 610; Conservative 139; Mismatches 204; Indels 17; Gaps 6;

QY 7 IVLLGFLFCLSLVATYSEGGATLLEIKSFKOVNNLVYMTSPSSDVCVMGVSCENV 66
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
12 LAWVGFM--VFGVASANNNEGKALMAIKGSFSLVNNLMDWDVHNSDLCSMGVFCDNV 69
QY 67 TFWVVALNLSLDLNDGEISPAIGDLKSLISIDLRGNRLSGOIPDEIGDCSSLOWLDSFN 126
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
70 SYVSVSLNLSLNDGEISPAIGDLKSLISIDLRGNRLSGOIPDEIGDCSSLOWLDSFN 129
QY 127 ELSGDIPFSISKUKQLEQLILKNNQLIGPISTLSQIPNPKLIDLAKNKLSGEIPRLIYW 186
DB 130 LLYGDIPFSISKUKQLEQLILKNNQLIGPISTLSQIPNPKLIDLAKNKLSGEIPRLIYW 189
QY 187 NEVLOYLGLGRGNLVGNISPDLCQLTGLMFPDVARNNSLTSIPTETNCATFQVLDLSYN 246
DB 190 NEVLOYLGLGRGNLVGNISPDLCQLTGLMFPDVARNNSLTSIPTETNCATFQVLDLSYN 249
```

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QY 247 QLTGEIPFDIGFQVATLTLSDGNQLSGKIPSVIGLQALAVLDLSGNLSSGIPILGNL 306
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
250 QITGEIPYNGFQVATLTLSDGNRLTGRIPVEYGLMALAVLDLSGNLSSGIPILGNL 309
QY 307 TFEKLYLHNSKLTGSIPEELGNMSKILYELNDNLTGHIPEELGLTDLPLVANND 366
DB 310 SFTGKLYLHGNMLTGPPIPESELGNMSRSLYQLNDNKLVTGPIPEELGLTDLPLVANNR 369
QY 367 LGGPIPDHSSCCNLSLNVHGNKPSGTIPRAFOKESMYLNLSSNNIIGPIPVLESRI 426
DB 370 LVGPPIPSNLSSCALNQFNVHGNLSGSIPLAFRNLGSITLYLNLSSNFKGKIPVELGHI 429
QY 427 GNDTDLNNSKINGIIPSSLADLEHLKKNLSRNHITGVVPGDFGNLRSIMEIDLSND 486
DB 430 INDKDLSGNMNSGSIPLTGLDLEHLILNLSRNHLSQGLPAEFGRLRSTQIMDIVSFNL 489
QY 487 ISGPPIBELNQLNIIILRIENNLTGVN-GLSLANCLSTVLNVSHNNLVGDIPIKNNNS 545
DB 490 LSGVIPLELQQLNLSLILNNKLTGKIPDQLTNGFTLVNLVSNFNNLSGIVPMKNFS 549
QY 546 RPSPDFRIGNPGICGSLNPSCHDSRRTVVSISRRAIIGIAGLVILMLVLIACRPH 605
DB 550 RFAPASVGNPVYLCGMVSGISGFLPKS-RV-FRGLALITVGVITLTCMIFLAVYKSM 607
QY 606 NPPFLDGLSDKPEVTYSTPKLVILHNMALHYEDIMRMTENLSEKXIIGHGASSTVYKC 665
DB 608 QOKKILQSSKKQ--AGSLTKLVILHMDMAHTDDIMRVTENLNEKFIIOGASSTVYKC 665
QY 666 VLKCKEPAVIAIKRLYSHNPOGMOFETELMSSIKRNLVSLQAYSLSHLGSLFFDYLE 725
DB 666 ALKSSPPIAKRLYNOYPNHLREFELETIGIRHRNIVSLGVALSPGNNLPFYDME 725
QY 726 NSGLMDLHGTCKKTLMDOTRLKIVGAAGLAVLHDCSPRIHRDVSSNIILDKDL 785
DB 726 NSGLMDLHGTCKKTLMDOTRLKIVGAAGLAVLHDCSPRIHRDVSSNIILDKDL 785
QY 786 EARLTDFIGIAKSLCVSKSHTSSTVYMGITGYIDPEYARTSRLETKSDVSYGIVLELTR 845
DB 786 EARLSDFIGIAKSLPAKSTHASTYVLGTGYIDPEYARTSRINXKSDIYSGIVLELTR 845
QY 846 RKAVDESNLHILIMSKTGNNEMEMADPITSTCDLGVYKVFQALALCTKROPDRP 905
DB 846 KKAVIDEAMHQLILSKADONTMEAVDPEVYTCMDLGHIRTFQALALCTKRNPLER 905
QY 906 TMOQTVRLGSFMLSPPAATDTSATLASCYVDEVANLKTSHSVNCSMSASDAQFL 965
DB 906 TMLSVSRVLSTLVPSTQ-----VAKLPSLDHSTKGLQENBVRNPDAEAGWFV 955
QY 966 RFQOVISONS 975
DB 956 QFREVISKSS 965

RESULT 12
AED28155
ID AED28155 standard; protein; 967 AA.
XX
AC AED28155;
XX
DT 01-DEC-2005 (first entry)
XX
DE Arabidopsis thaliana ERECTA paralog, ERL2 protein.
XX
KW plant growth regulation; transgenic plant; crop improvement; ERL2.
XX
OS Arabidopsis thaliana.
XX
PN US2005223428-A1.
XX
PD 06-OCT-2005.
XX
PF 30-DEC-2004; 2004US-00027304.
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XX 01-APR-2004; 2004US-0558529P.
XX (TORI/) TORII K U.
XX (SHPA/) SHPAK E D.
XX Torii KU, Shpak ED;
XX MPI: 2005-675788/69.
XX N-PSDB; AED28154.
PT Modulating plant height and organ shape comprises expressing, in plants,
PT a transgene encoding an ERECTA-like protein lacking an active kinase
PT domain.
XX
XX Claim 7; SEQ ID NO 8; 72pp; English.
XX
XX The present invention relates to a method for modulating plant height and
XX organ shape. The method involves expressing a transgene in a plant, where
XX the transgene encodes an ERECTA-like protein lacking an active kinase
XX domain and where expression of the transgene modulates plant height or
XX organ shape. ERECTA protein contains leucine-rich repeat receptor-like
XX kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and
XX functional Ser/Thr kinase activity. The invention is useful for producing
XX transgenic plant and for enhancing the yield of a crop plant. The present
XX sequence is the Arabidopsis thaliana ERECTA paralog, ERL2 protein.
XX
XX Sequence 967 AA;

Query Match 61.3%; Score 3089.5; DB 9; Length 967;
Best Local Similarity 62.2%; Pred. No. 6.4e-232;
Matches 605; Conservative 134; Mismatches 211; Indels 23; Gaps 6;

QY 11 GFLFCLSLV-----ATVTSEGATLLEIKSFKQVNNVLYDWTSPSSDYCVMRGVSC 63
DB 9 GFLFCLGAVVFMVLGSGVSPNNEGKALMAIKASFVNAVMMLDWDVHNHDFCWSRGVFC 68
QY 64 ENVTFFVNAVLTSDMLDGEISPAIDLSIDLRGRNRLSGIDSGIDSGISLQNLQD 123
DB 69 DNVSLVNAVLSNLSNLGGEISALDGLMNLQSIDLQNGQIDPEIDGNCVSLVYVD 128
QY 124 SFNELSGDIPFSISKLEQLILKNNQILGPISTLSQIPNLKIIDLAQNKLSGEIPRL 183
DB 129 STNLLFGDIPFSISKLEQLILKNNQILGPISTLSQIPNLKIIDLAQNKLSGEIPRL 188
QY 184 IYWNVEVLYLGRGNLVGNISPDLCQLTGLWTFDVRNNSLTGSIPTGICNCFQVYDL 243
DB 189 LYWNVEVLYLGRGNLVGNISPDLCQLTGLWTFDVRNNSLTGSIPTGICNCFQVYDL 248
QY 244 SYNQLGELIPDIFGLFOVATLSLQGNOLSGKIPSVIGLMOALAVLDSGLSGSIPRL 303
DB 249 STNQLTGVIPIYNGIQAVALTSLQGNKLTGRIPEVIGLMOALAVLDSGLSGSIPRL 308
QY 304 GNLTFTEKLYLSNKLGTGSIPELGNMSKLYLELDNHLTGHIPELGLTDLFPLANVA 363
DB 309 GNLSTFGKLYLHONKLTGQIPPELGNMSRLSYQLNDNELVGKITPELGLTDLFPLANVA 368
QY 364 NNDLGGPIPDHLSCTNLNSLVNHNKFSCTIPRAFQKESMTYLLNSNNIKGPIPEL 423
DB 369 NNNVLGLIPSNISSCAALNQFNHGNFLSGAVLEFRNLGSLTYLLNLSNSFGKIPAE 428
QY 424 SRIGNLDTLDSNNKINGIIPSSLDGLEHLKNNLSRNHITGVVPGDFGLRIMEIDLS 483
DB 429 GHINLDTLDSNNKINGIIPSSLDGLEHLKNNLSRNHITGVVPGDFGLRIMEIDLS 488
QY 484 NNDISGPIPEELNQLNIIILRLNNNLGTNV-GLSANCSTLVAVVSHNNLGVGDIPIKN 542
DB 489 FNLFLAVITPELQGLQNLINSLINNKKIKHCKIPDLQNLGCSLANLINSFNLSGIIIPMK 548
QY 543 NTSRSPDSFTIGNPGLCGWSLNSPCHDSRTTAVYSIRPAIIGLIGVILMLVLAAC 602
DB 549 NTSRSPDSFTIGNPGLCGWSLNSPCHDSRTTAVYSIRPAIIGLIGVILMLVLAAC 607

QY 603 RPHNPPFLDGSIDKPEVTYSTPLVILHNMALHVEDINRMTENISEKYLIGHGASSTV 662
DB 608 KSKQOKPVLKSGSKQP--EGSTGLVILHMDMAHTDIDIRVTENIDEXKIITGYSSTV 665
QY 663 YKCVLNCKRPAVKIRLYSHNPOSMMKOFETELEMSSIKRNLVSLQAYSLSHLGLLFPY 722
DB 666 YKCTSKSRPIAIKRIYNGYPSNFRFELETELETIGIRRNIVSLIGVALSPFGNLLFPY 725
QY 723 YLENGSLMDLHPPTKKKTLDMPTRLKIAVGAQAQGLAYLHHDCPRIIHRDVSSNILLD 782
DB 726 YMENGSIMDLHPGPKVKVLDWETRLKIAVGAQAQGLAYLHHDCPRIIHRDISSNILLD 785
QY 783 KDLERLTDFGLAKSICVSKSHTSTYMGITGYIDPEYARTSLTKSPDYSGIYLLBL 842
DB 786 GNFEARLSDFGIAKSLPATKTYASTYVLGTIGYIDPEYARTSLTKSNDYSGIYLLBL 845
QY 843 LTRKKAVDDESNIHLIMSKTGNEVEMADPDITSTCKDLGVKKVFPOLALICTRQPN 902
DB 846 LTRKKAVDNEANLHQMITLSKADNTVMEAVDAEVSVTCDMSGHKKTFQALALICTRQPN 905
QY 903 DRPTMQVTRVLSGFMLSQPPATDTSATLGSVCVDEYANKTSHSVNCSMSASDAQ 962
DB 906 ERPTMQEVSRRVLLSLVSPDP-----KKLPSPARVOGGEERRESHSDTTF-----PQ 953
QY 963 LFLRFGOVISONS 975
DB 954 WFOQFREDISKSS 966

RESULT 13
AED28153
ID AED28153 standard; protein; 966 AA.

XX AED28153;
XX
XX 01-DEC-2005 (first entry)
XX
XX Arabidopsis thaliana ERECTA paralog, ERL1 protein.
XX
XX Plant growth regulation; transgenic plant; crop improvement; ERL1.
XX
XX Arabidopsis thaliana.
XX
XX US2005223428-A1.
XX
XX 06-OCT-2005.
XX
XX 30-DEC-2004; 2004US-00027304.
XX
XX 01-APR-2004; 2004US-0558529P.
XX
XX (TORI/) TORII K U.
XX (SHPA/) SHPAK E D.
XX Torii KU, Shpak ED;
XX MPI: 2005-675788/69.
XX N-PSDB; AED28152.
PT Modulating plant height and organ shape comprises expressing, in plants,
PT a transgene encoding an ERECTA-like protein lacking an active kinase
PT domain.
XX
XX Claim 5; SEQ ID NO 6; 72pp; English.
XX
XX The present invention relates to a method for modulating plant height and
XX organ shape. The method involves expressing a transgene in a plant, where
XX the transgene encodes an ERECTA-like protein lacking an active kinase
XX domain and where expression of the transgene modulates plant height or
XX organ shape. ERECTA protein contains leucine-rich repeat receptor-like
XX kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and
XX functional Ser/Thr kinase activity. The invention is useful for producing
XX transgenic plant and for enhancing the yield of a crop plant. The present


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Db 241 LTGRIPFVIGLMOALAVLDLSDBNELTGPPIPIIGNLSTFGKLYHGKLTGQIPPELGNM 300
QY 331 SKLHYELNDNHLTGHIPEPELGLTDLFDLVANNDEGPDPHLSSTCTNLNSLVHGNK 390
Db 301 SRLSYLQNDNELVGKIPPELGLTEQLFELTANNLVLGIPSNISSCALNQPNVHGNF 360
QY 391 FSGTIPRAFOKLSMTYLNLSNNIKGPIPELSEIRIGNLDTLDLSNNKINGIIPSSIGDL 450
Db 361 LSGAVPLEFRNLGSLTYLNLSNSFKGKIPALGHIINLDTLDLSGNNFSGSIPLTIGDL 420
QY 451 EHLTKNLSRNHITGVVPGDFGNLSIMEIDLSNNDISGPIPELNLQNTIILRLNENN 510
Db 421 EHLILNLSRNHNLGTLPALFEGNLSRIQIIDVSFNFAGVIPTELGOQINLSILNNNK 480
QY 511 LTGNV-GSLANCLSLTVLVNSHNNLVGDI PKNNNSFRSPDSFGNGLGSMWNSPCHD 569
Db 481 IHKIDQLTNCFSLANLNISFNLSGIIIPMKNFTRFSPASFNGPFLCGMWVGSICGP 540
QY 570 SRRTVVSISSRAIIGIAGLVILLMVLIAACRPHPNPPELDGSLDKPVTSTPKLVIL 629
Db 541 SLPKSGV-FTRVAVICWVLGFIITLCMIFIAVYKSKQKQKVLKSSKQF--EGSTKLVL 597
QY 630 HNMALHYEDIMRMENISEKTIIGHGASTYKYCVLKKCKVAIKRLYSHNPQSKQF 669
Db 598 HMDMAHTDIDIRVTENLDEKYLIGGASTYKCTSKTSRDIKRIYNOYPSNFERF 657
QY 690 ETELEMLSSIKHRLNLSLQAYSLSHLSGLLFYDYLENGSLMDLHGPTKKTLDMPTRLK 749
Db 658 ETELELTGSIIRHNIYSLHGYSALSPFGNLLFYDMENGSLMDLHGPKKVKLDMETRLK 717
QY 750 IAVGAAGLAVLHHDSPRIIHRDVKSNILDLKDEARLTDEGIAKSLCVSKSHSTYV 809
Db 718 IAVGAAGLAVLHHDCTPRIIHRDKSNILDLGNFEARLSDGIAKSIPTATYASTYV 777
QY 810 MGTIGYIDEVARTSLTEKSDYVSGIYVLELTTRKAVDSDSNLHLLMSTGNNEVA 869
Db 778 LGTIGYIDEVARTSLNEKSDIYSGIYVLELTTRKAVDNEANLHOMLSYADNDNTVA 837
QY 870 ENADPITSTCKDLGVVKKVFOALCTCRQPNDRPTMHQVTRVLGSPMLSEOPRATPT 929
Db 838 EAVDAEVSTCMDSGHIKKTFOALALCTKRNPIERTMOEVSRLVLSLVPSPPP----- 891
QY 930 SATLAGSCYVDEVANLCTPHSVNCSMSASDAQLFARFGQVISQNS 975
Db 892 -KTLSPAKVQGEGERRESHSDTT-----PQWVFQFREDISKSS 931

RESULT 15
AD132620
ID AD132620 standard; protein, 932 AA.
XX
AC AD132620;
XX
DT 22-APR-2004 (first entry)
XX
DE Thale cress ERECTA homologue protein - SEQ ID 8.
XX
KM plant; transpiration efficiency; ERECTA; breeding; genetic engineering;
XX thale cress.
XX
OS Arabidopsis thaliana.
XX
OS
XX
XX Key Location/Qualifiers
XX PH Misc-difference 112..129
XX FT /note="Encoded by CTGACC"
XX
XX WO2004005555-A1.
XX
XX 15-JAN-2004.
XX
XX 02-JUL-2003; 2003WO-AU000854.
XX
XX 02-JUL-2002; 2002AU-00003339.
XX

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XX (AUSU ) UNIV AUSTRALIAN NAT.
PA
XX Masle J, Farguhar GD, Gilmore SR;
PI
XX WPI; 2004-091390/09.
DR
XX DR N-PSDB; AD132619.
PT Selecting plant having enhanced transpiration efficiency, useful for
PT producing plants with enhanced transcription efficiency comprising
PT selecting plant expressing a genetic marker linked to the ERECTA locus in
PT the genome of the plant.
XX
XX Claim 4; SEQ ID NO 8; 209pp; English.
XX
XX The invention relates to a novel method for selecting a plant having
CC enhanced transpiration efficiency comprising detecting a genetic marker
CC for transpiration efficiency, where the marker comprises a nucleotide
CC sequence linked genetically to an ERECTA locus in the genome of the plant
CC and selecting a plant that comprises or expresses the genetic marker. The
CC method of the invention may be useful for selecting a plant having
CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic
CC variant or protein-encoding region may be useful in the preparation of a
CC genetic construct for modulating the transpiration efficiency of a plant.
CC Furthermore, the ERECTA genes may be useful for producing plants having
CC enhanced transcription efficiency by both traditional plant breeding and
CC genetic engineering approaches. The current sequence is that of the thale
CC cress ERECTA homologue protein of the invention.
XX
XX Sequence 932 AA;
SQ
Query Match 60.7%; Score 3059; DB 8; Length 932;
Best Local Similarity 63.1%; Pred No 1.5e-229;
Matches 597; Conservative 131; Mismatches 202; Indels 16; Gaps 5;
QY 31 LEIKSFKDVNNVLYDMWTSPPSDYCVWRGSCENTFNVVALNLSDLMDGERISPAIGD 90
Db 1 MAIKASFNVAMNLLDMWDVHNHDFCSWRGVFCDDVSLNVVLSLNLSNLGGEISSALGD 60
QY 91 LKSLSIDLRGNRLSQIIDEIGDCCSLONLDSFNELSGDIPEFSISKUKOLEFQILKNN 150
Db 61 LNNLSIIDIQGNKLGQIIDEIGDNCVSLAYVDFSTLLRGDIPFISISKUKOLEFELMKNN 120
QY 151 QIIGPIPTLSQIIPNKKIDLAONKLSGRIPLTIWNEVLQYLGKGNLJVGNISPDLCQ 210
Db 121 QLTGPIPALTLQIPNKKIDLAONKLTGRIPLTIWNEVLQYLGKGNLGTLSPDWCQ 180
QY 211 LTGLWYFDVRNNSLNGSIPETIGNCTAFOVLDLSYNQLTGRIIPDIFGFOVATLSIQNQ 270
Db 181 LTGLWYFDVRGNNTIGTIPESIGNCTSFELDVSTNQIIGVFPYNGFQVATLSIQNK 240
QY 271 LSGKIPSVIGLMOALAVLDLSGNLSGSIPILGNLTFTKLYLHNSKLTGSIPELGNM 330
Db 241 LTGRIPFVIGLMOALAVLDLSDBNELTGPPIPIIGNLSTFGKLYHGKLTGQIPPELGNM 300
QY 331 SKLHYELNDNHLTGHIPEPELGLTDLFDLVANNDEGPDPHLSSTCTNLNSLVHGNK 390
Db 301 SRLSYLQNDNELVGKIPPELGLTEQLFELTANNLVLGIPSNISSCALNQPNVHGNF 360
QY 391 FSGTIPRAFOKLSMTYLNLSNNIKGPIPELSEIRIGNLDTLDLSNNKINGIIPSSIGDL 450
Db 361 LSGAVPLEFRNLGSLTYLNLSNSFKGKIPALGHIINLDTLDLSGNNFSGSIPLTIGDL 420
QY 451 EHLTKNLSRNHITGVVPGDFGNLSIMEIDLSNNDISGPIPELNLQNTIILRLNENN 510
Db 421 EHLILNLSRNHNLGTLPALFEGNLSRIQIIDVSFNFAGVIPTELGOQINLSILNNNK 480
QY 511 LTGNV-GSLANCLSLTVLVNSHNNLVGDI PKNNNSFRSPDSFGNGLGSMWNSPCHD 569
Db 481 IHKIDQLTNCFSLANLNISFNLSGIIIPMKNFTRFSPASFNGPFLCGMWVGSICGP 540
QY 570 SRRTVVSISSRAIIGIAGLVILLMVLIAACRPHPNPPELDGSLDKPVTSTPKLVIL 629

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Db 541 SLPKSQV-FTRVAVICMVLGFIILICMIFIAVYKSKQKPEVLKSSKQP--EGSTKLVL 597
QY 630 HMMALHVEDIMRMENISEKTIIGHGASSTYKCVLKNCKPVATKRLYSHNPQSMKQF 689
Db 598 HMDMAIHTFDIMRVTENLDEKTIIGHGASSTYKCTSKTSRPIAKRIYNQYPSNREF 657
QY 690 ETELEMSSIKHNLVSLQAVSLSHLGSLLFYDYLENGSLMDLLHGPTKKKTLMDWTRLK 749
Db 658 ETELETIGSIRHRNIVSLHGVALSPFGNLLFYDYMENGSLMDLLHGPGKKVXKLDWETRLK 717
QY 750 IAYGAAQGLAYLHHDCSPRIIHRDVKSSNILLDKLEARLTPGIAKSLCVSKSHSTYV 809
Db 718 IAVGAAQGLAYLHHDCPPRIIHRDIKSSNILLDGNFEARLSDFGIAKSIIPATKYASTYV 777
QY 810 MGTIGYIDPEYARTSRTEKSDVYSGIVLLELTRKAVDDSNLHHLMSKTGNNEVM 869
Db 778 LGTIGYIDPEYARTSRINEKSDIYSFGIVLLELTGKAAVDNEANLHQMTLSKADDTVM 837
QY 870 EMADPDITSTCKDLGVVKVYFQALALCTKRQPNDRPTMHQVTRVLGSFMLSEOPPATDT 929
Db 838 EAVDAEVSVCMDSGHKTKTFQALALCTKRNPLERPTMQEVSRLVSLVPSPP----- 891
QY 930 SATLAGSCYVDEYANLKTPHSVNCSSMSASDAQLFLEFGQVISON 975
Db 892 -KTLPSPAKVQEGEERRESHSDTT-----PQWFVQFREDISKSS 931
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Search completed: September 2, 2006, 06:50:45
Job time : 205 secs

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OM protein - protein search, using sw model

Run on: September 2, 2006, 06:58:10 ; Search time 37 Seconds
(without alignments)
1816.756 Million cell updates/sec

Title: US-10-519-135-2
Perfect score: 5043
Sequence: 1 MALFRDIVLGFCLSLVA.....SASDAQFLRFQGVQVQNSSE 976

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*

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2: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US08_NEW_PUB.pep:*

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6: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US11_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5043	100.0	976	6	US-10-519-135-2
2	5043	100.0	976	7	US-11-056-355B-46416
3	5043	100.0	976	7	US-11-056-355B-48175
4	3606	71.5	635	7	US-11-056-355B-46417
5	3606	71.5	635	7	US-11-056-355B-48176
6	3372.5	66.9	921	6	US-10-519-135-6
7	3364	66.7	647	7	US-11-056-355B-46418
8	3364	66.7	647	7	US-11-056-355B-48177
9	3113	61.7	966	6	US-10-519-135-4
10	3091.5	61.3	966	6	US-10-519-135-10
11	3059	60.7	932	6	US-10-519-135-8
12	2505.5	49.7	671	6	US-10-449-902-52071
13	2482	49.2	675	6	US-10-519-135-45
14	2247.5	44.6	550	6	US-10-953-349-22717
15	2055.5	40.8	504	6	US-10-953-349-22718
16	1966.5	39.0	481	6	US-10-953-349-22719
17	1446	28.7	1109	7	US-11-330-403-3817
18	1445	28.7	1210	7	US-11-056-355B-88228
19	1445	28.7	1210	7	US-11-056-355B-91984
20	1445	28.7	1252	7	US-11-056-355B-44895
21	1441	28.6	1109	7	US-11-330-403-9397
22	1421.5	28.2	985	7	US-11-056-355B-88230
23	1421.5	28.2	985	7	US-11-056-355B-91986
24	1421.5	28.2	1040	7	US-11-056-355B-88229
25	1421.5	28.2	1040	7	US-11-056-355B-91985

26	1417.5	28.1	448	6	US-10-519-135-20	Sequence 20, Appl
27	1416.5	28.1	1046	7	US-11-056-355B-79289	Sequence 79289, A
28	1413	28.0	1081	7	US-11-056-355B-44896	Sequence 44896, A
29	1410.5	28.0	1003	7	US-11-056-355B-50497	Sequence 50497, A
30	1409	27.9	1072	6	US-10-449-902-53937	Sequence 53937, A
31	1405.5	27.9	1003	7	US-11-056-355B-48695	Sequence 48695, A
32	1401	27.8	1012	6	US-10-953-349-13624	Sequence 13624, A
33	1401	27.8	1025	6	US-10-953-349-13623	Sequence 13623, A
34	1397.5	27.7	392	6	US-10-449-902-30892	Sequence 30892, A
35	1397	27.7	1123	6	US-10-953-349-4749	Sequence 4749, Ap
36	1380	27.4	942	7	US-11-056-355B-44897	Sequence 44897, A
37	1368.5	27.1	1102	7	US-11-056-355B-50734	Sequence 50734, A
38	1365.5	27.1	1192	7	US-11-056-355B-46297	Sequence 46297, A
39	1363.5	27.0	1040	6	US-10-449-902-41369	Sequence 41369, A
40	1354	26.8	386	7	US-11-056-355B-4049	Sequence 4049, Ap
41	1352.5	26.8	1041	7	US-11-056-355B-96010	Sequence 96010, A
42	1351.5	26.8	910	7	US-11-056-355B-79291	Sequence 79291, A
43	1351.5	26.8	970	7	US-11-056-355B-79290	Sequence 79290, A
44	1343	26.6	987	6	US-10-953-349-12072	Sequence 12072, A
45	1338.5	26.5	1000	7	US-11-056-355B-46298	Sequence 46298, A

ALIGNMENTS

RESULT 1									
US-10-519-135-2									
; Sequence 2, Application US/10519135									
; Publication No. US20060137041A1									
; GENERAL INFORMATION:									
; APPLICANT: The Australian National University									
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT									
; TITLE OF INVENTION: PLANTS PRODUCED THEREFROM									
; FILE REFERENCE: 94948/WMO									
; CURRENT APPLICATION NUMBER: US/10/519,135									
; CURRENT FILING DATE: 2004-12-22									
; PRIOR APPLICATION NUMBER: AU P63339									
; PRIOR FILING DATE: 2002-07-02									
; NUMBER OF SEQ ID NOS: 45									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 2									
; LENGTH: 976									
; TYPE: PRT									
; ORGANISM: Arabidopsis thaliana ERECTA allele									
US-10-519-135-2									
Query Match									
Best Local Similarity 100.0%; Score 5043; DB 6; Length 976;									
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MALFRDIVLGFCLSLVA	TATGSEGA	TLLETKSFKV	YNNVLY	YMTTSS	SSDY	CYWRG	60
DB	1	MALFRDIVLGFCLSLVA	TATGSEGA	TLLETKSFKV	YNNVLY	YMTTSS	SSDY	CYWRG	60
QY	61	VSCENATFNVA	LNALNDL	NDGEIS	PAIGDL	KSLSID	LRGN	RLSGQI	PEIGDCSS
DB	61	VSCENATFNVA	LNALNDL	NDGEIS	PAIGDL	KSLSID	LRGN	RLSGQI	PEIGDCSS
QY	121	LDLSFNEISG	DIPIFS	ISKUOLE	QILIK	NNOLG	IPSTLS	QIIPNL	KIIDLAK
DB	121	LDLSFNEISG	DIPIFS	ISKUOLE	QILIK	NNOLG	IPSTLS	QIIPNL	KIIDLAK
QY	181	PRLIYNEV	LQYIG	LRGN	NLVG	NIS	PDLC	QLTGL	WYFDR
DB	181	PRLIYNEV	LQYIG	LRGN	NLVG	NIS	PDLC	QLTGL	WYFDR
QY	241	LDLSYQNL	GEIP	FDIG	FOVAT	TL	SLQ	GNLSG	KISVGL
DB	241	LDLSYQNL	GEIP	FDIG	FOVAT	TL	SLQ	GNLSG	KISVGL
QY	301	PIVGNL	TFTEK	LYL	HSN	KL	TG	SIP	PEL
DB	301	PIVGNL	TFTEK	LYL	HSN	KL	TG	SIP	PEL
QY	360	PIVGNL	TFTEK	LYL	HSN	KL	TG	SIP	PEL
DB	360	PIVGNL	TFTEK	LYL	HSN	KL	TG	SIP	PEL

Qy	361	NNANNDLGGPIPDHSSSCCTNNLSLWGHGKREGCTIPRAQOKLESMTYLLSSNNIKGPIR	420
Db	361	NNANNDLGGPIPDHSSCTNNLSLWGHGKFGCTIPRAQOKLESMTYLLSSNNIKGPIR	420
Qy	421	VELSRIGMLDTLDLSNNKINGIIPSSLDGLEHLKKNLGRNHIITGVVPDFGNLRIMEI	480
Db	421	VELSRIGMLDTLDLSNNKINGIIPSSLDGLEHLKKNLSRNHIITGVVPDFGNLRIMEI	480
Qy	481	DLSSNDISGPIPEELNOLNIIILRLENNLTGNVNSLANCSGLTYLVANSNNLVGDIRE	540
Db	481	DLSSNDISGPIPEELNOLNIIILRLENNLTGNVNSLANCSGLTYLVANSNNLVGDIRE	540
Qy	541	NNNFSRSPDSFTGNPGLCGSMNLSPCHDSRRPTVRVISRAAIIIGIAGLVYLLMWLLA	600
Db	541	NNNFSRSPDSFTGNPGLCGSMNLSPCHDSRRPTVRVISRAAIIIGIAGLVYLLMWLLA	600
Qy	601	ACRPNNPPPLDGSIDKPYTSTPKVLVILHMNALHYEDIMKMTENTLSEKYIIIGHGASS	660
Db	601	ACRPNNPPPLDGSIDKPYTSTPKVLVILHMNALHYEDIMKMTENTLSEKYIIIGHGASS	660
Qy	661	TVYKCVLKNCKRVALIKRLYSHNPQSKQFETELMELSTIKHRLVSLQAYSLSHGSLIF	720
Db	661	TVYKCVLKNCKRVALIKRLYSHNPQSKQFETELMELSTIKHRLVSLQAYSLSHGSLIF	720
Qy	721	YDYLENGSLMDLIDHPPTKKKTLDMDRRLKIAVGAAGLVYLLHDCSPRIIHRDVKSSNII	780
Db	721	YDYLENGSLMDLIDHPPTKKKTLDMDRRLKIAVGAAGLVYLLHDCSPRIIHRDVKSSNII	780
Qy	781	LDKDLRLDTPFGIAKSLCVSKSHSTSYVMGTTGYIDPEYARTSRLTESDVYSYGIYLL	840
Db	781	LDKDLRLDTPFGIAKSLCVSKSHSTSYVMGTTGYIDPEYARTSRLTESDVYSYGIYLL	840
Qy	841	ELLTRKKAVDDESNNLHILMSKTGNNEVEMADPDITSTCKDLGVYKVFQALLCTCKRQ	900
Db	841	ELLTRKKAVDDESNNLHILMSKTGNNEVEMADPDITSTCKDLGVYKVFQALLCTCKRQ	900
Qy	901	PNDPRTHQVTRVLGSMLEQPPAATDTSATLAGSCYDEVANILKTPHSVNCSSMSASD	960
Db	901	PNDPRTHQVTRVLGSMLEQPPAATDTSATLAGSCYDEVANILKTPHSVNCSSMSASD	960
Qy	961	AQLFLRFGQVISQNSE 976	
Db	961	AQLFLRFGQVISQNSE 976	
RESULT 2			
US-11-056-355B--46416			
Sequence 46416, Application US/11056355B			
Publication No. US20060150283A1			
GENERAL INFORMATION:			
APPLICANT: Brover, Vyacheslav			
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding			
FILE REFERENCE: 2750-1590P052			
CURRENT APPLICATION NUMBER: US/11/056,355B			
PRIOR FILING DATE: 2005-02-14			
PRIOR APPLICATION NUMBER: 60/544,190			
PRIOR FILING DATE: 2004-02-13			
NUMBER OF SEQ ID NOS: 119966			
SEQ ID NO 46416			
LENGTH: 976			
TYPE: prt			
ORGANISM: Arabidopsis thaliana			
FEATURE:			
NAME/KEY: peptide			
LOCATION: (1)..(976)			
OTHER INFORMATION: Ceres Seq. ID no. 13576686			
US-11-056-355B--46416			

Query Match	100.0%;	Score 5043;	DB 7;	Length 976;
Best Local Similarity	100.0%;	Pred. No. 1.4e-218;		

Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALEPRDVLVLGEPFCLSLVAVATYSSGALLLSEIKSFKDNNVVLVDMWTSPESSDYCWARG	60
Db	1	MALEPRDVLVLGEPFCLSLVAVATYSSGALLLEIKSFKDNNVVLVDMWTSPESSDYCWARG	60
QY	61	VSCENVTFNVAVALNTDLMDLNDGEISPAIDLSLISIDLRGNRLSGQIPDEIGDCSSJON	120
Db	61	VSCENVTFNVAVALNTDLMDLNDGEISPAIDLSLISIDLRGNRLSGQIPDEIGDCSSJON	120
QY	121	LDSFNELSGSDIPFSISKULQOLEQILKNNOLIGPIPS7LSQIPULKILDLAQNKLSGEI	180
Db	121	LDSFNELSGSDIPFSISKULQOLEQILKNNOLIGPIPS7LSQIPULKILDLAQNKLSGEI	180
QY	181	PRLIYNNVEVQYGLRGNNLVGNI SPDLCQLGLMWFVDRNNLSLGSIPETIGNCTARQV	240
Db	181	PRLIYNNVEVQYGLRGNNLVGNI SPDLCQLGLMWFVDRNNLSLGSIPETIGNCTARQV	240
QY	241	LDSYNOLTEIEFPDIFGLQVATLSIQGNQLSGKIPSVIGLMOALAVLDSLGNLSGISIP	300
Db	241	LDSYNOLTEIEFPDIFGLQVATLSIQGNQLSGKIPSVIGLMOALAVLDSLGNLSGISIP	300
QY	301	PIIGNLTFTEKLYLHNSKULTGSIPEPELGNNKSLHYLELNDNLTHGIIPEELCKLTDLPDL	360
Db	301	PIIGNLTFTEKLYLHNSKULTGSIPEPELGNNKSLHYLELNDNLTHGIIPEELCKLTDLPDL	360
QY	361	NVANNDLEGGIPDHLSSCTNLNLANHGNNKFGSTIPRAFQKLESMTYLNLSNNIKGP1P	420
Db	361	NVANNDLEGGIPDHLSSCTNLNLANHGNNKFGSTIPRAFQKLESMTYLNLSNNIKGP1P	420
QY	421	VELSRIGNLDTDLNNKINGIIPSSLDGLLEHLKNLSRNHI7GVVPEDFQNLRSIMEI	480
Db	421	VELSRIGNLDTDLNNKINGIIPSSLDGLLEHLKNLSRNHI7GVVPEDFQNLRSIMEI	480
QY	481	DLSSNDISGDIPEELQOLONIILRLENNNTLGNVGSLANCISTLYANSHNNLVGD1PK	540
Db	481	DLSSNDISGDIPEELQOLONIILRLENNNTLGNVGSLANCISTLYANSHNNLVGD1PK	540
QY	541	NNNFSRSPSPFIGNFQGLCGSMWLNSEBCHDSRTRVVISIRAAI1LGIAIGLVI1LMVLIA	600
Db	541	NNNFSRSPSPFIGNFQGLCGSMWLNSEBCHDSRTRVVISIRAAI1LGIAIGLVI1LMVLIA	600
QY	601	ACRPHNPPEPLDGLDKPVY7STPKVILHMMNVALHYEDIRMTBNLSKX7IGHGASS	660
Db	601	ACRPHNPPEPLDGLDKPVY7STPKVILHMMNVALHYEDIRMTBNLSKX7IGHGASS	660
QY	661	TVYKCVLKNCKPAVKIRLYSHNPQSMKOPETELEMSS1KHNIVLSLOAY5LSHLSGLLF	720
Db	661	TVYKCVLKNCKPAVKIRLYSHNPQSMKOPETELEMSS1KHNIVLSLOAY5LSHLSGLLF	720
QY	721	YDYLENGLSLMDLHGPKTKKTLDPMDRLKIAVGAAGLAIYLHHDSPRI1IHRDVKSSN1L	780
Db	721	YDYLENGLSLMDLHGPKTKKTLDPMDRLKIAVGAAGLAIYLHHDSPRI1IHRDVKSSN1L	780
QY	781	LDKDLEARLTDPGIAGSLCVSKSHSTYVMGTIGYIDPEYARTSRLTESDYYSGIVLL	840
Db	781	LDKDLEARLTDPGIAGSLCVSKSHSTYVMGTIGYIDPEYARTSRLTESDYYSGIVLL	840
QY	841	ELILRRRAYVDESNLHLIMSKTGNNVENMEMADPDTISCKDLGVYKVFQALALCTKRO	900
Db	841	ELILRRRAYVDESNLHLIMSKTGNNVENMEMADPDTISCKDLGVYKVFQALALCTKRO	900
QY	901	PNDPRTHQVTRVLGSMLEQCPAATDTSATLAGSCYUDEYANLKTPHSVNCCSSMSAD	960
Db	901	PNDPRTHQVTRVLGSMLEQCPAATDTSATLAGSCYUDEYANLKTPHSVNCCSSMSAD	960
QY	961	AQLFARFGOV1SONSE 976	
Db	961	AQLFARFGOV1SONSE 976	

RESULT 3
US-11-056-355B-48175

```
; Sequence 48175, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48175
; LENGTH: 976
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(976)
; OTHER INFORMATION: Ceres Seq. ID no. 13578686
US-11-056-355B-48175
```

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Query Match      100.0%; Score 5043; DB 7; Length 976;
Best Local Similarity 100.0%; Pred. No. 1.4e-218;
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MALFRIIVLLGFLFCLSLVATVYSEBQATLETKSKFDVNNVLYDWTSPSSDYCYWRG 60
DB 1 MALFRIIVLLGFLFCLSLVATVYSEBQATLETKSKFDVNNVLYDWTSPSSDYCYWRG 60
QY 61 VSCENTFNVVALNLSDLNDEGISPAIGDKSLSTDLEKGNRLSGOIPPEIGDSSLON 120
DB 61 VSCENTFNVVALNLSDLNDEGISPAIGDKSLSTDLEKGNRLSGOIPPEIGDSSLON 120
QY 121 LDISFNEISGDIPIPSISKLEQLEQILKNNQLIGPIPSLISQIPNLKILDLAONKLSGEI 180
DB 121 LDISFNEISGDIPIPSISKLEQLEQILKNNQLIGPIPSLISQIPNLKILDLAONKLSGEI 180
QY 181 PRLIYNEVLYQYGLGKNNLVGNISPDLCQLTGLWYDVNNLSLTSIPTIGNCTAFQY 240
DB 181 PRLIYNEVLYQYGLGKNNLVGNISPDLCQLTGLWYDVNNLSLTSIPTIGNCTAFQY 240
QY 241 LDISYNQLTGEIIPFDIGFLOVATLSLOGNLSGKIPSVIGLMQALAVLDSGNLSSGIP 300
DB 241 LDISYNQLTGEIIPFDIGFLOVATLSLOGNLSGKIPSVIGLMQALAVLDSGNLSSGIP 300
QY 301 PILGNLTFEKLYLHNSKLTGSIPELGNMSKLYLELNDNHLTGHIPELGLKLTDLFDL 360
DB 301 PILGNLTFEKLYLHNSKLTGSIPELGNMSKLYLELNDNHLTGHIPELGLKLTDLFDL 360
QY 361 NVANNLEGIIPHLSSCTNLNSLVNHNKFSGTTIPPAFOKLESMTYLNSSNNIKGPIP 420
DB 361 NVANNLEGIIPHLSSCTNLNSLVNHNKFSGTTIPPAFOKLESMTYLNSSNNIKGPIP 420
QY 421 VELSRIGNLDLTLNNKINGIIPSSIGDLEHLKNNLSRNHITGVYVPGDGNLRSIMEI 480
DB 421 VELSRIGNLDLTLNNKINGIIPSSIGDLEHLKNNLSRNHITGVYVPGDGNLRSIMEI 480
QY 481 DLSNNDISGIPBELNQLQNIILLRLENNNTLGNVGLANCLSLTVLVNSHNNLVGDIPK 540
DB 481 DLSNNDISGIPBELNQLQNIILLRLENNNTLGNVGLANCLSLTVLVNSHNNLVGDIPK 540
QY 541 NNNFSFSPDSFGNGGLCGSMUNSPCHDSRRVTVRSISRAAILGLAIGGLVILLMWLA 600
DB 541 NNNFSFSPDSFGNGGLCGSMUNSPCHDSRRVTVRSISRAAILGLAIGGLVILLMWLA 600
QY 601 ACRPHNPPELDGSLDKPVTYSTPKVILHNNMALHYEDIMMNTENLSKYYIIGHGASS 660
DB 601 ACRPHNPPELDGSLDKPVTYSTPKVILHNNMALHYEDIMMNTENLSKYYIIGHGASS 660
QY 661 TVYKCVLKNCKPAVKRLYSHNPQSMKQFETLEMLSSIKGRNLVSLQAVSLSHLGSLLF 720
DB 661 TVYKCVLKNCKPAVKRLYSHNPQSMKQFETLEMLSSIKGRNLVSLQAVSLSHLGSLLF 720
```

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DB 661 TVYKCVLKNCKPAVKRLYSHNPQSMKQFETLEMLSSIKGRNLVSLQAVSLSHLGSLLF 720
QY 721 YDYLENGSLMDLHGPPTKKTLDMDRLKAYAGAOLAYLHHDGSPRIIHRPVKSNIL 780
DB 721 YDYLENGSLMDLHGPPTKKTLDMDRLKAYAGAOLAYLHHDGSPRIIHRPVKSNIL 780
QY 781 LDLDLEARLTDGFIASLCSKSHSTYVWGTTGYIDPEYARTSRUTEKSDVYSYGIVL 840
DB 781 LDLDLEARLTDGFIASLCSKSHSTYVWGTTGYIDPEYARTSRUTEKSDVYSYGIVL 840
QY 841 ELITRRKAVDDESNLHLHLSKTKGNNEVEMADPDITSTCKDGVVKKVQALALCTKRQ 900
DB 841 ELITRRKAVDDESNLHLHLSKTKGNNEVEMADPDITSTCKDGVVKKVQALALCTKRQ 900
QY 901 PNDRPTMHOVTRVLSGFMISEOPPAATDTSATLASCYVDEVANLKTPHSVNCSMSASD 960
DB 901 PNDRPTMHOVTRVLSGFMISEOPPAATDTSATLASCYVDEVANLKTPHSVNCSMSASD 960
QY 961 AOLFLRFQVYISQNSE 976
DB 961 AOLFLRFQVYISQNSE 976
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RESULT 4

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US-11-056-355B-46417
; Sequence 46417, Application US/11056355B
; Publication No. US20060150283A1
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; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 46417
; LENGTH: 695
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(695)
; OTHER INFORMATION: Ceres Seq. ID no. 13578687
US-11-056-355B-46417

Query Match      71.5%; Score 3606; DB 7; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.8e-154;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 301 AIIIGIAGGVIIILMVLIAACRPHNPFLDGLDKDKEVTYSTPKLVILHMMMLHYVEDI 360
Qy MRMTENISEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPSOMKOFETELEMSSIKH 701
Db 361 MRMTENISEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPSOMKOFETELEMSSIKH 420
Qy 702 RNVLISQAYSLSHLSGLLPDYLENGSLMDLHGPTKKKTLMDWTRKLIAYGAAGLAVL 761
Db 421 RNVLISQAYSLSHLSGLLPDYLENGSLMDLHGPTKKKTLMDWTRKLIAYGAAGLAVL 480
Qy 762 HHDCSPRIIHRDVKSSNILLDKDLEARLTDGIAKSLCVSKSHSTYVMGTIGYIDPEYA 821
Db 481 HHDCSPRIIHRDVKSSNILLDKDLEARLTDGIAKSLCVSKSHSTYVMGTIGYIDPEYA 540
Qy 822 RTSRLTEKSDVYSYGIVLELLETRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 881
Db 541 RTSRLTEKSDVYSYGIVLELLETRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 600
Qy 882 DLGVKKVFPQALLCTKROPNDRPTMHQVTRVLGSPMLSEOPPAATDTSATLAGSCYVDE 941
Db 601 DLGVKKVFPQALLCTKROPNDRPTMHQVTRVLGSPMLSEOPPAATDTSATLAGSCYVDE 660
Qy 942 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 976
Db 661 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 695
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RESULT 5
US-11-056-355B-48176
; Sequence 48176, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48176
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(695)
; OTHER INFORMATION: Ceres Seq. ID no. 13578687
US-11-056-355B-48176
```

```
Query Match 71.5%; Score 3606; DB 7; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.8e-154;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 MOALAVADLSGNLSGSIPIPLGNLFTTEKYLHNSNKLTSIPPELGNSMKLHYLENDN 341
Db 1 MOALAVADLSGNLSGSIPIPLGNLFTTEKYLHNSNKLTSIPPELGNSMKLHYLENDN 60
Qy 342 HLTGHIPELQKLTDLFDLVANNNDLGGPIPDHLSSCTNLNSLVNHNKESGTTIPRAFOK 401
Db 61 HLTGHIPELQKLTDLFDLVANNNDLGGPIPDHLSSCTNLNSLVNHNKESGTTIPRAFOK 120
Qy 402 LBSMTYINLSSNNIKGPIPELBSRIQNLDTLDSNNKINGIIPBSGLDLEHLKMNLSRN 461
Db 121 LBSMTYINLSSNNIKGPIPELBSRIQNLDTLDSNNKINGIIPBSGLDLEHLKMNLSRN 180
Qy 462 HITGVVGDGRNSRISMEIDLSSNDISGPIPEELNOKONTIILRLLENNNLTGAVGSLANC 521
Db 181 HITGVVGDGRNSRISMEIDLSSNDISGPIPEELNOKONTIILRLLENNNLTGAVGSLANC 240
```

```
Qy 522 LSLTLVNSHNNLVGDI PKNNNFSRSPDSFGNPGLCGSMWNSPCHDSRRTRVVISIRA 581
Db 241 LSLTLVNSHNNLVGDI PKNNNFSRSPDSFGNPGLCGSMWNSPCHDSRRTRVVISIRA 300
Qy 582 AIIIGIAGGVIIILMVLIAACRPHNPFLDGLDKDKEVTYSTPKLVILHMMMLHYVEDI 641
Db 301 AIIIGIAGGVIIILMVLIAACRPHNPFLDGLDKDKEVTYSTPKLVILHMMMLHYVEDI 360
Qy 642 MRMTENISEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPSOMKOFETELEMSSIKH 701
Db 361 MRMTENISEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPSOMKOFETELEMSSIKH 420
Qy 702 RNVLISQAYSLSHLSGLLPDYLENGSLMDLHGPTKKKTLMDWTRKLIAYGAAGLAVL 761
Db 421 RNVLISQAYSLSHLSGLLPDYLENGSLMDLHGPTKKKTLMDWTRKLIAYGAAGLAVL 480
Qy 762 HHDCSPRIIHRDVKSSNILLDKDLEARLTDGIAKSLCVSKSHSTYVMGTIGYIDPEYA 821
Db 481 HHDCSPRIIHRDVKSSNILLDKDLEARLTDGIAKSLCVSKSHSTYVMGTIGYIDPEYA 540
Qy 822 RTSRLTEKSDVYSYGIVLELLETRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 881
Db 541 RTSRLTEKSDVYSYGIVLELLETRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 600
Qy 882 DLGVKKVFPQALLCTKROPNDRPTMHQVTRVLGSPMLSEOPPAATDTSATLAGSCYVDE 941
Db 601 DLGVKKVFPQALLCTKROPNDRPTMHQVTRVLGSPMLSEOPPAATDTSATLAGSCYVDE 660
Qy 942 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 976
Db 661 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 695
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```
RESULT 6
US-10-519-135-6
; Sequence 6, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU PS3339
; PRIOR FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Sorghum ERECTA
US-10-519-135-6
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Query Match 66.3%; Score 3372.5; DB 6; Length 921;
Best Local Similarity 68.4%; Pred. No. 6.7e-144;
Matches 666; Conservative 96; Mismatches 141; Indels 71; Gaps 8;

Qy 13 LFCLSIVATVTSREGATLEIKKSPKDVNNVLDWMTTSPSSDYCWVRGVCENVTENVVA 72
Db 9 LVALDLVAVAADGATLVEIKKSPKDVNNVLDWMTTSPSSDYCWVRGVCENVTENVVA 65
Qy 73 LNLSDNLDELISPAIGDLKSLSIDLRGNRLSGQIPDEIGDCSSIQNLNLSFNEISGDI 132
Db 66 LNLSDNLDELISPAIGDLKSLSIDLRGNRLSGQIPDEIGDCSSIQNLNLSFNEISGDI 125
Qy 133 PFSISKLKQLEQLILKNQNLIGPIPTLSQIPVUKLIDLAQNKLSGEIPLLIYWNEVLOY 192
Db 126 PFSISKLKQLEQLILKNQNLIGPIPTLSQIPVUKLIDLAQNKLSGEIPLLIYWNEVLOY 185
Qy 193 LGRGNLVENISPDLCQLGLWYFVDRNNSLGSIPETIGNCTAROVLDLSNOLTGEI 252
Db 186 L-----DVKNNSLTGVLPDITIGNCTSFQVLDLSNRRFTGPI 221
```

Qy	25	PRIGELQVATLSTLSGNOU:SGKIPSVYIGMOALVLDLSGNLSGSGIPILIGNLTPEKL	31.2
Dp	222	PFNIGFQVATLSTLSGNKFTGPIPSYIGMOALVLDSTYNOLSGSPISIGNLTPEKL	281
Qy	313	YLSNKLGTGSIPELGNMSKLAHYLELNDHLGH:PELIGKLTDLFDLVANNDLEGP	372
Dp	282	YIGGNLTGSIPELGNMSTLHYLELNDQLTGSIPELIGKLTGFDLVANNDLEGP	341
Qy	373	DHLSCTNLNLVNHGNKFSGII:PRAFOKLESMTYLANSSNNIKGPIPELSIRIGNDLT	432
Dp	342	DNLSGCYNLNSFFAAYGNKNGITIPSRIRKLESMTYLANSSNFISSGPIELSRINNDLT	401
Qy	433	DLSNNKINGIIPSSGLDEHLKMLSRNHLITGVYGGFGNLSRIMEIDLSNNDISGPI	492
Dp	402	DLSNNMTGPIPSISGLSRLRLNLSKGLGFI:PAFGNLSRIMEIDLSYNLGLIP	461
Qy	493	EEINLOQNIILLRLENNMLTGNVGS:LANCLSTLVANSHNLVGDIPANNFSRFSDFS	552
Dp	462	QELMNQNLML-----LNVSNNLAGVPAIDNNFTFRSDFS	498
Qy	553	IGNPGLGSMNSPCHDSRRYRV:ISRAIIGIAGLVLLAVLLAACPNNPPEFLD	612
Dp	499	IGNPGLCGWLGSSCSSTGHHEKPRISKAAIIGVAVGLVILLMLVAVCPHRPRAFXD	558
Qy	613	GSLDKVTYSTPLVTLIHNMMALHYEDIMRTNLSKRYIIIGGASSTYVKCVLKNCKP	672
Dp	559	VTVSKPRNAPPLVTLIHNMMALHYDDIMRTNLSKRYIIIGGASSTYVKCVLKNCKP	618
Qy	673	VAIKRLVYSHNPQSMOKFETELMELSGIKRNLVSIQOASLSHLGSLFYDYLEWEGSLMDL	732
Dp	619	VAIKRLVYAHYPSQIKMFETEELETVGSIKRNLVSIQGSISLPVGNLIFYDMEGSLMDV	678
Qy	733	LH-GPTKKKTLDMWTRLK:IAVGAAGLAVLHHDCSPRIIHRDVYSSNILLDKDLEARTD	791
Dp	679	LHGSSKKKKLDWETRLRI:ALGAOGLAVLHHDCSPRIIHRDVYSSKNILLDKDYEALTD	738
Qy	792	FGIAKSLCVSKMSTSYVMGTTGYIDPEYARISRLTEKSDVY-----SYGVLLELLTRR	846
Dp	739	FGIAKSLCVSKMSTSYVMGTTGYIDPEYARISRLNEKSDVRYLHMGAG-----	788
Qy	847	KAVDDSNLHLHLSKTYGNNEVWEMADPITSTCKDLGVYKAVFOLALLCTKRPQNDPT	906
Dp	789	-AADMDEASGGRI:LSKTASNEVMDVYDPIIGTCKDLGEBYKKLQVALLCTKRPQSPRPT	847
Qy	907	MHOVTRVLSFMLSQPP---AATDSATLAGSCYVDEYANIKTPHVSNC-SSNSASDAQ	962
Dp	848	MHEVTVLCLVNPDPKPRSAHQ:POPEPAVPSYINEYVLSRGALSCANSTSTSDAE	907
Qy	963	LFIRFGQVISONSE 976	
Dp	908	LFIRFGQVISONNME 921	

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RESULT 7
US-11-056-355B-46418
; Sequence 46418, Application US/11056355B
; Publication NO. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brewer, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1530PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 46418
; LENGTH: 647
; TYPE: prt
; ORGANISM: Arabidopsis thaliana

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; ; FEATURE:
; ; NAME/KEY: peptide
; ; LOCATION: (1)..(647)
; ; OTHER INFORMATION: Ceres Seq. ID no. 135786688
US-11-056-355B-46418

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Query Match	66.7%;	Score 3364;	DB 7;	Length 647;
Best Local Similarity	100.0%;	Pred. No. 1.1e-143;		
Matches 647;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	330	MSKJHYEILNDNHLTGHIPELGLGTLDFLDVYANNDLEGIIPHLSCTNLNSLVNHCN	389
Dh	1	MSKJHYEILNDNHLTGHIPELGLGTLDFLDVYANNDLEGIIPHLSCTNLNSLVNHCN	60
Qy	390	KFSGTTIPRAFOKLESMTYMLNSNNIKGPIPEVLSRIGNLDTLDSNNKINGIIPSSIGD	449
Dh	61	KFSGTTIPRAFOKLESMTYMLNSNNIKGPIPEVLSRIGNLDTLDSNNKINGIIPSSIGD	120
Qy	450	LEHLKXNLESRNHITGVVPDGFGLRSIMEIDLSNNDISGPIPELNOLONIILRLLENN	509
Dh	121	LEHLKXNLSRNIHTGVVPDGFGLRSIMEIDLSNNDISGPIPELNOLONIILRLLENN	180
Qy	510	NLTGNVSLANCJSLTVLVNYSHNNLVGDIPIKNNNFSRFSPPDSFIGNPLCGSMINSPCHD	569
Dh	181	NLTGNVSLANCJSLTVLVNYSHNNLVGDIPIKNNNFSRFSPPDSFIGNPLCGSMINSPCHD	240
Qy	570	SRRTVRVSRPAALIGLIGLVYLLMVLIAACRPHNPRLDGLDKPYTYSTPKVYL	629
Dh	241	SRRTVRVSRPAALIGLIGLVYLLMVLIAACRPHNPRLDGLDKPYTYSTPKVYL	300
Qy	630	HNNALHYVEDIRMTENLSEKIYIGHGASVYKCYLKNCKPVAIKRLYSHPQSMQOF	689
Dh	301	HNNALHYVEDIRMTENLSEKIYIGHGASVYKCYLKNCKPVAIKRLYSHPQSMQOF	360
Qy	690	ETELEMLSSIKHRNLVSLQVYSLSHLSGLFYDYLENGSLMDLLHGPTKXKTLDMDTRLK	749
Dh	361	ETELEMLSSIKHRNLVSLQVYSLSHLSGLFYDYLENGSLMDLLHGPTKXKTLDMDTRLK	420
Qy	750	IAYGAAGLAVLHHDCSPRIIHRVKSNNILBDLEARLTDPSIAKSLCYKSHTSYV	809
Dh	421	IAYGAAGLAVLHHDCSPRIIHRVKSNNILBDLEARLTDPSIAKSLCYKSHTSYV	480
Qy	810	MGTIGYIDPEYARSRLTEKSDVYSYIVLELITRKAADVDSNLSHLIMSKGNNEVM	869
Dh	481	MGTIGYIDPEYARSRLTEKSDVYSYIVLELITRKAADVDSNLSHLIMSKGNNEVM	540
Qy	870	EMADPDITSTCKDGLVVKVYFOLALCTKROPNDRPTMHQVTRVLGSGFMLSSEOPPAATDT	929
Dh	541	EMADPDITSTCKDGLVVKVYFOLALCTKROPNDRPTMHQVTRVLGSGFMLSSEOPPAATDT	600
Qy	930	SATLAGSCYDVEYANLKTPIHSVNCSSMSASDAQULFAPGOVISONSE	976
Dh	601	SATLAGSCYDVEYANLKTPIHSVNCSSMSASDAQULFAPGOVISONSE	647

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RESULT 8
US-11-056-355B-48177
? Sequence 48177, Application US/11056355B
? Publication No. US2006015023A1
? GENERAL INFORMATION:
? APPLICANT: Brover, Vyacheslav
? APPLICANT: Alexandrov, Nikolai
? TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
? TITLE OF INVENTION: Polypeptides Encoded Thereby
? FILE REFERENCE: 2750-1590PUS2
? CURRENT APPLICATION NUMBER: US/11/056,355B
? CURRENT FILING DATE: 2005-02-14
? PRIOR APPLICATION NUMBER: 60/544,190
? PRIOR FILING DATE: 2004-02-13
? NUMBER OF SEQ. ID NOS: 119966
? SEQ ID NO 48177
?
? LENGTH: 647
? TYPE: prt

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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)-(647)
OTHER INFORMATION: Ceres Seq. ID no. 13578688
US-11-056-355B-48177

Query Match 66.7%; Score 3364; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 1,1e-143; Indels 0; Gaps 0;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 MSKIHVELENDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNSLVNHN 389
DB 1 MSKIHVELENDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNSLVNHN 60
QY 390 KFSGTIPRAFOKESMYLNLSSNNIKGPIPELSRIGNLDTLDLSNNKINGIIPSSIGD 449
DB 61 KFSGTIPRAFOKESMYLNLSSNNIKGPIPELSRIGNLDTLDLSNNKINGIIPSSIGD 120
QY 450 LEHLKKNLSRNHITGVPGDFGNLRSGIMEIDLSNNDISGPIPEELNQLONIILRLENN 509
DB 121 LEHLKKNLSRNHITGVPGDFGNLRSGIMEIDLSNNDISGPIPEELNQLONIILRLENN 180
QY 510 NLGNVGSLANCLSLTVLNVSHNNLVGDIPEKNNFSRPSDPTGNPGLCGSWLNSFCHD 569
DB 181 NLGNVGSLANCLSLTVLNVSHNNLVGDIPEKNNFSRPSDPTGNPGLCGSWLNSFCHD 240
QY 570 SRRVRVSRRAALIGLIGLVLVLLMVLTAACRPHNPPPELDGSLDKPVYTSFKLVIL 629
DB 241 SRRVRVSRRAALIGLIGLVLVLLMVLTAACRPHNPPPELDGSLDKPVYTSFKLVIL 300
QY 630 HNNMALVVEDIMMTEENLSEKYLIGHGASSTVVCVLKNCPPAIRLYSHNPSMKOF 689
DB 301 HNNMALVVEDIMMTEENLSEKYLIGHGASSTVVCVLKNCPPAIRLYSHNPSMKOF 360
QY 690 ETELEMLSSIKHNLVSLQAVSLSHLSGLFYDYLENGSLMDLHGPTKKTLDWTRLK 749
DB 361 ETELEMLSSIKHNLVSLQAVSLSHLSGLFYDYLENGSLMDLHGPTKKTLDWTRLK 420
QY 750 IAYGAAGGLAYLHHDGSPRIIHRDVKSNNILDDKLEARLTDPGIASLCSKSHSTYV 809
DB 421 IAYGAAGGLAYLHHDGSPRIIHRDVKSNNILDDKLEARLTDPGIASLCSKSHSTYV 480
QY 810 MGTIGYIDPEYARTSRLTESKDVSYSGIVLLELLTRRKAVDDESNNLHLMSTGNNEV 869
DB 481 MGTIGYIDPEYARTSRLTESKDVSYSGIVLLELLTRRKAVDDESNNLHLMSTGNNEV 540
QY 870 EMADPDTSTCKDGVVKKVFOALLCTKQPNDRPTMHQVTRVLGSPMLSEOPPAATDT 929
DB 541 EMADPDTSTCKDGVVKKVFOALLCTKQPNDRPTMHQVTRVLGSPMLSEOPPAATDT 600
QY 930 SATLAGSCYDEYANLKTPHSNCSSMSASDAQFLRFQGVISONSE 976
DB 601 SATLAGSCYDEYANLKTPHSNCSSMSASDAQFLRFQGVISONSE 647

RESULT 9
US-10-519-135-4
Sequence 4: Application US/10519135
Publication No. US20060137041A1

GENERAL INFORMATION:
APPLICANT: The Australian National University
TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY
FILE REFERENCE: 94948/MRO
CURRENT APPLICATION NUMBER: US/10/519,135
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: AU PS3339
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 999

TYPE: PRT
ORGANISM: rice RECTA
US-10-519-135-4

Query Match 61.7%; Score 3113; DB 6; Length 999;
Best Local Similarity 63.1%; Pred. No. 2,9e-132;
Matches 618; Conservative 135; Mismatches 182; Indels 44; Gaps 9;

QY 26 EGATLEIKKSFDDVNNVLYDWTTPSPSDCVWRGVSCCEVTFNNVALNSDNLDOEIS 85
DB 35 EGKALMGVKAQFGANALVDW--DGADHCAMRGVTCDNASFAVALNLSNLTNGEIS 92
QY 86 PAIGDKSLSLIDLRGNRLSGQIPDEIGDSSQLONLDSFNEISGDIPEISIKLKQLEQL 145
DB 93 PAIGELKNLQFVLDKGNKLTGQIPDEIGDCISLKYLDLGNLNLGYDIPFISIKLKQLEEL 152
QY 146 ILKKNQLGPIPESTLSGIPMLKTLDLAQNLTSGEIPRLIYWNVEVLYLGKGNLVGNIS 205
DB 153 ILKKNQLGPIPESTLSGIPMLKTLDLAQNLTGDIPEPLIYWNVEVLYLGKGNLSTGTL 212
QY 206 PDLCOLTGLWYFDVRRNLSLGSIPETIGNCTAFQVLDLSYNQLTGEIPDFIGLQVATLS 265
DB 213 PDMCQLTGLWYFDVRRNLSLGSIPETIGNCTAFQVLDLSYNQLTGEIPDFIGLQVATLS 272
QY 266 LQGNQLSGKIIPYIIGMQLAVLDSGNLSSGIPILGNLTFTKLYLHNSKLTGSIIP 335
DB 273 LQGNRLTGKIPDYIIGMQLAVLDSGNLSSGIPILGNLTFTKLYLHNSKLTGSIIP 332
QY 326 ELGNMSKTLHLENDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNSLVN 385
DB 333 ELGNMSKTLHLENDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNSLVN 392
QY 386 VHGKFSGTIPRAFOKESMYLNLSSNNIKGPIPELSRIGNLDTLDLSNNKINGIIP 445
DB 393 VGNKLNLSGIPAGFQKLESITVNLSSNNKNGIPBELGHIILDTLDLSYNFSGEVPA 452
QY 446 SLGDLLEHLKKNLSRNHITGVPGDFGNLRSGIMEIDLSNNDISGPIPEELNQLONIILRL 505
DB 453 TIGDLLEHLKKNLSRNHITGVPGDFGNLRSGIMEIDLSNNDISGPIPEELNQLONIILRL 512
QY 506 LENNNLTVGNV--GSLANCLSLTVLNVSHNNLVGDIPEKNNFSRPSDPTGNPGLCGSW 550
DB 513 LENNNLTVGNV--GSLANCLSLTVLNVSHNNLVGDIPEKNNFSRPSDPTGNPGLCGSW 555
QY 551 -----SFIGNPGLCGSMWNSPCHDSRRTRVVSISRAALIGLIGLVLV 598
DB 566 ISDCNQYIHNKCSFGLGNPLHVVQDSSCGSHSGQ--RVNISKRAIACIIIGFIILCVLL 624
QY 599 IACRPHNPPPELDGSLDKVYTSFKLVILHNNMALVVEDIMMTEENLSEKYLIGHG 658
DB 625 IATYKTQPPPLVYKGS--DKPV--CGPPKLVYLQMDMAIHTEEDIMRLTENLSEKYLIGHG 682
QY 659 SSTYVVCVLKNCPPVAIRLYSHNPSMKOFETELEMLSSIKHNLVSLQAVSLSHLSGL 718
DB 683 SSTYVVCVLKNCPPVAIRLYSHNPSMKOFETELEMLSSIKHNLVSLQAVSLSHLSGL 742
QY 719 LFYDYLENGSLMDLHGPTKKTLDWTRLKLIAYGAAGGLAYLHHDGSPRIIHRDVKSN 778
DB 743 LFYDYNGSLMDLHGPTKKTLDWTRLKLIAYGAAGGLAYLHHDGSPRIIHRDVKSN 802
QY 779 ILDDKLEARLTPBGIAKSLCSKSHSTYVMGTIGYIDPEYARTSRLTESKDVSYSGIV 838
DB 803 ILDDENFEAHLSPFGIAKCPVSAKSHASTVLTGIGYIDPEYARTSRLTESKDVSYSGIV 862
QY 839 LLELLTRRKAVDDESNNLHLMSTGNNEVEMADPDTSTCKDGVVKKVFOALLCTK 898
DB 863 LLELLTRRKAVDDESNNLHLMSTGNNEVEMADPDTSTCKDGVVKKVFOALLCTK 922
QY 899 ROPNDPRTMHQVTRVLGSPMLSE--OPPAATDTSATLAGSCYDEYANLKTPHSNCSSM 956
DB 923 RHPSDRPTMHQVTRVLGSPMLSE--OPPAATDTSATLAGSCYDEYANLKTPHSNCSSM 979
QY 957 SASDAQFLRFQGVISONSE 975

Db 980 SSSDEQWFRGEVTSKHT 998

```

RESULT 10
US-10-519-135-10
; Sequence 10, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIEN
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU P53339
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana ERECTA homolog
US-10-519-135-10

```

Query Match 61.3%; Score 3091.5; DB 6; Length 966;
 Best Local Similarity 62.9%; Pred. No. 2.6e-131;
 Matches 610; Conservative 139; Mismatches 204; Indels 17; Gaps 6;

```

7 IVLLGFLCLSLVATVTSBQATLLEIKSFQVNNVLYDMTTPSSSDYCVWRGVCENV 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
12 LAWVGFV-VFQVSAANNNGKALMAIKGFSNLYNNLLDMDDVHNDGSMRGVPCDNV 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 TENVAVALNSDLNDGSIAPALGDKLSLIDLRGNRLSGQIPPEIDGCSLQNLDSFN 126
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
70 SYSVSNLNTSLNMGISPAIGLRNLOSIDLGKLAGQIPDEINCCASLYVLDSEN 129
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
127 ELGSDIPFSISKQLEQLIKNNQLGPIPSLTSQIPNLKIIDLAONKSGEIPRLIYW 166
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
130 LLYGDIPFSISKQLEQLIKNNQLGPIPSLTSQIPNLKIIDLAONKSGEIPRLIYW 189
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
187 NEVLYQVIGLRGNMLVGNISPDLCQITGLWYFDVNNLSLTSIPETIGCTAFQVLDL 246
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
190 NEVLYQVIGLRGNMLVGNISPDLCQITGLWYFDVNNLSLTSIPETIGCTAFQVLDL 249
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
247 QLTGEIPFDIGFLOVATLSLQGNOLSGKISVIGLMALAVLDLSGSLSPILIGNL 306
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
250 QLTGEIPYNTGFLQVATLSLQGNKLTGRIPFVIGLMALAVLDLSGSLSPILIGNL 309
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
307 TTFEKLVLHNNKLTGSIPELGNNSKLHYLELNDNHLTGHIPPELGLKLTDLFDLVANN 366
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
310 SFTGKLYLHGNNMLTGPPELGNNSRLSYQLNDNKLVTGPPELGLKLTDLFDLVANN 369
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
367 LBPPIPDHSSCTNLNSLVNHNKFSCTIPPAFOKLESMTYLNSNNIKGPIPELVLSRI 426
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
370 LVGPPIPNSSCAALNQFNHGNLSLGSIPPLAFNLSGLTYLNNSSNPFKGIPELVGHI 429
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
427 GNDITDLSNNKINGITPSSIGDLEHLKRNLSRNHITGVVPGDFGNLRSIMEIDLSND 486
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
430 INLDKDLSSGNFSGSIPLTGLDLEHLILNLSRNHLSGQLPAFEGNLSRIOMIDVSFNL 489
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
487 ISGPIPELNLQNLIIILRLNNNLVGNV-GLANCLSLTVLVNHNHILAGDIPIKNNFS 545
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
490 LSGVITPELQDLQNLNLSLNNKLGKIPDQNLNCTLVNANLNSFNLSGIVPEPMKFS 549
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
546 RFPSPDFIGNPGLCGSWLNSPCHDSRTVVSISRAAILGAIAGVLLMLVLAACRPH 605
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
550 RFAFASVAGNPIYLCGNWVSGICGLPKS-RV-PSRGLALICIVGLVITLMLFLAVYKSM 607
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
606 NPPPELDGSLDKPYTSTPKLVILHNMALHVEDIKRMTENSEKTIIGHGASSTYYKC 665
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
608 QOKKILIQGSSKQ-ABGLTRVLILHMDMAIHFDIDIKRMTENNEKPIIGYASSTYYKC 665

```

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QY 666 VLAKCKPVAIKRLYSHNPQKOFETELMSSIKERNLVSLOAYSLSHLSLLFYDYLE 725
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 666 ALKSSRIAIKRLYNOYPNHLREFETELTIGSIRHNISYSLGYSALSPGNNLFYYME 725
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 726 NSLMDLLHGPYTKKTLDMWDTLRUKIAYGAAQGLAYLHHDCSPRIHRDVKSNILDKL 785
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 726 NSLMDLLHGLSKVKKLDWETRLKIAVGAQAQGLAYLHHDCPTPRIHRDIKSNILDENF 785
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 786 EARLTDPGIAKSLCVSHSTYVMGTIGYIDPEYARTSLTEKSDPYSGYIVLELLTR 845
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 786 EARLSDGIAKSLPASKTHASTYVLTGTYIDPEYARTSRINRSDIYSGVILELLTG 845
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 846 RKAVIDESNLNHLIMSKTGNNEWEMADPDITSCDGLGVKKVFOALALCTKROPDRP 905
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 846 KKAVIDEANLHOLLISGADNTWMEAVDPYVTCNDLGHIRKTFQALALCTKRNPLERP 905
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 906 TMAQVTVLGSFMLSQPPATDTSATLACSQVDEYANLKTPHSVNCSMSASDAQFL 965
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 906 TMAEVSRLVLLSLVPSIQ-----VAKKLPDLHSTKKGLOEENVRPDAASQMFV 955
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 966 RFGQVISOQS 975
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 966 QFREVISKSS 965
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 11
US-10-519-135-8
; Sequence 8, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIEN
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU P53339
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana ERECTA homolog
US-10-519-135-8

```

Query Match 60.7%; Score 3059; DB 6; Length 932;
 Best Local Similarity 63.1%; Pred. No. 7.1e-130;
 Matches 597; Conservative 131; Mismatches 202; Indels 16; Gaps 5;

```

QY 31 LKIKSFQVNNVLYDMTTPSSSDYCVWRGVCENVTFNNVVALNSDLNDGEISPAIGD 90
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAIKASFQVNNVLYDMTTPSSSDYCVWRGVCENVTFNNVVALNSDLNDGEISPAIGD 60
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 91 LKSLSDLRGNLNSLQGIPEIDGCSLQNLDSFNEISGDIPIFSISKQLEQLIKNN 150
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LNNLOSIDLGKNGKLGQIPDEINCCASLYAVDSTMLFSGDIPFSISKQLEQLIKNN 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 151 QLTGPIPSLTSQIPNLKIIDLAONKLSGEIPRLIYNEVLYQVIGLRGNMLVGNISPDLCQ 210
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 QLTGPIPATLTQIPNLKIIDLAONKLTGEIPRLIYNEVLYQVIGLRGNMLVGNISPDLCQ 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 LTLGWYFDVNNLSLTSIPETIGCTAFQVLDLSYNOULGEIPFDIGFLOVATLSLQGN 270
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 LTLGWYFDVNNLSLTSIPETIGCTAFQVLDLSYNOULGEIPFDIGFLOVATLSLQGN 240
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 LSGKISVIGLMALAVLDLSGSLSGSIPILIGNTTFEKLVLHNNKLTGSIPELGNM 330
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 LTRGIPFVIGLMALAVLDLSGSLSGSIPILIGNTTFEKLVLHNNKLTGSIPELGNM 300
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 331 SKLHYLELNDNHLTGHIPPELGLKLTDLFDLVANNLDEGPIDHSSCTNLNSLVNHNK 390
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 SRLSYQLNDNDELVGKIPPELGLKLTDLFDLVANNLVLGIPISNISSCAALNQFNHGNF 360

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```

Qy      391 FGGTIRAPQKLESMYTYLNLSSNNIKGPIPVBLSTIGMLDTLDLSNKNINIIIPSSIGDL 450
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      361 LSGAVPEEFENGLSLYYLNLSSEFGAKI PAELGHI INLDITDLSGNFSSSILETLTGDL 420
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      451 EHLILKNLNSNHITGVVDPDFGNLSRIMEIDLSNNDISGAPIPEELNQLONIILRENNN 510
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      421 EHLLIILNSNHNLNGTLPAEPFNLSIQIIDVSFPFLAGVIPTELGOQLNINSILANNK 480
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      511 LTGNV-GSLANCLSTLVNLVSHNNLVGDI PKANNFSRPSPDSFIGNPGLCGSWLNSPCHD 565
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      481 IHKIPDOLNCFPSLANLINISFNNLSGII PPMKNFTFRSPASFPGNPFLCGNWGISICGP 540
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      570 SRRTVASISRALLIGAIAGVLIMLMVLAACRHANPEPPFDSDJDXPTVYSIPXIVIL 629
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      541 SLPKSOV-FTRVAIVCMVGFTLLICMTPIAAYKSQOKPVLKGSKP--EGSTKLIVIL 597
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      630 HNMALHVEDIIRMWTEENISEKYIIGHGASTVYCVCUKNCQPYALKLYSHNPQSKOF 689
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      598 HMOMALHTPDIMRYENDEKTIICYGASSIVYCTSKTSRAIKRIYNQYSNREF 657
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      690 ETELEMLSIKARNVLSDAYSLSHGSLLPDYIENGSLMDLHGPTYKKTLDDWTRLK 749
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      658 ETELETIGSI RHRNIVLSLHGVALSPFGNLLPFYDMENSGSLMDLHGPKKVKYLDMEETRLK 717
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      750 IAVGAOGLAYLIHHDCSPRIHRDVYSSNILDKOLEARLNDPFIAGSLCXSHTSYV 809
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      718 IAVGAOGLAYLIHHDCTPRIHRDIKSSNILDGFEARLSFGIASIPATKIYASTIV 777
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      810 MGTIGYIDPEYARTSRLTREKSDVYSYGIVLLELTRRAVDDESNTLHLIMSKTGNNEVM 865
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      778 LGTIGYIDPEYARTSNLRKESKDYSISGYVLELLLGKAVDENANLHQMILSKADNVTM 837
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      870 EMADPDITSCDKLGVYKKVPQIALICTRKQDNDRPTMHQYTRYUGSWMLEOPPAATDT 929
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      838 EAADAESVTCMDSGHKIKTFQALACTGRNPLERPTQAEVSRYLSLVSPRP----- 893
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      930 SATLAGSCYDEVANKTSPHSVNCSSMASDAQLFLRFGOYISONS 975
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      892 -KLLPBAKVQGEGERRESHSDTT-----PQWVVQFREDISKSS 931
       :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 12
US-10-449-902-52071
; Sequence 52071, Application US/104499902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-209269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52071
; LENGTH: 671
; TYPE: PRt
; ORGANISM: Oryza sativa
; OS-10-449-902-52071
```

```

Query Match      49.7%; Score 2505.5; DB 6; Length 671;
Best Local Similarity 73.7%; Pred. No.2-9e-105;
Matches 479; Conservative 68; Mismatches 100; Indels 3; Gaps 1.

    13 LFCLSLVATVTSSEGAATLLEIKKSKVDNNVNYLDWTTTSSSDSYCWARGVSCENNTFENVVA 72
       | ||| :::::|||||:::||||| ||| ||||| :||| |
```

Db 1 LVALLVAAVAADDSSTLEIEIKKSRANVDNVLGYMA---GGDYCSMRGVLCMDVTFVAVA 69

Qy 73 LMSDLMDLGEISPAIGDKSLMSIDLGRNRLSGQIPDEIGDSSLONDLSPNEISGD1 132

Db 70 LMSGLNLTGGEISPAVGRKGVISIDLSKMSLSQGPDEIGDSSLSLTDLSPFNSLDGD1 129

Qy 133 PFSISLXOLDELIKKNOLIGPISLTSQIPNLIKIDLAQNKLSGSIPLIYWNELQY 192

Db 130 PFSVSLKRIEBSILKKNOLIGVPISTLSQIPNLKIDLAQNKLSGSIPLIYWNELQY 189

Qy 193 LGLRGNLNGNISPDLCQLTGLMYEDVYNNLSLTSIPETIGNCTAPQVLDLSYNOLTGEI 252

Db 190 LGLRGNLNBGSISPDIQCLTGLMYEDVYNNLSLTGPETIGNCTSPQVLDLSYNKLSGSI 249

Qy 253 PPIGRLQVATISLQGNOLSGKIPSVITGMALAVLDLSGNLSGSIPIPLIGNLTPEKL 312

Db 250 PPIGRLQVATISLQGNMFTGPISPIDLMQALVLDLSYNOLSGSIPISITGMLTYTEKI 309

Qy 313 YLHSNLTGSIPEPLGNNSKLHYELBNHNLTGHPPELGLTDPPLTYANNDDLEGP1R 372

Db 310 YMGKNCLTGPPEPLGNNSLTHYLELNDNOLSGPPEPFGLKLTGLFPLTYANNDFSP1P 369

Qy 373 DHLSSCTNLNSLVNHGNKFSGTIPRAFOKLEBSMTYLNLSNNIKGP1PVELSRIGLDTL 432

Db 370 DNISSCVNLNSFNAYGNRLNGTIPSLHKLESMTYLNLSNFFLSGSIPIELSRINLDTL 429

Qy 433 DLSNNKINGITIFSSIGDLEHLLKNNLSNNHTGYVPDGFGLRISIMEDISNNDISGP1R 492

Db 430 DLSNNMTIPISITIGSLEHLRLMLSNNGVGFIPAEIGLRISIMEDISNNHNLGLG1P 489

Qy 493 BELNOLQNTIFILRLENNMLTGNVGSJLANCLSLTYLVNYSNNHNLVDIPKNNNFSRSPDSF 552

Db 490 QELIGMLQNLMLNLKNNITIGDVSSLMNCFSPLNLTNLSYNNLAGVETDNNFSRSPDSF 549

Qy 553 IGNPGLCGSMWNSPCHDSRRTRVISISRAALIGIAIGLVILLMVLVLAACRPHNPEPLD 612

Db 550 IGNPGLCGYWLSSCRSGHQOKPLISKALIGIAVGLVILLMVLVAVCRPHSPVFKD 609

Qy 613 GSLDRKVTYSTPKVILHNNALNYHEIDIMNTENLSBKTYIIGGASSTV 662

Db 610 VVSXSKRVSVPRLVILHNNLSLLEYEDIMNTENLSBKTYIIGGASSTV 659

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RESULT 13
US-10-519-135-45
Sequence 45, Application US/10519135
Publication No. US20060137041A1
GENERAL INFORMATION:
APPLICANT: The Australian National University
TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY
TITLE OF INVENTION: PLANTS PRODUCED THEREFROM
FILE REFERENCE: 94948/MRO
CURRENT APPLICATION NUMBER: US/10/519,135
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: AU PS3339
PRIOR FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patencin version 3.1
SEQ ID NO 45
LENGTH: 675
TYPE: PRT
ORGANISM: maize ERECTA
US-10-519-135-45

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[illegible]

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Db 64 SCNNISFNAYGKNTGTTIRSLRKLESMTYLNLSNPFISGSIPIELSRILNNIDTDLSC 123
Qy 437 NKINGIIPSSLDGLLEHLKKNLSRNHITGVVPGDFGLASIMEIDLSNNDISGPPELN 496
Db 124 NMTGPIPSISIGLLEHLRLNLKNDLVGFI PAEFGRLRSVMEIDL SYNHGLIIPOLG 183
Qy 497 QLONNILRLNENNLGNVSLNCLSLTVLANSYSHNNLVGDIPKNNPFSFSDSFGNP 556
Db 184 MLONNMLKLKNNNTGDSVSLMNCESLNLNVSYNLAGAVPDNNFTFSHDSFGNP 243
Qy 557 GLCGSWNSPCHDSRRTVRVSIISRAAILGIAIGLVILMLVLIACRPHNPPELDGSLD 616
Db 244 GLCGWNLGSSCRGTGRDRPKISKALIGVAVGLVILMLIIVAVCRPHNPFAKATVS 303
Qy 617 KPVYTSPTKLVIIHMMNALHYEDIMRTENLSEKTIIGHGASSTVYKCVLKNCKPVAIK 676
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Qy 677 RLYSHNPQSKOPETELEMSSIKHRVLVSLQAVSLSHLGLSLFYDYLENGSLMDLH-G 735
Db 364 KLVAHVQSLKEFELETELVGSIKHRVLVSLQGSLSVGNLLFYAVMESGLMDVLHG 423
Qy 736 PTKKTLMDWTRKIAVGAAGLAVLHDCSPRIIHRDVKSNNILDKDEARLTFGIA 795
Db 424 SSKKNLMDWTRIRIALGAAGLAVLHDCSPRIIHRDVKSNNILDKDYEALHTDREGIA 483
Qy 796 KSLCVSKSHTSTYVMTGTYIDPEYARTSLTEKSDVSYGYVLELTLTRKAVDESNL 855
Db 484 KSLCVSKSHTSTYVMTGTYIDPEYARTSLTEKSDVSYGYVLELTLTKKPDVNECNL 543
Qy 856 HHLIMSKTGNNEVEMADPDITSTCKDLGVYKVFQALICTKROPDRPTMHQVRVLG 915
Db 544 HHLILSTASNEVETVDPVGDTCCKDLGEVKKLFQALICTKROPDRPTMHEVAVLD 603
Qy 916 SFMLSEOP-----AATDTSATLAGSCYVDEYANIKTPHSVNC-SMSASDAQLF 964
Db 604 CLVNPPEPPOQOQKAAHHHQLPPSPPAYVDEYVSLRGICALSCANSSSTSDAEFL 663
Qy 965 LRFQVISON 974
Db 664 LKFGAISQN 673

RESULT 14
US-10-953-349-22717
; Sequence 22717, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22717
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22717

Query Match 44.6%; Score 2247.5; DB 6; Length 550;
Best Local Similarity 77.7%; Pred. No. 8.3e-94;
Matches 429; Conservative 51; Mismatches 63; Indels 9; Gaps 2;
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Db 61 PEEISLOQNMISLRLENNKLTDGVASLSCLSLSLNVSYNKLVGVIPTSSNFTREPPDS 120
Qy 552 FIGNPGICGSWNSPCHDSRRTVRVSIISRAAILGIAIGLVILMLVLIACRPHNPPELF 611
Db 121 FIGNPGICGSWNLPCHGAPSERVTLSTRAILGITGALVILMLVLIACRPHNSPPF 180
Qy 612 DGLDKPVTYSTPTKLVIIHMMNALHYEDIMRTENLSEKTIIGHGASSTVYKCVLKNCK 671
Db 181 DGSFDPKINFPSPKLVIIHMMNALHYEDIMRTENLSEKTIIGHGASSTVYKCVLKNCK 240
Qy 672 PVAIKRLYSHNPQSKOPETELEMSSIKHRVLVSLQAVSLSHLGLSLFYDYLENGSLMD 731
Db 241 PVAIKRIYSHNPQCIKEFELETELVGSIKHRNVSLSQGSLSFYGHLFPDYMENSLMD 300
Qy 732 LHLGPTKTKLMDWTRKIAVGAAGLAVLHDCSPRIIHRDVKSNNILDKDEARLTFD 791
Db 301 LHLGPTKTKLMDWTRKIAVGAAGLAVLHDCSPRIIHRDVKSNNILDKDEARLTFD 360
Qy 792 FGIASLCSKSHSTYVMTGTYIDPEYARTSLTEKSDVSYGYVLELTLTRRAVD 851
Db 361 FGIASLCSKSHSTYVMTGTYIDPEYARTSLTEKSDVSYGYVLELTLTRRAVD 420
Qy 852 ESNLHRLIMSKTGNNEVEMADPDITSTCKDLGVYKVFQALICTKROPDRPTMHQVT 911
Db 421 ESNLHRLIMSKATNAVMTVDPDITATCKDLGAVKVFQALICTKROPDRPTMHEVT 480
Qy 912 RVLSFMLSEOP-----PAATDTSATLAGSCYVDEYANIKTPHSVNC-SMSASDAQLF 964
Db 481 RVLSGLVPSSTPEKQLADLPAPNSPAKV--PCYVEIYANIKTPHVNCSMSTSDAQLF 538
Qy 965 LRFQVISON 976
Db 539 LKFGAISQN 550

RESULT 15
US-10-953-349-22718
; Sequence 22718, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22718
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22718

Query Match 40.8%; Score 2055.5; DB 6; Length 504;
Best Local Similarity 77.9%; Pred. No. 2.9e-85;
Matches 394; Conservative 43; Mismatches 60; Indels 9; Gaps 2;
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 2, 2006, 06:57:15 ; Search time 186 Seconds
(without alignments)
2430.633 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043

Sequence: 1 MALFRIVLGFCLSLVA.....SASDAQFLRFQGVQVQNSSE 976

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

2097797

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5043	100.0	976	US-11-027-304-2	Sequence 2, Appl1
2	3602.5	71.4	838	US-10-425-114-58433	Sequence 58433, A
3	3592.5	71.2	985	US-10-424-599-171008	Sequence 171008, A
4	3372.5	66.9	921	US-10-389-566-1452	Sequence 1452, App
5	3167	62.8	614	US-11-027-304-4	Sequence 4, Appl1
6	3141.5	62.3	907	US-10-437-963-123824	Sequence 123824, A
7	3089.5	61.3	967	US-11-027-304-8	Sequence 8, Appl1
8	3079.5	61.1	966	US-11-027-304-6	Sequence 6, Appl1
9	2931	58.1	909	US-10-425-115-367213	Sequence 367213, A
10	2921.5	57.9	885	US-10-437-963-169553	Sequence 169553, A
11	2791	55.3	764	US-10-425-114-58448	Sequence 58448, A
12	2712	53.8	764	US-10-425-115-262277	Sequence 262277, A
13	2484.5	49.3	962	US-10-437-963-121441	Sequence 121441, A
14	2384.5	47.3	578	US-10-425-114-45783	Sequence 45783, A
15	2322.5	46.1	611	US-11-027-304-87	Sequence 87, Appl1
16	2259.5	44.8	613	US-11-027-304-86	Sequence 86, Appl1
17	2236.5	44.3	541	US-10-425-114-43982	Sequence 43982, A
18	2215	43.9	713	US-10-425-114-58001	Sequence 58001, A
19	2010	39.9	621	US-11-027-304-88	Sequence 88, Appl1
20	1968.5	39.0	619	US-11-027-304-12	Sequence 12, Appl1
21	1956.5	38.6	458	US-11-027-304-10	Sequence 10, Appl1
22	1596	31.1	502	US-10-425-114-53788	Sequence 53788, A
23	1568	31.1	502	US-10-101-464A-945	Sequence 945, App
24	1568	31.1	502	US-10-864-252-945	Sequence 945, App
25	1543	30.6	426	US-10-425-114-59439	Sequence 59439, A
26	1529.5	30.3	464	US-10-424-599-268366	Sequence 268366, A
27	1489	29.5	1102	US-11-096-568A-27957	Sequence 27957, A

28	1484	29.4	1097	6	US-11-096-568A-27959	Sequence 27959, A
29	1484	29.4	1098	6	US-11-096-568A-27958	Sequence 27958, A
30	1474.5	29.2	402	4	US-10-425-115-242582	Sequence 242582, A
31	1446	28.7	1109	4	US-10-389-566-2378	Sequence 2378, App
32	1441	28.6	1109	4	US-10-389-566-1136	Sequence 1136, App
33	1432.5	28.4	998	4	US-10-101-464A-931	Sequence 931, App
34	1432.5	28.4	998	5	US-10-864-252-931	Sequence 931, App
35	1424.5	28.2	1029	4	US-10-437-963-164029	Sequence 164029, A
36	1421.5	28.2	1057	4	US-10-437-963-191288	Sequence 191288, A
37	1404.5	27.9	998	4	US-10-101-464A-895	Sequence 895, App
38	1404.5	27.9	998	5	US-10-864-252-895	Sequence 895, App
39	1401.5	27.8	1010	4	US-10-424-599-195812	Sequence 195812, A
40	1399.5	27.8	1030	4	US-10-437-963-158754	Sequence 158754, A
41	1393.5	27.6	370	4	US-10-101-464A-944	Sequence 944, App
42	1393.5	27.6	370	5	US-10-864-252-944	Sequence 944, App
43	1386	27.5	452	4	US-10-425-115-222873	Sequence 222873, A
44	1384.5	27.5	1021	4	US-10-101-464A-954	Sequence 954, App
45	1384.5	27.5	1021	5	US-10-864-252-954	Sequence 954, App

ALIGNMENTS

RESULT 1									
US-11-027-304-2									
; Sequence 2, Application US/11027304									
; Publication No. US20050223428A1									
; GENERAL INFORMATION:									
; APPLICANT: Torii, Keiko U.									
; APPLICANT: Shpak, Elena D.									
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH									
; FILE REFERENCE: UMOT122663									
; CURRENT APPLICATION NUMBER: US/11/027,304									
; PRIOR FILING DATE: 2004-12-30									
; PRIOR APPLICATION NUMBER: US 60/558,529									
; NUMBER OF SEQ ID NOS: 88									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 2									
; LENGTH: 976									
; TYPE: PRT									
; ORGANISM: Arabidopsis Thaliana									
US-11-027-304-2									
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Best Local Similarity 100.0%; Score 5043; DB 6; Length 976;									
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Qy	61	VSCENTYFNVALNLSLNDLNDGEISPAIGDKLSLIDLRGNLSGOIPDEIGDCSSLON	120						
Db	61	VSCENTYFNVALNLSLNDLNDGEISPAIGDKLSLIDLRGNLSGOIPDEIGDCSSLON	120						
Qy	121	LDLSFNELSGDIPIFSISKQLEQLILKNNOILGIPSTISOIPNKILDLAONKLSGEI	180						
Db	121	LDLSFNELSGDIPIFSISKQLEQLILKNNOILGIPSTISOIPNKILDLAONKLSGEI	180						
Qy	181	PRLIYNEVLYQYGLGNLNVGNISPDLCOLTLAFYDVYNNLSLTGSIPIETIGNCTAFQV	240						
Db	181	PRLIYNEVLYQYGLGNLNVGNISPDLCOLTLAFYDVYNNLSLTGSIPIETIGNCTAFQV	240						
Qy	241	LDLSYNQLTGEIPFDIGLOVATLSIQGNQSGKIPSVIGLMQALAVLDISGNLSGISIP	300						
Db	241	LDLSYNQLTGEIPFDIGLOVATLSIQGNQSGKIPSVIGLMQALAVLDISGNLSGISIP	300						
Qy	301	PIIGNLTPEKLYLHNNKLTGSIPELGNMSKJHYELNDNHTLGHIPPELGLKTLDFDL	360						
Db	301	PIIGNLTPEKLYLHNNKLTGSIPELGNMSKJHYELNDNHTLGHIPPELGLKTLDFDL	360						
Qy	361	NVANNLEGPDPHLSSTCTNLSLNVGNKFSGTIPPAFOKLESMTYLNLSNNIKGPIP	420						

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Db 361 NVANNDEGP1PDLSSCTNLNSLVHGNKRSGTTPPAFQKLESMYTLNLSNNIKGP1P
Qy 421 VELSRIGLDTLDLSNNKINGIIPSSIGDLLEHLLKMLSRNHTIGVYPGDFGNLRSTMEI
Db 421 VELSRIGLDTLDLSNNKINGIIPSSIGDLLEHLLKMLSRNHTIGVYPGDFGNLRSTMEI
Qy 481 DLSNNDISGPIPELNLQNIILRLNENNLTVGVSLANCLSTVLNVSNNLVGIPIK
Db 481 DLSNNDISGPIPELNLQNIILRLNENNLTVGVSLANCLSTVLNVSNNLVGIPIK
Qy 541 NNNFSRSPDSFIGNPGLCGSWLNSPCHDSRTYVRSISRALLGIAIGGLVILLMVLIA
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Qy 601 ACRPHNPPPLDGLDKPVYTPKVLVILHNNMALHYEDIMRTENLSEKYLIGHGASS
Db 601 ACRPHNPPPLDGLDKPVYTPKVLVILHNNMALHYEDIMRTENLSEKYLIGHGASS
Qy 661 TYKCVLKNCKPVAIKRLYSHNPQSMKOFETELMSSIKHRNLVSLQAVSLHSLGLF
Db 661 TYKCVLKNCKPVAIKRLYSHNPQSMKOFETELMSSIKHRNLVSLQAVSLHSLGLF
Qy 721 YDYLENGSLMDLHGPTKKKTLMDTRUKIAYGAQGLAYLHHDSPRIIHRDVXSNIL
Db 721 YDYLENGSLMDLHGPTKKKTLMDTRUKIAYGAQGLAYLHHDSPRIIHRDVXSNIL
Qy 781 LDKDLERLIDFGIAKSLCVSKSHSTYVWGTTIGYIDPEVARTSLTEKSDVSYGVL
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Qy 841 ELTRRAVAVDESULHLLINSGKTGNNEMVEMADPITSTCKDLGVKKVFOALLCTKRQ
Db 841 ELTRRAVAVDESULHLLINSGKTGNNEMVEMADPITSTCKDLGVKKVFOALLCTKRQ
Qy 901 PNDRPTMHQVTRVLGSEFMLESEOPPAATDTSAITLAGSCYVDEYANLKTPHSVNCSMSASD
Db 901 PNDRPTMHQVTRVLGSEFMLESEOPPAATDTSAITLAGSCYVDEYANLKTPHSVNCSMSASD
Qy 961 AOLFLRFGVIVSONSE 976
Db 961 AOLFLRFGVIVSONSE 976
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RESULT 2
US-10-425-114-58433
; Sequence 58433, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 58433
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-GMFL02220115B11_Flt.peg
US-10-425-114-58433
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Query Match 71.4%; Score 3602.5; DB 4; Length 838;
Best Local Similarity 82.0%; Pred. No. 9e-241;
Matches 688; Conservative 66; Mismatches 76; Indels 9; Gaps 2;

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Qy 145 LILKNQILIPISLTSQIPNLKILDLAQNKLSGEIPRLIYNNENVLYQLRGNNLVGNI 204
Db 2 LILKNQILIPISLTSQIPNLKILDLAQNKLSGEIPRLIYNNENVLYQLRGNNLVGSL 61
Qy 205 SPDLQQLTGLMYDVRNNSLTGSIPEITGNCTAPQVLDLSYNOLTGEIPPDIGLOYATL 264
Db 62 SPDMCQLTGLMYDVRNNSLTGSIPEITGNCTAPQVLDLSYNOLTGEIPNIFLOVATL 121
Qy 265 SLOGNOLSGKIPSYIGMQLAVLVLDSGNLSSGIPILGNLFTETKLYHNSKLTGSIP 324
Db 122 SLOGNOLSGKIPSYIGMQLAVLVLDSGNLSSGIPILGNLFTETKLYHNSKLTGSIP 181
Qy 325 PELGNNSKLYLELNDNHLTGHIPEELGKLTDFDLVANNNDGPIPDHLSCTNLNSL 384
Db 182 PELGNNSKLYLELNDNHLTGHIPEELGKLTDFDLVANNNDGPIPDHLSCTNLNSL 241
Qy 385 NVHGNKFSGTTPPAFQKLESMYTLNLSNNIKGP1PELSRIGLDTLDLSNNKINGIIP 444
Db 242 NVHGNKLTGSIIPSLQLESMTSLNLSNNLQGAIPLELSRIGLDTLDLSNNNLVGSIP 301
Qy 445 SSIQDLLEHLLKMLSRNHTIGVYPGDFGNLRSTMEIDLSNNDISGPIPELNLQNIIL 504
Db 302 SSIQDLLEHLLKMLSRNHTIGIIPAEFGNLRSTMEIDLSNNDISGPIPELNLQNIISL 361
Qy 505 RLENNNLTVGVSLANCLSTVLNVSNNLVGDIPKNNFSRSPDSFIGNPGLCGSWLN 564
Db 362 RLENNNLTVGVSLANCLSTVLNVSNNLVGDIPKNNFSRSPDSFIGNPGLCGSWLN 421
Qy 565 SPCHDSRTYVRSISRALLGIAIGGLVILLMVLIAACRPHNPPPLDGLDKPVYTP 624
Db 422 LPCGARPSEERVLISKAALIGITGALVILLMVLIAACRPHSPSPFPDGSFDPKRVNFSPP 481
Qy 625 KLVILHNNMALHYEDIMRTENLSEKYLIGHGASSVYKCVLKNCKPVAIKRLYSHNPQ 684
Db 482 KLVILHNNMALHYEDIMRTENLSEKYLIGHGASSVYKCVLKNCKPVAIKRLYSHNPQ 541
Qy 685 SMKOFETELMSSIKHRNLVSLQAVSLHSLGLFYDYLENGSLMDLHGPTKKKTLMD 744
Db 542 CIKEFETELTVGSIKHRNLVSLQAVSLHSLGLFYDYLENGSLMDLHGPTKKKTLMD 601
Qy 745 DTRUKIAYGAQGLAYLHHDSPRIIHRDVXSNILDKDLERLIDFGIAKSLCVSKSH 804
Db 602 ELRLKIALGAQGLAYLHHDCCPRIIHRDVXSNILDLADFEELHIDFGIAKSLCVSKSH 661
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Db 722 TNVMEVEMVEMADPITSTCKDLGVKKVFOALLCTKRQPNDRPTMHQVTRVLGSEFMLESEOP- 781
Qy 924 -----PAATDTSAITLAGSCYVDEYANLKTPHSVNCSMSASDAOLFLRFGVIVSONSE 976
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RESULT 3
US-10-424-599-171008
; Sequence 171008, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 171008
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LENGTH: 985
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1), (985)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT847_125435C.1.pep
US-10-424-599-171008

Query Match 71.2%; Score 3592.5; DB 4; Length 985;
Best Local Similarity 72.3%; Pred. No. 5.5e-240;
Matches 715; Conservative 94; Mismatches 163; Indels 17; Gaps 6;

QY 1 MALFRDVLVGLFCLSLVATVTSSECATLLEIKSKFDVNNVLYDMTTPSSDYCYWRG 60
DB 1 MAFRFGLIALLICLS-VNSVESDDGATLLEIKSKFRVDNVLVDMTSPSSDYCAMRG 59
QY 61 VSCENVTENVVALNLSDLNLDGEISPAIGDKSL---SIDLRGNRLSGQIPDEIGDCSS 117
DB 60 IACDNVTENVVALNLSGLNLDGEISPAIGDKSLAGRAKAVDNESN-LHHLIWSKAATNAV 118
QY 118 LQNLDSLNFNELSGDIPFS---ISKLKQLEQLIKNNQLIGRIPSTLSQIPNLKILDLAQN 174
DB 119 METVDPDITATGDKLXSKLIISLYAAQKGIKIGQLIGVTVVLSQIPDKILDLAQN 178
QY 175 KLSGEIPRLIYMWNVLOYLGRGNLVGNISPDLCQLTGLMFPVRRNSLTGSIPTETIGN 234
DB 179 NLGGEIPSLISKDEVLQYLYVNLTLHLVTSPLXLCLOTGSSSCLEKOSKTYXSERILN 238
QY 235 CTAPOVDLSYNQUTGSEIPDIFLOVATLSLQCNQISGIPSYIGLMOALVLDLSGNL 294
DB 239 XKSFSIDLSYNKTEERIPNIGLOVATLSLQCNKLSGHIPEYIGLMOALVLDLSGNL 298
QY 295 LSGSIPILGNLTFTTEKLYLHNSKLTGSIPELGNMSKLYLELNDHNLTGHIPELGLK 354
DB 299 LSSSIPILGNLTFTTEKLYLHNSKLTGSIPELGNMSKLYLELNDHNLTGHIPELGLK 358
QY 355 TDLFDLVANNDEGPIPDHLSCTNLSLNVHGNKFSGTPRAFOKLESMTYNLSSNN 414
DB 359 TDLFDLVANNDEGPIPDHLSCTNLSLNVHGNKFSGTPRAFOKLESMTYNLSSNN 418
QY 415 IKRPIPELSRIGNLDTLDLSNNKINGIIPSSIGDLHLKMLSRHITGVPGDGNL 474
DB 419 LQALPIELSRIGNLDTLDLSNNKINGIIPSSIGDLHLKMLSRHITGVPGDGNL 478
QY 475 RSIMEIDLNSNDISGPIPEELNQLNIIILRLNNNLTVGNVSLANCLSLTVLVSHNLT 534
DB 479 RSIMEIDLNSNDISGPIPEELNQLNIIILRLNNNLTVGNVSLANCLSLTVLVSHNLT 538
QY 535 VGDIPKNNNSRSPDSFNGPGLCGSWLNSPCHDSRTYRVVISRAAIIIGIAGLVIL 594
DB 539 FGVIPTSNNTFRPPSPFIGNPGLCGWMLNPGHGAPESEKVTLSKAAIIGITLGAIVIL 598
QY 595 LAMVLIACRHPNPFPDGLDKPVYTPPKLYVLHNNMALHYVEDIMRMTNLSKXYII 654
DB 599 LAMVLIACRHPNPFPDGLDKPVYTPPKLYVLHNNMALHYVEDIMRMTNLSKXYII 658
QY 655 GHGASSTVYKCVLKNCKPVAIKRLYSHNPQSMKOFETELEMSSIKRNLVSLQVSLSH 714
DB 659 GHGASSTVYKCVLKNCKPVAIKRLYSHNPQSMKOFETELEMSSIKRNLVSLQVSLSH 718
QY 715 LGSLLFPDYLENGSLMLHGPYKKTLDMDTRLKIVGAAGCAIYAHHCSPRIHRDV 774
DB 719 YGHLFPDYLENGSLMLHGPYKKTLDMDTRLKIVGAAGCAIYAHHCSPRIHRDV 778
QY 775 KSSNIIILDKLEARLFGIAXSLCVSKSHSTVVMGTIGYIDPEVARTSRILEKSVYS 834
DB 779 KSSNIIILDKLEARLFGIAXSLCVSKSHSTVVMGTIGYIDPEVARTSRILEKSVYS 838
QY 835 YGIVLELLTRRAKAVDNESNLHLLMSKGTGNNEVMENADPDITSTCKDLGVVKKVFOAL 894
DB 835 YGIVLELLTRRAKAVDNESNLHLLMSKGTGNNEVMENADPDITSTCKDLGVVKKVFOAL 894

DB 839 YGIVLELLTRRAKAVDNESNLHLLMSKATNAVMETVPDITATCKDLGVVKKVFOAL 898
QY 895 LCTKROPDRPTMHOVTRVGSFMLSEOP-----PAADTSATLAGSCYVEYANLKT 947
DB 899 LCTKROPDRPTMHOVTRVGSFMLSEOP-----PAADTSATLAGSCYVEYANLKT 956
QY 948 PHNSVCSMSASDAQLEFLRGOVISONSE 976
DB 957 PHNSVCSMSASDAQLEFLRGOVISONSE 985

RESULT 4

US-10-389-566-1452
Sequence 1452, Application US/10389566
Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
CURRENT APPLICATION NUMBER: US/10/389,566
PRIOR FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1452
LENGTH: 921
TYPE: PRT
ORGANISM: Sorghum bicolor
US-10-389-566-1452

Query Match 66.9%; Score 3372.5; DB 4; Length 921;
Best Local Similarity 68.4%; Pred. No. 9.1e-225;
Matches 666; Conservative 96; Mismatches 141; Indels 71; Gaps 8;

QY 13 LFCLSIATVTSSEGATLLEIKSKFDVNNVLYDMTTPSSDYCYWRGSCENVTENVVA 72
DB 9 LVALLVAVAVAADGATLVLEIKSKFRNVGVLYDYDMA---GDYCSWRGVLCDDVFAVAA 65
QY 73 LINSDLNLDGEISPAIGDKSLSLIDLRGNRLSGQIPDEIGDCSSLQNLDSLNFNELSGDI 132
DB 66 LINSDLNLDGEISPAIGDKSLSLIDLRGNRLSGQIPDEIGDCSSLQNLDSLNFNELSGDI 135
QY 133 PFSISKLKQLEQLIKNNQLIGRIPSTLSQIPNLKILDLAQNLSGEIPRLIYMWNVLOY 192
DB 126 PFSISKLKQLEQLIKNNQLIGRIPSTLSQIPNLKILDLAQNLSGEIPRLIYMWNVLOY 185
QY 193 LGRGNLVGNISPDLCQLTGLMFPVRRNSLTGSIPTETIGNCTAFOVLDLSYNQLTGEI 252
DB 186 LGRGNLVGNISPDLCQLTGLMFPVRRNSLTGSIPTETIGNCTAFOVLDLSYNQLTGEI 251
QY 253 PDIIGLOVATLSLQCNQISGIPSYIGLMOALVLDLSGNLSSGIPITIGLTFTEK 312
DB 222 PDIIGLOVATLSLQCNQISGIPSYIGLMOALVLDLSGNLSSGIPITIGLTFTEK 301
QY 313 YLHNSKLTGSIPELGNMSKLYLELNDHNLTGHIPELGLKTDLPDLVANNDEGPI 372
DB 282 YLHNSKLTGSIPELGNMSKLYLELNDHNLTGHIPELGLKTDLPDLVANNDEGPI 361
QY 373 DNLSSCVNLNSFAYANKLNGTIPRSLRKLSEMTYLNLSNFISSGIPIELSRINNDTL 401
DB 342 DNLSSCVNLNSFAYANKLNGTIPRSLRKLSEMTYLNLSNFISSGIPIELSRINNDTL 401
QY 401 DNLSSCVNLNSFAYANKLNGTIPRSLRKLSEMTYLNLSNFISSGIPIELSRINNDTL 401
DB 402 DNLSSCVNLNSFAYANKLNGTIPRSLRKLSEMTYLNLSNFISSGIPIELSRINNDTL 401
QY 433 DLSNNKINGIIPSSIGDLHLKMLSRHITGVPGDGNLPSIMEIDLNSNDISGPI 492
DB 402 DLSNNKINGIIPSSIGDLHLKMLSRHITGVPGDGNLPSIMEIDLNSNDISGPI 492
QY 492 DLSNNKINGIIPSSIGDLHLKMLSRHITGVPGDGNLPSIMEIDLNSNDISGPI 492
DB 492 DLSNNKINGIIPSSIGDLHLKMLSRHITGVPGDGNLPSIMEIDLNSNDISGPI 492
QY 493 BEINQNLNIIILRLNNNLTVGNVSLANCLSLTVLVSHNLTGDIIPKNNNFSRFPDPS 552
DB 493 BEINQNLNIIILRLNNNLTVGNVSLANCLSLTVLVSHNLTGDIIPKNNNFSRFPDPS 552

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Db 462 OELEMLQNLML-----LNTSYNNLAGVVPADNNFRFPSPDSF 498
QY 553 IGNPGLGSLNSPCHDSRRTRVVISIRAAIILGAIIGVILMLVLIACRPHNPFLD 612
Db 499 LGNPGGLGVLGSSCRGTGHEKEKPPISKAALIGVAVGLVILLMLIIVAVCRPHRPPAFKD 558
QY 613 GSIIDKPVTYTPKVLILHMMALHVEDIMRMTENLSEKYYIGHGASTYVKCVLKKCKP 672
Db 559 VYTSKPRRNAPKVLILHMMALHVEDIMRMTENLSEKYYIGHGASTYVKCVLKKCKP 618
QY 673 VAIKRLYSHNPQSMKQFETELMLSSIKHNLVSLQAYSLSHGSLIPYDLENGSLMDL 732
Db 619 VAIKRLYAHYPOSLKEFETELTVGSIKHNLVSLQAYSLSPVGNLLIFYDMEGCSLMDV 678
QY 733 LH-GPTKKKTLDMQTRKIAVGAAGLAVYHHDCSPRIHRDVSKNILLDKOLEALTD 791
Db 679 LHGGSSKKKKLDWETRIRIALGAAQGLAVYHHDCSPRIHRDVSKNILLDKOLEALTD 738
QY 792 FGIASLSLVSCKSHSTYVMGTIGYIDPEYARTSRLTESKSPDY-----SYGIVLELTLTRR 846
Db 739 FGIASLSLVSCKSHSTYVMGTIGYIDPEYARTSRLTESKSPDY-----SYGIVLELTLTRR 788
QY 847 KAVDDESNLHLIMSKTGNNEVEMADPDITSTCKDGVVKKVFOALALCTKQPNDRPT 906
Db 789 -AADWQASGQRLISKTSASNEVMDTVDPDIDTCKDLGEVKKLFQALALCTKQPNDRPT 847
QY 907 MHQVTRVLSFMLEQPP---AATDTSATLAGSCVVEYVANKLTPHSVNC--SSMSASDAQ 962
Db 848 MHEVVRVLDCLVMPDPKPSAHQLPQSPAPVPSYINEYVSLKGTGALSCANSTSTSDAE 907
QY 963 LFLRFQGVISONSE 976
Db 908 LFLKFGGAISONME 921
```

```
RESULT 5
US-11-027-304-4
; Sequence 4, Application US/11027304
; Publication No. US20050223428A1
; GENERAL INFORMATION:
; APPLICANT: Torii, Keiko U.
; APPLICANT: Snpak, Elena D.
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
; FILE REFERENCE: UMOTL22663
; CURRENT APPLICATION NUMBER: US/11/027,304
; PRIORITY FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/558,529
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
US-11-027-304-4
```

Query Match 62.8%; Score 3167; DB 6; Length 614;

Best Local Similarity 100.0%; Pred. No. 9.3e-211; Indels 0; Gaps 0;

Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MALFRDIVLLGFLECLSLVAVTSEEGATLLEIKKSFQDVNNVLYDWTSPSSDYCVMRG 60
Db 1 MALFRDIVLLGFLECLSLVAVTSEEGATLLEIKKSFQDVNNVLYDWTSPSSDYCVMRG 60
QY 61 VSCENVTNNVALNLSLNDGEISPAIGDKSLSLDLGNRISGQIPDEIGCSSLQNL 120
Db 61 VSCENVTNNVALNLSLNDGEISPAIGDKSLSLDLGNRISGQIPDEIGCSSLQNL 120
QY 121 LDISFNLSGSDIPSPISKQLQLEQILIKNNQLIGPITSTISQIPNLTIIDLAQKLSGEI 180
Db 121 LDISFNLSGSDIPSPISKQLQLEQILIKNNQLIGPITSTISQIPNLTIIDLAQKLSGEI 180
```

```
QY 181 PRLIYNEVLOYLGLRGNLNVGNISPDLCQLTGLWYFDVRNNSLTGSIPETIGNCTAFQV 240
Db 181 PRLIYNEVLOYLGLRGNLNVGNISPDLCQLTGLWYFDVRNNSLTGSIPETIGNCTAFQV 240
QY 241 LDISYNQLTGEIIPFDIGFLOVATLSIQGNQLSKIFSVIGLMALAVLDLSGNLSGSIP 300
Db 241 LDISYNQLTGEIIPFDIGFLOVATLSIQGNQLSKIFSVIGLMALAVLDLSGNLSGSIP 300
QY 301 PILGNLTFTFKLYLHNSKLTGSIIPPELGNMSKLYLELNDNHLTGHIPELGLKTLDFDL 360
Db 301 PILGNLTFTFKLYLHNSKLTGSIIPPELGNMSKLYLELNDNHLTGHIPELGLKTLDFDL 360
QY 361 NVANNDLEGPIDPHLSSCTNLNSLVNHNKFSCTGIPRAFOKLESMTYLNLSNNIKGPIP 420
Db 361 NVANNDLEGPIDPHLSSCTNLNSLVNHNKFSCTGIPRAFOKLESMTYLNLSNNIKGPIP 420
QY 421 VELSRIGNLDLTLSSNNKINGITIPSSIGDLEHLILKNLSNNHTTGVVPDQFGLRSTIMEI 480
Db 421 VELSRIGNLDLTLSSNNKINGITIPSSIGDLEHLILKNLSNNHTTGVVPDQFGLRSTIMEI 480
QY 481 DLSNNDISGPIPEELNQLQNIILLRLNNNLTGNGSLANCLSTVLYNLSHNNLVGDIPK 540
Db 481 DLSNNDISGPIPEELNQLQNIILLRLNNNLTGNGSLANCLSTVLYNLSHNNLVGDIPK 540
QY 541 NNNFSRSPDSFIGNFGLCGSWLNSPCHDSRRTRVVISIRAAIILGAIIGLVILLMWLIA 600
Db 541 NNNFSRSPDSFIGNFGLCGSWLNSPCHDSRRTRVVISIRAAIILGAIIGLVILLMWLIA 600
QY 601 ACRPHNPPELDGS 614
Db 601 ACRPHNPPELDGS 614
```

```
RESULT 6
US-10-437-963-123824
; Sequence 123824, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIORITY FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 123824
; LENGTH: 907
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(907)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_26620C.1.pep
US-10-437-963-123824
```

Query Match 62.3%; Score 3141.5; DB 4; Length 907;

Best Local Similarity 65.1%; Pred. No. 9.2e-209; Indels 81; Gaps 11;

Matches 631; Conservative 94; Mismatches 164; Indels 81; Gaps 11;

```
QY 13 LFCLSIVATVTESEGATLLEIKKSFQDVNNVLYDWTSPSSDYCVMRGVSCENVTNNVA 72
Db 13 LVALLLVAVAVADGSLTLEIKKSFQDVNNVLYDWA---GGDVCSMRGVLCADVTFVAA 69
QY 73 LNSDLNLDGEISPAIGDKSLSLI-DLRGNRLSGQIPDEIGCSSLQNLDISFNLSGSD 131
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Db 70 LNTSGNLGGEISPAVRLKGVSMYGRGGVL-----CCCLEMM-----LAGA 113
QY 132 IPPSISLKLQLEQLKKNQOLIGPIBSTLSQIPMLKLDLAONKLSSEIPRLIYMWELQ 191
Db 114 WTRS-----MLTKNNQOLIGVIPSTLSQIPMLKLDLAONKLSSEIPRLIYMWELQ 165
QY 192 YLGRGNLTVGNISPDLCQTLGMYFDVRNNLSLGSIPETIGNTAQOVLDSLNOLTGE 251
Db 166 YLGRGNLTVGNISPDLCQTLGMYFDVRNNLSLGSIPETIGNTAQOVLDSLNOLTGE 201
QY 252 IPPDIGLOVATLSLQGNOLSGKIPSVIGLMOALAVLDLSGNLSGSIPIPLIGLTFTEK 311
Db 202 IPPNIGLOVATLSLQGNMFTGPIPSVIGLMOALAVLDLSGNLSGSIPIPLIGLTFTEK 261
QY 312 LYHSNKLTSIPPELGNSKLHYLELDNHLGHIPEPLGKLTDFDLVANNDEGPI 371
Db 262 LYMOGNKLTGPIPEPLGNMSTLHYLELDNHLGHIPEPLGKLTDFDLVANNDEGPI 321
QY 372 PDHLSCTNLNSLVHGNKFSGTIPRAFOKLESMTYLNLSNNIKGPIPEVLSRIGLDT 431
Db 322 PDHSSCVNLNSFNAAGNRLNGTIPSLHKLDESMTYLNLSNPLSGSIPLELSRINLDT 381
QY 432 LDISNNKINGIIPSSIGDLEHLKKNLSRNHITGVPGDFGNLRSIMEIDLNNDISGPI 491
Db 382 FNLSN---NOLV-----GFPAEIGNLRSIMEIDMNNHGLGLI 417
QY 492 PEBLNQNLIIILRENNLITGVNSLANCLSLTVLNVSHNNLVGDIPIKNNNFSRSPDS 551
Db 418 POELGMLQNMMLNLTNNNTIGDVSILMCFSLNVLNVSYNLAGVPTDNNSRSPDS 477
QY 552 FIGNPGICSGWNSPCHDSRRTRVVISRAIIGIAIGLVILMLVLAACRPNNPPEL 611
Db 478 FLNPNGLCGWLLSSSCSGHQOKPLISKAIIIGIAGVGLVILMLVLAACRPSPPEVK 537
QY 612 DGSIDPVTSTPKLVIILHNNMALHYVEDIMRMTENLSEKIIIGHGASSTVYKCVLKNCK 671
Db 538 DVSVPKRVSNVPPKLVILHNNLSLHYVEDIMRMTENLSEKIIIGHGASSTVYKCVSNKR 597
QY 672 PVALKLYSNPOSKOFELEMLSSIKRNLVSLQAYSLSHLGSILFPDYLENSLMD 731
Db 598 PVAVKKLYAHYPOSFKFEFETELEVGSIKHRNLVSLQAYSLSPVGNLLFPDYMENGLMD 657
QY 732 LTH-GPRTKKKTLMDPRLKIAYGAAQGLAYLHDCSPRIIHRDVKSNILLDOLERLT 790
Db 658 VLHEGPKKKKLMERLRIALGAQGLAYLHDCSPRIIHRDVKSNILLDOLERLT 717
QY 791 DFGIAKSLCVSKSHTSYVMGTIGYIDPEYARTSRLTEKSDVYSYGIVLELLTRKAVD 850
Db 718 DFGIAKSLCVSKSHTSYVMGTIGYIDPEYARTSRLTEKSDVYXLMHCSAXADRKASG 777
QY 851 DESNLHLHNSKTGNNEVEMADPDITSTCKDLGVKKVFOALLCTKROPNDRTMHQV 910
Db 778 QRVQSPSXISLSTKANNAMVETVPDIDACTCKDLGEVKKVFOALLCTKROPNDRTMHV 837
QY 911 TRVLSFMSLSEQPPAADTSA---TLAGCYVDEYANLKTTPHVSNGSMS-ASDAQFLR 966
Db 838 VRLVLDCLVRDPPPKSAQOLAMPQRPVPSYINEYVLSRGTSVLSGANSSTSDAELFLK 897
QY 967 FGQVISONSE 976
Db 898 FGEVISONTE 907

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RESULT 7
US-11-027-304-8
; Sequence 8, Application US/11027304
; Publication No. US2005023428A1
; GENERAL INFORMATION:
; APPLICANT: Torii, Keiko U.
; APPLICANT: Shpak, Elena D.
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
; FILE REFERENCE: UMO122663

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; CURRENT APPLICATION NUMBER: US/11/027,304
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/558,529
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
US-11-027-304-8

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Query Match 61.3%; Score 3089.5; DB 6; Length 967;
Best Local Similarity 62.2%; Pred. No. 4e-205;
Matches 605; Conservative 134; Mismatches 211; Indels 23; Gaps 6;

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QY 11 GFLFCULV-----ATVYSEGAATLEIKSKPKVNNVLYDMTSPSSDYCVWRGVSC 63
Db 9 GLFFCLGMVFMVLGVSVMNNEGKALMAIKASFNVANMLDMDDVHNHDFCSMRGVFC 68
QY 64 ENYTFNVVNLNSDLNLDGEISPAIGDKLSLSDIRGNRLSQIPDEIGDCSSLONLD 123
Db 69 DNVSLNVVSLNSLNLMDGELSSGALDMLNLOSIDLQGNKLGQOIPDEIGNCVSLAYVD 128
QY 124 SFNELSGDIPFISIKLQLEQLIKNNQOLIGPIBSTLSQIPMLKLDLAONKLSSEIPRL 183
Db 129 STNLPFGDIPFISIKLQLEQLIKNNQOLIGPIBSTLSQIPMLKLDLAONKLSSEIPRL 188
QY 184 IYMWELQYLGRLGNLVGNISPDLCQTLGMYFDVRNNLSLGSIPETIGNTAQOVLDT 243
Db 189 LYMWELQYLGRLGNLVGNISPDLCQTLGMYFDVRNNLSLGSIPETIGNTAQOVLDT 248
QY 244 SYNQLTGEIPFDIGLOVATLSLQGNOLSGKIPSVIGLMOALAVLDLSGNLSGSIPIPL 303
Db 249 SYNQLTGEIPFDIGLOVATLSLQGNOLSGKIPSVIGLMOALAVLDLSGNLSGSIPIPL 308
QY 304 GNLTFPEKLYHSNKLTSIPPELGNSKLHYLELDNHLGHIPEPLGKLTDFDLVANN 363
Db 309 GNLTFPEKLYHSNKLTSIPPELGNSKLHYLELDNHLGHIPEPLGKLTDFDLVANN 368
QY 364 NNDLEGPIDHLSCTNLNSLVHGNKFSGTIPRAFOKLESMTYLNLSNNIKGPIPEV 423
Db 369 NNDLEGPIDHLSCTNLNSLVHGNKFSGTIPRAFOKLESMTYLNLSNNIKGPIPEV 428
QY 424 SRIGNDITDLSNNKINGIIPSSIGDLEHLKKNLSRNHITGVPGDFGNLRSIMEIDL 483
Db 429 GHIIINDITDLSNNKINGIIPSSIGDLEHLKKNLSRNHITGVPGDFGNLRSIMEIDL 488
QY 484 NNDISGPIPELNQNLIIILRENNLITGVNSLANCLSLTVLNVSHNNLVGDIPIKNN 542
Db 489 NNDISGPIPELNQNLIIILRENNLITGVNSLANCLSLTVLNVSHNNLVGDIPIKNN 548
QY 543 NPSRFPDSFTGNPGICSGWNSPCHDSRRTRVVISRAIIGIAIGLVILMLVLAAC 602
Db 549 NPSRFPDSFTGNPGICSGWNSPCHDSRRTRVVISRAIIGIAIGLVILMLVLAAC 607
QY 603 RPHNPPPELDGSLDKVYVSTPKLVIILHNNMALHYVEDIMRMTENLSEKIIIGHGAS 662
Db 608 RPHNPPPELDGSLDKVYVSTPKLVIILHNNMALHYVEDIMRMTENLSEKIIIGHGAS 665
QY 663 YKCVLNKCKPVVALKRLVSNPOSKOFELEMLSSIKRNLVSLQAYSLSHLGSILFPDY 722
Db 666 YKCVLNKCKPVVALKRLVSNPOSKOFELEMLSSIKRNLVSLQAYSLSHLGSILFPDY 725
QY 723 YLENGSLMDLHGPRTKKKTLMDPRLKIAYGAAQGLAYLHDCSPRIIHRDVKSNILLD 782
Db 726 YLENGSLMDLHGPRTKKKTLMDPRLKIAYGAAQGLAYLHDCSPRIIHRDVKSNILLD 785
QY 783 KDLERLTPRGIAKSLCVSKSHTSYVMGTIGYIDPEYARTSRLTEKSDVYSYGIVLEL 842
Db 786 GNFERLSPFGIAKSLCVSKSHTSYVMGTIGYIDPEYARTSRLTEKSDVYSYGIVLEL 845
QY 843 LTRKKAVIDESNLHLHNSKTGNNEVEMADPDITSTCKDLGVKKVFOALLCTKROPN 902

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125 GNSLTGTLSPDMCQTLGLWYFDIRGNMNLGTIPGICNCTSFELIDISYNQISGEIPYNI 184
257 GFLQVATLSIQNGQSGKIPSVIGLMOALVLDISGULLSGSPILIGNLTFFEKLYLHS 316
185 GYLQVATLSLHRRNLKIPKIPVIGLMOALVLDISENELVGPILPILGNLSYSGKLLHG 244
317 NKLTSIPPELGMSKLAHYLELNDNLHGTGHIPEELGKLTDLFDLVANNDLEGPIDHLS 376
245 NKLGTGHIPEELGMSKLSYQLNDNLVGTIPALGKLTDFELNLANNNLEGHIPANIS 304
377 SCTNLNSLVHGNKFSGTIPRAPOKLESMTYLNLSNNIKGPIPELSRIGNIDTDLNLSN 436
305 SCGALKNFENYGNRLNGSIPAGFOKLESLTYLNLSNFSFGQIPSELGHIVNIDTDLNLSY 364
437 NKLNGIIPSSLGDELHLLKNNLSRNHITGVPGDGLRSLMEIDLSNNIDSGIPBELN 496
365 NEFSGPVPPITGDELHLELNLKNNLTGSVPAEFGMLRSVQVIMSSNNLSGLPELGL 424
497 QLQNIILRLNENNLGTGNV-GSLANCLSLVLANVSHNNL-----VGDIPKNNNFRSPSP 550
425 QLQNLDSLILANNLSLAGEIPQAOLANCFSLVTLAYIQQLMARPIEKLKVPN-----GX 479
551 SFTGNPGLCGSWINSPCHDSRRTRVVISISRAILGIAIGLVILLMVLIAACRPHNPPF 610
480 SFGNLMELHYCCDSSCGSHSGT-KVISRTAVACMLGFIILLCIYLAIFYKT-NQPOL 537
611 LDGSLDKPVTYSPKLYILHMNMAHYEDIMRTENLSKYIIGHASSTYVCYLKNC 670
538 PEKASDKPV-QGPPKIVLQMDMAVHTYEDIMRLTEMLSEKYIIGHASSTYVRCDLKSG 596
671 KPAVKRLVSHYNQSMKOFETELEMSSIKHRNLVSLQAVSLSHLSGLLFPDYLENGSLM 730
597 KAIIVKRLVSHYNQSMKOFETELEMSSIKHRNLVSLHGSLSHGKULLYDYWENGSLM 656
731 DLLHGPTKKKTLDMDTRELKIAVGAQGLAVLHDCSPRIIHRDVKSSNILLDKLEARLT 790
657 DLLHGPTKKKTLDMDTRELKIAVGAQGLAVLHDCSPRIIHRDVKSSNILLDKLEARLT 716
791 DFGIACSLVSKSHSTYVNGTIGYIDPEYARTSRLTEKSDVSYGVLLLELTRCAVD 850
717 DFGIACSLVSKSHSTYVNGTIGYIDPEYARTSRLTEKSDVSYGVLLLELTRCAVD 776
851 DEGNLHLILMSKGTGNNEVEMADPDITSTCKDGVVKKVFOALLCTKROPNDPRTMGOV 910
777 NESENHQLILSKADDDTVMCAVDPEVSVTCTDMVLKAKAFQALCTKRPADRPMTAEV 836
911 TRVLGSFMLEQPPAA-TDTSATLAGSCYVDEYAN-LKTPHSV-----NCSMSASD 960
837 ARVL-----LSLPPAKKPPASKAAASAAAGDYTRFLATAADLRGGVADDDTGDNSSD 892
961 AQLFLRFGOYISONS 975
893 EQWFRFGEVITSKHT 907

RESULT 10
; Sequence 169553, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Roga, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Bing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

```

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169553
; LENGTH: 885
; TYPE: PRN
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(885)
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67963C.1.pep
; US-10-437-963-169553

Query Match      57.9%; Score 2921.5; DB 4; Length 885;
Best Local Similarity 60.1%; Pred. No. 1.6e-193;
Matches 599; Conservative 96; Mismatches 147; Indels 155; Gaps 13;

13 LPCLSLVATVTSSEGAATLEIKKSPFDVNNVLYDWT-TSPSDYCVWRGVSCENVTPNV 71
11 LAAIILAVAAADDDGQTLLEIKKSPFRVNDVLYDMAGDGAPRRYCSWRGVLCNVTPAVA 70
72 ALNLSLNDLDETSIPAIGDKLSLIDKGNRLSGQIPDEIGCCSLQNLDSLFPNELSGD 131
71 AL-----DLKSNELSGQIPDEIGCCTSIKT----- 95
132 IFFSISKLQLEOLILKNNQILPPTLSQIPNLKILDAONKLSGEIPRLIYMEVLQ 191
96 -----LILKNNLVGMITPSTLSQPNLKLIDLAONKLSGEIPRLIYMEVLQ 142
192 YL-----GLRGNLVGNISPDLCQTLGLWYFVDRNNSLTGSIPTIGNCTAFQ 239
143 YLRNLICNVQIYRGLRSNNLEGSLEPMQQLGWY----- 179
240 VDLSTYNQLTGEIPDYGLOVATLSIQNGQSGKIPSVIGLMOALVLDISGULLSGSI 239
180 -LDLSYRNLGEIPFNIQVAVATLSIQNGQSGKIPSVIGLMOALVLDISFNQLSGPI 238
300 PPIIGNLTFFEKYLYHSNKLKTSIPPELGMSKLAHYLELNDNLHGTGHIPEELGKLTDLFD 359
239 PSILGNLTYTEKLYLQGNRLTGSIPPELGMSKLAHY----- 274
360 LNVANNLDEGPIPDHLSCTNLNSLVHGNKFSGTTIPRAFQKLESMTYLNLSNNIKGPI 419
275 LNVANNLDEGPIPDHLSCTNLNSLVHGNKFSGTTIPRAFQKLESMTYLNLSNNIKGPI 310
420 PVELSRIGNLDTLDSNNKINGIIPSSLGDELHLLKNNLSRNHITGVVPDGFNLRSIME 479
311 PIELAKKKNLDTLDSNNVAGIIPSAIGSELHLLRLNFNNMLVGYIPAEFGNLRSIME 370
480 I-----DLSNNDISGPIPEELNOLQNTIILRLNENNLGTGNGLANCLSLVLANVSHN 532
371 IFLLCFSDLSNHLGGLIPQEVGMQLNLILLEBSNNITGVDSLSLNCFSVLNVANVSN 430
533 NLVGDIPKNNNFRSPDSFTGNPGLCGSWINSPCHDSRRTRVVISISRAIILGIAIGLV 592
431 NLAGIVPTDNNFRSPDSFTGNPGLCGSWINSPCHDSRRTRVVISISRAIILGIAIGLV 490
593 ILLMVLIAACRPHNPPFIDGSLDKPVTYS-----TPKLVILHMNMAHYEDIMKMT 646
491 ILLMVLIAACRPHNPPFIDGSLDKPVTYS-----TPKLVILHMNMAHYEDIMKMT 550
647 NLSEKYLIGHASSTYVCYLKCKCKVVAIKRLYSHNPQSMKOFETELEMSSIKHRNLVS 706
551 NLSEKYLIGHASSTYVCYLKCKCKVVAIKRLYSHNPQSMKOFETELEMSSIKHRNLVS 610
707 LQAVSLSHGSLIFDYLENGSLMDLLH-GPTKKKTLDMDTRELKIAVGAQGLAVLHDC 765
611 LQAVSLSHGSLIFDYLENGSLMDLLH-HAGSSKKQKLDHEARIRILGAAQGLAVLHDC 670
766 SPRIIHRDVKSSNILLDKLEARLTDFGIASLVCVSKSHSTYVMGTIGYIDPEYARTSR 825
671 NPRIIXRDVSKNILLDKLEARLTDFGIASLVCVSKSHSTYVMGTIGYIDPEYARTSR 730
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```
QY 826 LTRKSDVYSYGIUVELLETRKKAVDDESNTLHLLIMSTGNNEWMADPDITSTCKDLGY 885
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 731 LNEKSDVYXIMHCEPPGATYQKASXNECNLHLLLSQAADYVEMWDPDIADTCKDLGE 790
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 886 VKKVFQALLCTKRPQNDPRTMHQVTRVLSFMLSEOP-----PAATDSATLAGSCYVD 940
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 791 VKKVFQALLCSKRPQSDRPTMHEVVRVLDCLVYDPDPSPKALPPALPQSTVPS--YVN 848
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 941 EYANLKTPHSVNC-SSMSASDAQFLRFGQYISQNSE 976
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 849 EYVSLRGSTLSCENSSASDAQFLRFGQYISQNSE 885

RESULT 11
US-10-425-114-58448
/ Sequence 58448, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 58448
/ LENGTH: 764
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: UC-ZWFLB73041E04_FLI.pep
US-10-425-114-58448

Query Match 55.3%; Score 2791; DB 4; Length 764;
Best Local Similarity 71.8%; Pred. No. 1,56-184;
Matches 535; Conservative 85; Mismatches 113; Indels 12; Gaps 3;

QY 242 DLSYNQLTGEIPFDIGFLQVATLSLQGNQLSGKIPSYIGMQLAVLDSGNLSGSIIP 301
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 18 DLSYNRTGPIPNIGFLQVATLSLQGNKKTGPISYIGMQLAVLDSYNQLSGSIIP 77
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 302 ILGNLFTTEKLYHSNKLGTSGIPPELGNSKLYLELNDNHLTGHIPPELGKLTDLFDLN 361
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 78 ILGNLFTTEKLYMQGNRLTSGIPPELGNSMTLHYLELNDNQLTSGIPPELGRLTGLFDLN 137
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 362 VANNDEGPIPDHLSCTNLNSLVHGNKPSGTIPRAFOKLESMTYLNLSNNIKGPIPV 421
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 138 LANNHLEGPDPNLSVCVNLNSFNAYGKUNGTIPSLRKLSEMTYLNLSNFTSGSIPI 197
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 422 ELSRIGNLDTLDSNNKINGIIPSSLDLEHLKMLSRNHTGVVGDGFLRSIMEID 481
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 198 ELSRINNLDLDSNNMTGPISSIGNLEHLRLNLSKNDLVGFIPAEFGNLSRVSWEID 257
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 482 LSNNDISGPIPEELNQLNITLLRLENNNTLGNVSLANCLSTVLNVSHNNLVGDI 541
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 258 LSYNHLGLIPQELGMLQNLMLLKLENNNTIGDVSSLMNCFSLNVLNVSYNNLAGAVPTD 317
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 542 NNSRSEPDGFIQNGICGSWLNSPCHDSRTTVVSVSRRAIIGLAIAGVYLLMLVIA 601
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 318 NNFRRFSDHDFLGNPGCGVWLGSSCRSTGRDPRPISKAAIIGVAVAGVLLMLLVAV 377
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 602 CRPNRPPEFDGSDKDVYVSTPKLYILHNMALHVEDIMRMENTSEKTIIGHGASST 661
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 378 CRPHHPAFADATYSKPVSNPFLKYLILHNMALHVEDIMRMENTSEKTIIGHGASST 437
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 662 VYKCVLKNCKRPAIKRLYSHNPQMKOFETELMLSIKHRLNVSLQAYSLSHLSLIFY 721
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
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DB 438 VYKCVLKNCKRPAIKRLYAHYPSQSLKEFETELTVGSIKRLNVSLQYSLSPVGNLLFY 497
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 722 DYLENGSLMDLH-GPTKKKTLMDTRLKTAAGAOLAIYHDCSPRIIHRPVKSSNLT 780
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 498 DYMSGSLMDVLEHSGSKKKKLDWVTRLRALCAQGLAIYHDCSPRIIHRPVKSKNLT 557
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 781 LDLDLEARLDTFGIANSKLVSKSHTSYVNGTIGYIDPEYARTSRLTESKDVSYGIVLL 840
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 558 LDKDYEHLDTDFGIANSKLVSKSHTSYVNGTIGYIDPEYARTSRLTESKDVSYGIVLL 617
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 841 ELTRKKAVDDESNTLHLLIMSTGNNEWMADPDITSTCKDLGYKVFQALLCTKRPQ 900
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 618 ELTGKRPVNECNLHLLLSKTAENEVETVPDVGDTCKDLGEVKKLFGALLCTKRPQ 677
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 901 PNDPRTMHQVTRVLSFMLSEOP-----PAATDSATLAGSCYDEVANLKTPHS 950
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 678 PSDRPTMHEVVRVLDCLVNEPPEPPOQOQKAAHHLQLPQSPRAYVDEYVSLGTGA 737
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 951 VNC-SSMSASDAQFLRFGQYISQNSE 974
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 738 LSCANSSTSDAEFLKFGQYISQNSE 762

RESULT 12
US-10-425-115-262277
/ Sequence 262277, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(5322)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 262277
/ LENGTH: 764
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)-(764)
/ OTHER INFORMATION: unsure at all Xaa locations
/ OTHER INFORMATION: Clone ID: MRT4577_17080C.1.pep
US-10-425-115-262277

Query Match 53.8%; Score 2712; DB 4; Length 764;
Best Local Similarity 70.1%; Pred. No. 4,4e-179;
Matches 522; Conservative 85; Mismatches 126; Indels 12; Gaps 3;

QY 242 DLSYNQLTGEIPFDIGFLQVATLSLQGNQLSGKIPSYIGMQLAVLDSGNLSGSIIP 301
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 18 DLSYNRTGPIPNIGFLQVATLSLQGNKKTGPISYIGMQLAVLDSYNQLSGSIIP 77
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 302 ILGNLFTTEKLYHSNKLGTSGIPPELGNSKLYLELNDNHLTGHIPPELGKLTDLFDLN 361
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 78 ILGNLFTTEKLYMQGNRLTSGIPPELGNSMTLHYLELNDNQLTSGIPPELGRLTGLFDLN 137
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 362 VANNDEGPIPDHLSCTNLNSLVHGNKPSGTIPRAFOKLESMTYLNLSNNIKGPIPV 421
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 138 LANNHLEGPDPNLSVCVNLNSFNAYGKUNGTIPSLRKLSEMTYLNLSNFTSGSIPI 197
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 422 ELSRIGNLDTLDSNNKINGIIPSSLDLEHLKMLSRNHTGVVGDGFLRSIMEID 481
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 198 ELSRINNLDLDSNNMTGPISSIGNLEHLRLNLSKNDLVGFIPAEFGNLSRVSWEID 257
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 482 LSNNDISGPIPEELNQLNITLLRLENNNTLGNVSLANCLSTVLNVSHNNLVGDI 541
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 258 LSYNHLGLIPQELGMLQNLMLLKLENNNTIGDVSSLMNCFSLNVLNVSYNNLAGAVPTD 317
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
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Oy 542 NNFSPSPSPFNGPCLGSMWLSNPOCHDSRRTRVRSIRAAIIGAIAGVILMLVIAA 601
Dy 318 NNFITFSHDSFNGPCLGSMWLSNPOCHDSRRTRVRSIRAAIIGAIAGVILMLVIAV 377
Oy 602 CRPNPPEPLDGSLDKPVTVYTPKVLILHNMALHYVEDIMRMTENLSEKYLIGHGASST 661
Dy 378 CRPHHPAPFKDQATVSKPVVNGPKVLILHNMALHYVEDIMRMTENLSEKYLIGHGASST 437
Oy 662 VYKCVLKNCKPVALIKRLYSHNPQSMKQFETELMELSSITKRNLYSLQAYSLSHLGLLPY 721
Dy 438 VYKCVLKNCKPVALIKRLYSHNPQSMKQFETELMELSSITKRNLYSLQAYSLSHLGLLPY 497
Oy 722 DYLENGSLMDLH-GPTKKKTLDMWTRLRKAYGAAGSLATLHDCSPRIIHRDVKSNIL 780
Dy 498 DYMEGSLMDVHLBEGSSKKOKLDMWTRLRKAYGAAGSLATLHDCSPRIIHRDVKSNIL 557
Oy 781 LDKDLEARLTDEGIAKSLCVSKSHTSTYVWGTIGYIDPEYARTSRLTEKSDVYSYGIVL 840
Dy 558 LDKDLEARLTDEGIAKSLCVSKSHTSTYVWGTIGYIDPEYARTSRLTEKSDVYSYGIVL 617
Oy 841 ELTRKRAVDDESNLHHLIMSKTGNNEVEMADPDITSTCKDYGAVKVFQALALCTKRQ 900
Dy 618 GAADQOASGQRXNLHHLILSKTASNEVETVPDVGDTCKDGEVVKLLQALALCTKRQ 677
Oy 901 PNDRPTMHQVTRVLSGFMLEQPP-----AATDTATLTAAGSCYUVEYANLKTTPHS 950
Dy 678 PSDRPTMHQVTRVLSGFMLEQPP-----AATDTATLTAAGSCYUVEYANLKTTPHS 737
Oy 951 VNC-SSMSASDAQFLRFGQVISON 974
Dy 738 LSCANSSSTDABELFLKFGSAISON 762

RESULT 13
US-10-437-963-121441
; Sequence 121441, Application US/10437963
; Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437, 963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 121441
LENGTH: 962
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(962)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_24466C.1.pcp
US-10-437-963-121441

```

Query Match	49.3%	Score 2484.5	DB 4	Length 962
Best Local Similarity	53.0%	Pred. No. 3.5e-163		
Matches 528; Conservative	140;	Mismatches 19c;	Indels 133;	Gaps 18;

QY	26	EGATLLEIKKFKVNNVNYLYDMTSSPSDDYCWMRGSCSENYTFNVVA	-----	73
Db	35	EGKALMGVKAFGFGNAANALVDM--DGGADHDCAMRCVTLCDNASFALATSLDISAILEFVM		92

[illegible]

```

RESULT 14
US-10-425-114-45783
; Sequence 45783, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingsong
; APPLICANT: Zhou, Yinhua
; APPLICANT: Kovacic, David K.

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APPLICANT: Screen, Steven E
APPLICANT: Tabaka, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 73128
SEQ. ID NO: 45783
LENGTH: 578
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700954473_FLI.pep
US-10-425-114-45783

Query Match 47.3%; Score 2384.5; DB 4; Length 578;
Best Local Similarity 78.4%; Pred. No. 1.5e-156;
Matches 455; Conservative 53; Mismatches 63; Indels 9; Gaps 2;

QY 404 SMYLNSSNNKIPVEISRGINDTLDSNNKINGIIPSSIGDEHLKNNLSNHI 463
1 SMTSLNLSNNLQGAIPDIELSRIGNLDTLDIINNVLGSIPLSSIGDEHLKNNLSNHI 60
QY 464 TGVVPGDFGNLSIMEIDLSNNDISGIPPELNQONIIILRLNENNLGTGVSILANCLS 523
61 TGIIPAFGNLRSMEIDLSNNOISGLIPBELSQLOMMISIRLENNKLTGDDVASLSICIS 120
QY 524 LTVLVNHNVLVDIPKNNNFSRSPDSFGNPGGLCGSWLNSPCHDSRRVVSISPAAI 583
121 LSLVLNYSNKLFGVPTSNFTPRPPDSFGNPGGLCGSWLNLPCHGAPSERVTLSSKAI 180
QY 584 LGALIGLVLLMWLIAACRPHNPBPLDGLDKPVYVSTPKVILMMNALHYVEDIMR 643
181 LGITLGLVLLMWLIAACRPHSPSPDPSFDPKVPNVPSPKVLILMMNALHYVEDIMR 240
QY 644 MTELSKTYIIHGASSTVYKCVLKNCKPVAIKLYHNPOSMKQFETELMLSSIGHRN 703
241 MTELSKTYIIHGASSTVYKCVLKNCKPVAIKLYHNPOSMKQFETELMLSSIGHRN 300
QY 704 LVSLQAVSLHSGSLFYDYLENGSLMDLHGPTKKKTLMDTRKLIAYGAQGLAYLHH 763
301 LVSLQAVSLHSGSLFYDYLENGSLMDLHGPTKKKTLMDTRKLIAYGAQGLAYLHH 360
QY 764 DCCPRIIHRVKSNNILLDDLEARLDPFGIAKSLCVSKSHTSYVNGGTGYIDPEYART 823
361 DCCPRIIHRVKSNNILLDDLEARLDPFGIAKSLCVSKSHTSYVNGGTGYIDPEYART 420
QY 824 SRLTEKSDVSYGIVLELTLRRKAVDDESNLHILMSKTGNNEVEMADPDITSTCKDL 883
421 SRLTEKSDVSYGIVLELTLRRKAVDDESNLHILMSKTGNNEVEMADPDITSTCKDL 480
QY 884 GVVKKVQALALLCTKROPNDPRTMHQVTRVLGSPMLSEOP-----PAATDTSATLAGS 936
481 GAVKKVQALALLCTKROPNDPRTMHQVTRVLGSPMLSEOP-----PAATDTSATLAGS 538
QY 937 CYVDEVANLKTSPHVSNCSSMSASDAOLFIRGOVISONSE 976
539 CYVDEVANLKTSPHVSNCSSMSASDAOLFIRGOVISONSE 578

RESULT 15
US-11-027-304-87
Sequence 87, Application US/11027304
Publication No. US20050223428A1
GENERAL INFORMATION:
APPLICANT: Torii, Keiko U.
APPLICANT: Shpak, Elena D.
TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
FILE REFERENCE: UMO0122663
CURRENT APPLICATION NUMBER: US/11/027,304
CURRENT FILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: US 60/558,529
PRIOR FILING DATE: 2004-04-01
NUMBER OF SEQ. ID NOS: 88
SOFTWARE: PatentIn version 3.2
SEQ. ID NO: 87
LENGTH: 611
TYPE: PRT
ORGANISM: Oryza Sativa
US-11-027-304-87

Query Match 46.1%; Score 2322.5; DB 6; Length 611;
Best Local Similarity 73.4%; Pred. No. 3.3e-152;
Matches 442; Conservative 63; Mismatches 94; Indels 3; Gaps 1;

QY 13 LFCLSIVATVTSSEGAATLEIKKSPKDVNNVLYDWTTPSSPSDYCVARGVSCENVTEVVA 72
13 LVALLVAVAVADGSLTLEIKKSPKDVNNVLYDWTTPSSPSDYCVARGVSCENVTEVVA 69
QY 73 LNLSDNLDEISPAIGDLKSLISIDLRGNLSGQIPDEIGDCSSLQNLDSFNLSGDI 132
70 LNLSDNLDEISPAIGDLKSLISIDLRGNLSGQIPDEIGDCSSLQNLDSFNLSGDI 129
QY 133 PESTSKLQLEBOLILKQNLGIPSTLSQIPMLKTLDLAONKLSGEIPRLIYMNVLQY 192
130 PESTSKLQLEBOLILKQNLGIPSTLSQIPMLKTLDLAONKLSGEIPRLIYMNVLQY 189
QY 193 LGRGNLVGNISPDLCQTLGTLVYFVRNNSLTGSIIPETIGNCTARQVLDLSYNQLTGEI 252
190 LGRGNLVGNISPDLCQTLGTLVYFVRNNSLTGSIIPETIGNCTARQVLDLSYNQLTGEI 249
QY 253 PEDIGLOVATSLSQNLQSGKIPSVIYGLMOALAVLDLSGNLSGSIIPILGNLTTEKL 312
250 PEDIGLOVATSLSQNLQSGKIPSVIYGLMOALAVLDLSGNLSGSIIPILGNLTTEKL 309
QY 313 YHSNKLGTGIPPELGNMSKLYLELNDNHLTGHIPELGLKTLDPDLVANNDLGPIR 372
310 YHSNKLGTGIPPELGNMSKLYLELNDNHLTGHIPELGLKTLDPDLVANNDLGPIR 369
QY 373 DHTSSCTNLNSLVHGNKFSGTIPRAFOKLESMTYVNLSSNNIKGPIPELSRIGNLDTL 432
370 DHTSSCTNLNSLVHGNKFSGTIPRAFOKLESMTYVNLSSNNIKGPIPELSRIGNLDTL 429
QY 433 DLSNNKINGIIPSSIGDEHLKNNLSRNHITGVVPGDFGNLRSIMEIDLSNNDISGPIR 492
430 DLSNNKINGIIPSSIGDEHLKNNLSRNHITGVVPGDFGNLRSIMEIDLSNNDISGPIR 489
QY 493 BELNOLNIIILRLNENNLGTGVSILANCLSLTVLVNHNVLVDIPKNNNFSRSPDSF 552
490 BELNOLNIIILRLNENNLGTGVSILANCLSLTVLVNHNVLVDIPKNNNFSRSPDSF 549
QY 553 IGNPGCGSWLNSPCHDSRRVVSISRAAILGIALGVLILMVLIACRPHNPPEFLD 612
550 IGNPGCGSWLNSPCHDSRRVVSISRAAILGIALGVLILMVLIACRPHNPPEFLD 609
QY 613 GS 614
610 VS 611

Search completed: September 2, 2006, 07:01:06
Job time : 190 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 2, 2006, 06:56:20 ; Search time 51 Seconds

(without alignments)
1675.096 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043

Sequence: 1 MALFRIVLLGFPLCLSLVA.....SASDAQPLRFQGVISQNSE 976

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /EMC Celerra SIDS3/prodata/2/iaa/5 COMB.pep:*

2: /EMC Celerra SIDS3/prodata/2/iaa/6 COMB.pep:*

3: /EMC Celerra SIDS3/prodata/2/iaa/7 COMB.pep:*

4: /EMC Celerra SIDS3/prodata/2/iaa/H COMB.pep:*

5: /EMC Celerra SIDS3/prodata/2/iaa/PCTUS COMB.pep:*

6: /EMC Celerra SIDS3/prodata/2/iaa/RE COMB.pep:*

7: /EMC Celerra SIDS3/prodata/2/iaa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1568	31.1	502	2	US-10-101-464A-945
2	1432.5	28.4	998	2	US-10-101-464A-931
3	1404.5	27.9	998	2	US-10-101-464A-895
4	1393.5	27.6	370	2	US-10-101-464A-944
5	1384.5	27.5	1021	2	US-10-101-464A-954
6	1360.5	27.0	990	2	US-10-101-464A-814
7	1355	26.9	984	2	US-10-101-464A-919
8	1341.5	26.6	996	2	US-10-101-464A-889
9	1341.5	26.6	996	2	US-10-101-464A-933
10	1305	25.9	998	2	US-10-101-464A-914
11	1300.5	25.8	980	1	US-08-473-553A-6
12	1293.5	25.6	985	1	US-08-473-553A-2
13	1293	25.6	999	1	US-08-473-553A-5
14	1275	25.3	1166	2	US-10-101-464A-900
15	1264.5	25.1	974	2	US-10-101-464A-921
16	1242	24.6	1133	2	US-10-101-464A-809
17	1227.5	24.3	1196	2	US-08-881-706-2
18	1227.5	24.3	1196	2	US-09-823-394-2
19	1206	23.9	919	2	US-10-101-464A-642
20	1140.5	22.6	910	2	US-09-228-986-72
21	1140.5	22.6	910	2	US-10-101-464A-72
22	1136.5	22.5	947	2	US-09-228-986-73
23	1136.5	22.5	947	2	US-10-101-464A-73
24	1133	22.5	1025	1	US-08-567-375-4
25	1133	22.5	1025	1	US-08-587-680A-4
26	1133	22.5	1026	2	US-09-623-551-18

27	1112.5	22.1	1012	1	US-08-475-891A-4	Sequence 4, Appl
28	1035.5	20.5	864	2	US-10-101-464A-896	Sequence 896, App
29	999	19.8	968	2	US-09-228-986-76	Sequence 76, Appl
30	999	19.8	968	2	US-10-101-464A-76	Sequence 76, Appl
31	960.5	19.0	1112	2	US-09-353-585-3	Sequence 3, Appl
32	959.5	19.0	1112	2	US-09-353-585-2	Sequence 2, Appl
33	939	18.6	968	2	US-09-180-439-3	Sequence 4, Appl
34	937	18.6	968	2	US-09-180-439-3	Sequence 3, Appl
35	933	18.5	1016	2	US-09-180-439-8	Sequence 8, Appl
36	904	17.9	697	2	US-10-101-464A-940	Sequence 940, App
37	878	17.4	1023	1	US-08-475-891A-2	Sequence 2, Appl
38	878	17.4	1023	1	US-08-567-375-2	Sequence 2, Appl
39	878	17.4	1023	1	US-08-587-680A-2	Sequence 2, Appl
40	869.5	17.2	843	2	US-10-101-464A-893	Sequence 893, App
41	842	16.7	705	2	US-10-101-464A-894	Sequence 894, App
42	823.5	16.3	828	2	US-10-101-464A-934	Sequence 934, App
43	822	16.3	692	2	US-10-101-464A-897	Sequence 897, App
44	817.5	16.2	799	2	US-09-180-439-6	Sequence 6, Appl
45	811.5	16.1	804	2	US-10-101-464A-890	Sequence 890, App

ALIGNMENTS

RESULT 1

US-10-101-464A-945

Sequence 945, Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.102002

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 945

LENGTH: 502

TYPE: PRT

ORGANISM: Pinus radiata

US-10-101-464A-945

Query Match

31.1%; Score 1568; DB 2; Length 502;

Best Local Similarity 62.0%; Pred. No. 1.3e-113;

Matches 310; Conservative 75; Mismatches 107; Indels 8; Gaps 6;

481 DISNDISGIPBELNOLNIIILRLNNLIGNV.GSLANCISLVLVSHNNLVGDIP 539

3 DISANDLSGIPBELNOLNIIILRLNNLIGNV.GSLANCISLVLVSHNNLVGDIP 62

540 KNNRPFPSDSTIGNPGCGSWLNSPCDHSRTVAVSIRAIILGAIAGVILMLVLI 599

63 VTQNFRTFTESEFFGNPGGLGVIWISLGCISAOAPASVSTTAVICISLASVILVCVITI 122

600 AACRPHNPPEFLDGLDKPVTSTPKLVILHNMALHVEDIMRMTENISEKTIIGGAS 659

123 ALVLSQHKRFTTGSSSK-TGQSSPRLVILHNMALYMDIMRMTENISEKTIIGGAT 181

660 STYKCVLKNCKRPAIKRLYSHNPGSKQFTELEMLSTIKRNLVSLQAYSLSHGSL 719

182 STYKCVLKNCKRPAIKRLYSHNPGSKQFTELEMLSTIKRNLVSLQAYSLSHGSL 241

QY	720	FVYVLENGSLWDLHPETKTKTLLMDPTRTKIAVYGAAGLAIYHHDCSPRIITHRQVKSNI	779
Db	242	FVYVWNGSLMDLHSSSKKIKLMDMTKRIKLGAAQGLAIYHHDCNRIITHRQVKSNI	301
QY	780	LDDKDLEARLTDEGIAKSLDVSCKSHSTIYVMGTIGYIDPEYARTSLTEKSDVYSYGIVL	838
Db	302	LDDNDEAHLSDEGIACKIPSAKTHASTIYVMGTIGYIDPEYARTSLTEKSDVYSYGIVL	361
QY	840	LELTTERKANDESNLHHLIMSKTGNNEMEAADDISTCKDGLVYKVVQALLCTKR	899
Db	362	LELTGKRPVNDNSNHLHQLILSGADNMNMEVDEPVATCIDETAKTITQLALLCTKR	421
QY	900	QPNDRPTMQVTVTLGSGFM-LSEQPPAATDTSATLAGSC--VYDEY--ANLKTPHSVNC	954
Db	422	QPNDRPTMPDVAVQLSLPFSKQAPSRSRVNQPAASNNYRRYLDEYTGHRNDRVGSSTS	481
QY	955	SMASDAQFLFRGQVYISQN	974
Db	482	S-STSDQGLFVRGVEISQN	500

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RESULT 2
US-10-101-464A-931
Sequence 931, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 931
LENGTH: 998
TYPE: prt
ORGANISM: Pinus radiata
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(998)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-101-464A-931

```

Query Match	28.4%;	Score 1432.5;	DB 2;	Length 998;
Best Local Similarity	36.5%;	Pred. No. 1.3e-102;		
Matches 361;	Conservative 157;	Mismatches 374;	Indels 97;	Gaps 19;

Qy	10	UGFLFCLSLVATVYS-----EEBATLLEIKKSRDNNVNVLDYTTSSSDPYCYWRGVS	62
	7	LHFLF-FCFVLTVRSCFAIRGMQDDELIQELKRGDDPSGAERNNENNDSN- CWMGTGT	64
Db	63	CENATFNVALNLSPLNDGEISPAIDGLKSLSLDLRGNRLSGQIPDEIGCSSLQNIID	122
Qy	65	CDAGEKFEVEEDLSKNIIGPPPTVYCRIDGLAKSLANNYNGSIIPAGLRCHGLEFLVD	124
Db	123	LSFNELSGDIPIFSISKLEQLEILKNNQLIGPIPSTLSQIPNLKILDLAQNKLSGEIIPR	182
Qy	125	LSQULIIGGLDFISELFRKLKHLDSGNNLSSGPVPAPGRPLPELVNLVSNLMTTPIIP	184
Db	183	LIYNNEVLYIQLRGNNLVGNISPLCOQTGLMYDVRNNSLTGSIPEPTIGACTPAFOYLD	242
Qy	185	FCVGLPNILOQNLNANPLTGVTPPELIGLKKQLQNLMLAGCNLVGSIPEPLTGLNLSLTIIND	244

QY	243	LSVNOITGSIIPDIEGL-QVATLSIQGNQISGKTPSVIGLMQALAVLDSGNLLSGSIPP	304
Db	245	LSNKRISGSGIPESITKLDKVOIETLYQNLLSGPIPVAMGELKALKRPDASNNMLDGSIPA	304
QY	302	ILGNLTFETKELYHSNKLGSIPPELGMMSKLHYLELDNHLTGHIPEPELGLTDLFDLNL	361
Db	305	GLGSILNL-ESLNDYQNNLVGEIIPPELGSFTSLKELKFPNSNLTSLSLENIGRNSDILLALD	363
QY	362	VA-----NNDEGGPIPDHLSCTTNINSLNHGKFRSGTTPR	397
Db	364	IAONLISGRLPDLCCKKKLEILISIFNNELGQNPESIGTCTISINRVALGKNGKNGSVPS	423
QY	398	APQKL-----ESMTYLNLSNNIKKPIVELSRIGNDTLTD	433
Db	424	LEFGLRHVSULLEIKONVEFGFISPIDIAKAKSLKLVISGNIPSGSLPETSLENNLSSETI	483
QY	434	LSNNKINGIIPSGISGLDEHLKMNLSRHHITGVVPGDFGNLSIMEIDLSNNDISGPIPE	493
Db	484	ASNMLITGALPSLGLQLGLGLDLSNNQLSGELPAELISSCKQGEINLSNQQLSGSIPA	543
QY	494	ELNQONIIILRLNENNLTVNGVNSLANCLSLTVLVNSHNLVGDIP--KNNFSRSPSD	550
Db	544	SVGTLPLVNLVLDSDNLTLGPPIPESELGNKLKNTPEVDSNRLSGAVPLAFENPYEK----	599
QY	551	SFTGNQGLCG--SWANSRPHDSRRIVRVRISIRAAITLGAIGVILMLVLLAORPHNPP	608
Db	600	SFLGNELSCSREAFNGTSCSEVRESEKAKRQRMWMLRLCLPALSIIILFVLGLAFYRRYR	659
QY	609	PFLDGLDPVTYVSTPKVLILHMNNAUVYEDIMRMTENLSEKYLIGHGASSTYYKCVLK	668
Db	660	NFANAERKKSVDKSSMLTSFPH-RIGPSEYE----ILDCLDEBDVIGSGAGKYYKATLS	714
QY	669	NCKRPVALIKRLYSH--NPSMKOFETELBMLSSIKRNLVSLQAYLSLHGSLLPDYULE	725
Db	715	NGELVAIKRLMSNGKTNASTDNGFOAEVDLGIKRNKVIIVLMOCCSKSDSNLLVYEMP	774
QY	726	NGSLMULLHGPTKKYKKTLDWDTRKLAAYGAAGGLAYLHNDSPKRIINRDYVSSNILLDKDL	785
Db	775	NGSLGDLRHP-KASVLDMPRIYKKTALAAAGGLAYLHNGCVPSIVNHDVSSNNLLDEDY	833
QY	786	EALTLDPFGIAKSL--CVSKSHTSYVMGTIGYIDPEYARTSLREKSDVSYGVLIELL	843
Db	834	GAIVADPFGVAKFLQSGSGADSMYLAASGYCIAEYATLKVNKEKDYSFGVILIELV	893
QY	844	TREKAVDDESN-----LHHLINSKTGNNEVEMADPDITSTCKDLGVVKKVFOALL	895
Db	894	TGRAPVDPERGENKDLVKWLCKNKIETKGNLNEVL--DPKLVDFCKE--EWTVMWKGLL	948
QY	896	CTKRQPNDRPTMQOIVRVULGSFMLSQOPR	924
Db	949	CTSVLPRLINRPSMRVVE-----MOEANP	972

RESULT 3
US-10-101-464A-895
Sequence 895, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OR INVENTION: Compositions Isolated from Plant Cells
TITLE OR INVENTION: and their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724
 PRIOR FILING DATE: 2000-01-11
 NUMBER OF SEQ ID NOS: 989
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 895
 LENGTH: 998
 TYPE: PRT
 ORGANISM: Pinus radiata
 US-10-101-464A-895

Query Match 27.9%; Score 1404.5; DB 2; Length 998;
 Best Local Similarity 36.0%; Pred. No. 1.9e-100;
 Matches 347; Conservative 168; Mismatches 362; Indels 87; Gaps 24;

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12 FLFCL-----SLVATVTSSEGC--ATLEIKKSPFDVNNVYDMTSSPSDYCWRG 60
11 FICFIFSMALVDFGVAVPAQQTQIQLIRKMEALDPFNALRWDGSDSE--CWRG 69
61 VSGENVTFNVVALNLSDNLDEISPAIGDKLSLIDLRGNLSGQIPPEIGDCSSLON 120
70 IDC-NDEGAVTRIQHSSLSIGRLPDICNLQSLIIFELDRNSLYGNPFPEFSCRL 128
121 LDLSFNLSDGIPPSISIKLQLEOLIKNNQIGPISTSQIPNLKILDLOAKLSGE- 179
129 LNLSSNLNGSLP-DLSKTKALKYLDLSNNRFSGEFVSQNLNLSLSLGIIMFNRRT 187
180 IPELIVNEVLYQYLGKGNLNGISPDLCQLTGLWTFVDRNNSLTGSIPTGNCATFQ 239
188 IPELWMLTRLSWLYLTCNCFYSGIPASLSNLSELGNLEISMMDLTIRIPELGS 247
240 VLDLSYNQLTGEIIPFDIGPL-QVATLTSLQGNQSGKIPSYIGMQLAVLDLSGN 298
248 QLELFSLNLSEIPELGNLTSLRDPASRNSLCGRIPAPFGKLERHFIQVYQNL 307
299 IPELGNLTETKLYHSNKLTGSIPELGNMSKLYLELNDHLTGHIPPEL--GKLT 355
308 IPEGFGLKMLIGISWQNYLTGPIPKLGSVSEFNMI DVSQNMLSGPLEPDLCSG 367
356 DLFEDLVANNDDGPIPDHLSSTCNLSLWVHGKFPSCGTIPRAFOKLESTMYL 415
368 YIL--VLDNEFTGQIPESYGNCKSMRFRSKYKLTGRIPRGIEWEPHYSILDS 424
416 KGPVPELSRIGNLDLTDLNNKINGIIPSLGDLLEHLKMLNLSRNHITGVDP 475
425 EGEIAPRIGARNLSLEYIQNGSSGLPRAIEGASOLIKIDVSGNLTGAVSEIK 484
476 SIWEIDISNDISGPIPEELNOLNIIILRLNENNLGVN--GSLANCLSLTVL 534
485 LLSLSLQENNLSPGIPAQIGCHKFSLSIMLAYNELTGPIPGSLGFWEVLSNL 544
535 VGDIPL-----KNNNFSRFS-----PDSFIGNPGLCGSMWLN--PCHDS 570
545 SGEIPNTLAALKLSSVFSRNSLTGPVPIELISQTNRSFSGNPGLOGGLESIQ 604
571 RRTAVRVSISPAALIGIAGLV--ILLMTVLIACRPHNPPLDGLDRPVYSTK 627
605 TRDY--YGRWITGAVSGVTFFTLIGMLIRGCRLLH---RDSKKNANRTFWE 655
628 ILHNNALHAYE-DIMKMTENLSEKYLIGHASSTYKCVLKCKCPAIVKRLYS--H 681
656 -----SFHLNPFDEHVESMDEHIIIGGSGSTVRIQLDSNESAVAVKMLCK 709
682 NPGSM--KQETELMNLSSIKRNLVSLQAVSLSHLSLLFYDYLENGSLMDLHG 739
710 GGQGLINRELKAEVETLGTIRHRNIVKLYCFNSGNDNMMLVEYEMPGNLMES 769
740 KTLIDMDTRLKIAYGAAGLAVLHHDGSPRIIHRDVKSNLILDLDDARLTFD 798
770 ASDMPTRYKIALGVANGLAVLHMDCPGIIHRVKSNTIILDBENQARVADGFA 829
799 CVSKSHTSYVMGTIGYIDPEYARTSRLEKSDVSYGYVLELLELTKRKAVD 854
830 ACPRGDSVAITGTHGYIAPEYAVSSVTEKSDIYSGVVLLELTGRPVEAF 889

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QY 855 ----LHLIMSKTGNNEVMADPDITSTCKDGVYKVFOLALCTKRPNDPTMHQV 910
DB 890 IYWMISRKILTRGAREVL---DYRIYLYKQEMI--QALKIAVRTSKLPNVRPS 944
QY 911 TRVL 914
DB 945 VQML 948

```

RESULT 4
 US-10-101-464A-944
 Sequence 944, Application US/10101464A
 Patent No. 6768041
 GENERAL INFORMATION:
 APPLICANT: Strabala, Timothy
 APPLICANT: Nieuwenhuizen, Nicolaas
 APPLICANT: Higgins, Colleen M.
 TITLE OF INVENTION: Compositions Isolated from Plant Cells
 TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
 FILE REFERENCE: 11000.1020c2
 CURRENT APPLICATION NUMBER: US/10/101,464A
 CURRENT FILING DATE: 2002-03-18
 PRIOR APPLICATION NUMBER: 09/704,302
 PRIOR FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: 09/228,986
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/162,866
 PRIOR FILING DATE: 1999-11-01
 PRIOR APPLICATION NUMBER: PCT/US00/00724
 PRIOR FILING DATE: 2000-01-11
 NUMBER OF SEQ ID NOS: 989
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 944
 LENGTH: 370
 TYPE: PRT
 ORGANISM: Pinus radiata
 US-10-101-464A-944

Query Match 27.6%; Score 1393.5; DB 2; Length 370;
 Best Local Similarity 76.7%; Pred. No. 3.2e-100;
 Matches 270; Conservative 39; Mismatches 42; Indels 1; Gaps 1;

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QY 9 LGFLFCLSLVATVTSSEGCATLEIKKSPFDVNNVYDMTSSPSDYCWRGVCENT 68
DB 20 LVTFLYFGLLSAV--SDDGNTILATKKSFRSDNVLYNMIDSASHSCMRGTC 78
QY 69 NVVALNLSIDNLDEISPAIGDKLSLIDLRGNLSGQIPPEIGDCSSLONLDSF 128
DB 79 AVVALNLSHNLGGEISPIYGNKLSLESIDKNGNLSGQIPPEIGDCSALKIDV 138
QY 129 SGDIPPSISIKLQLEOLIKNNQIGPISTSQIPNLKILDLOAKLSGEIPL 188
DB 139 YGDIPEISIKLQLEOLIVANNQIMGPISLTSQLPKMFPADNQLSGEIPRL 198
QY 189 VLOYLDRGNLVGNISPDLCQLTGLWTFVDRNNSLTGSIPTGNCATFOV 248
DB 199 VLOYLDRGNLVGNISPDLCQLTGLWTFVDRNNSLTGSIPTGNCATFOV 258
QY 249 TGEIIPNIGFLOVATISLQGNQSGKIPVIGIMQALAVLDLSGNLSGSIPI 308
DB 259 TGEIIPNIGFLOVATISLQGNQSGKIPVIGIMQALAVLDLSGNLSGSIPI 318
QY 309 TEKLYHSNKLTGSIPELGNMSKLYLELNDHLTGHIPPELGLKTLDFDL 360
DB 319 TDKLYHSNKLTGSIPELGNMTKLGYLQINDNQLTGQIPPELGNLEOLFEL 370

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RESULT 5
 US-10-101-464A-954
 Sequence 954, Application US/10101464A
 Patent No. 6768041
 GENERAL INFORMATION:

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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101.464A
PRIOR FILING DATE: 2002-03-18
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 954
LENGTH: 1021
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-101-464A-954
```

Query Match 27.5%; Score 1384.5; DB 2; Length 1021;
Best Local Similarity 34.6%; Pred. No. 7.3e-99;
Matches 348; Conservative 170; Mismatches 368; Indels 119; Gaps 22;

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3 LFRIVVLGLFCLSL-----VATVSEGATLLEIKSKFK-DVNVVLYDWTSS-- 52
1 MMRFFLLLLLLHLHRRGAASAAPRRLTEPLALSLRAVTDPOSSALSWTSAAN 60
53 -SDCVARVSCENVTFVVALNLSIDNLDEISPAICDLKSLSIDLRGRLSGOIPDE 111
61 GSSHSQGVTCDAARRHVHTALDLSLELAALBPVVAHRLFLSLVAANQSLGPIPPQ 120
112 IGDCSSQONLDLSNEISGDIPIFSISKQLEQILKNNQILGPIPTSLQIPNKLIDL 171
121 ISALAAARYLNLNNVFNNGTFRPRLGLRLNRVLDLYNNMTGDLPVAVAMPPQLRLHL 180
172 AONLSEIRPLIYWNVLOVYLGKGNLVGNISPDLCQLTG-----LWYDVANNSLTG 226
181 GGNFGRIRPEYGRMEFTEYLAWSGDLTAIPPEIGNLTTRELYGYV---NSYDG 236
227 SIPTIGNCTAFQVLDLSYNQLTGEIPEDIGLQ-VATLSQGNQSLGKIPSVIGLMAQL 285
237 SLPEIENLSQLVRLDAASGCLSGEIPPEIAKQNLDTLFLQVNGFPGSLPAEIGYINSL 296
286 AVLDLSGNLSSGIPPLIGNLTFTEKLYLHSNKL-----TG 321
297 KSLDLSNNMFAGEIPESFSQLKNLTLLHLFRNKINGESPFIADLPLOVQLWENNFTG 356
322 SIPELGNMSTKLHLELNDNLHTGHIPELGLKLDLPDLVANNNDLGGPIPDHSSCTNL 381
357 SIPEGLGNKNGHLQIVDSSNKLTTGLTPDLCYNQLOLILASLYLIGPIRESIGKRSLL 416
382 NSLWVHGNKSGTIPRAFQKLESMTYLNLSNNIKGPIPELSRIG-NLDTLDSNNKIN 440
417 ERIMGNVYNGSLPRGLFGLPELNQVEFQDNLLVGEFPVSDSIALTKLQITLNNKLG 476
441 GIIPSSIGDLEHLKMLSRNHTIGVVGDFGNLRISMEIDLNNDSIGPIPELANO--- 497
477 GSLEPTIGNSGVOKLLLDGNNSFGOIPPEIGRLQOLAKIDPSSNRYSGPIPAOISOCKL 536
498 -----LQNIILLRENNNLTVGNV-GSLANCLSLTYLVANSHNNLY 535
537 LTFPDLSCNELSGEIPPEITGMRLINLYLNLSNLSGSIPIPSISTMOSLTSVDPSYNNLS 596
536 GDIPKNNFSRFSDFEIGNPGLCGSWLNSPCHDSRRF-----VRVSIIRAAILG 585
597 GLVGTGQGFVFNYSFLGNPELGPYL-GPCXKGEMTGIMQAHVKGPLASVALLVIG 655
586 IATGGVILLMVLIAACRPHNPPEPLDGLDKPVYTSIPKL-VILHNMALHVEDIMRM 644
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656 LVCSSIFALVAITKA-----RSLKKASDARAWFSAFORLDFSC---EDVL-- 699
645 TENSEKYYIIIGHASSTVYKCVLKNCKPVAIKRL-----YSHNPSMKQFETELEWLS 698
700 -DSLKENITIGKGCAGIVYSGMNGDHAVAKLPLVMGRSSSID---HGFNAIEIQLGK 754
699 IKRNLVSLQAVSLSHLSGLLFPYDLENGSLMDLHGPTKKTLMDWTRLKIAVGAAGL 758
755 IRRHRIYRLGFCPSNHEHTNLVVEYMPNGSLGEVLHG-KKGHLLINSVRYKIALBAKGL 813
759 AYIHHDCSPRIIRRDVSSNILLDKLEAPLTPGIAKSLCVS-KSHTSYVWGTIGYID 817
814 CYLHHDCSPRIIRRDVSSNILLDSDFEAVADFGIAKFLQDSGASGSAIAGSYGYIA 873
818 PEYATRLTEKSDVYSYGVLELLELTRKAVDDESNLHLLI-----MSKTNNEVWEMA 872
874 PEYATRLTEKSDVYSYGVLELLELTRKAVDDESNLHLLI-----MSKTNNEVWEMA 933
873 DPDITSTCKDLGVVKKVQFQALLCTKRQPNDRPTMHQYTRVLGSF 917
934 DPRINTV--PLHEAMHLFYVAMLVEEQAVERRPTMEVQILTEF 976
```

RESULT 6
US-10-101-464A-814
Sequence 814, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101.464A
PRIOR FILING DATE: 2002-03-18
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 814
LENGTH: 990
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-101-464A-814

Query Match 27.0%; Score 1360.5; DB 2; Length 990;
Best Local Similarity 33.3%; Pred. No. 5.2e-97;
Matches 336; Conservative 178; Mismatches 397; Indels 97; Gaps 19;

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7 IVLLGFLFCLSLVATVTS-BEGATLLEIKKSFQDVNNVLYDWTSSSDYCVARVSCEN 65
6 IVLGVULLCTVIRGSSSSVSDVDVLLAKGFPSPERALLTWSSSSSVCLWYGRCSR 65
66 VTFNVVALNLSIDNLDEISPAICDLKSLSIDLRGRLSGOIPDEIGDCSSQONLDLSF 125
66 --GRVSVLELTLDINTLGGSVPLVSRLSHLSIVELSLAGNPFSGTI--VIANLSIKFLINISN 121
126 NELSGDIPFSISKQLEQILKNNQILGPIPTSLQIPNKLIDLDAONLTSGEIRPLIY 185
122 NLFSGSLDMWYSSIANLKVFDAVDNNFTGLLPTGVLDLKKIRYLSLGGNYFGGEIPKSYG 191
186 MNEVLYLGLRGNNLVGNISPDLCQLT-----GLAWYFDVR 220
182 ELAALEYLSVAGNGLNKPLPSELGNLTLEIREIYLVGYVNFEEGIPREFGSLINLVHMDLS 241
```


QY 835 YGIVLELLTRKAVDESN-----LHLMSTKGNNEVMEMADPITSTCKDL-GV 885
 Db 874 YGVVLMEMLSGKRSVDREFGSGNSVDWVRKIKSGKIGIRVL---DKNGASCAPVREE 930
 QY 886 YKVVFOALLCTKQCPDRPTMHQVTRVLSFMLSQPP 924
 Db 931 MLELLRVALLCTAASPADRPMSRDV-----LMLQEARP 964

RESULT 8

US-10-101-464A-889
 ; Sequence 889, Application US/10101464A
 ; Patent No. 6768041
 ; GENERAL INFORMATION:
 ; APPLICANT: Strabala, Timothy
 ; APPLICANT: Nieuwenhuizen, Nicolaas
 ; APPLICANT: Higgins, Colleen M.
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells
 ; FILE REFERENCE: 11000.1020C2
 ; CURRENT APPLICATION NUMBER: US/10/101,464A
 ; PRIOR FILING DATE: 2002-03-18
 ; PRIOR APPLICATION NUMBER: 09/704,302
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/228,986
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/162,866
 ; PRIOR FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/00724
 ; NUMBER OF SEQ ID NOS: 989
 ; SOFTWARE: FaSeq for Windows Version 4.0
 ; SEQ ID NO 889
 ; LENGTH: 996
 ; TYPE: PRT
 ; ORGANISM: Pinus radiata
 US-10-101-464A-889

Query Match 26.6%; Score 1341.5; DB 2; Length 996;
 Best Local Similarity 35.4%; Pred. No. 1,6e-95;

Matches 346; Conservative 164; Mismatches 375; Indels 93; Gaps 20;

QY 13 LFCLSLVATVTSSEGATLLEIKSFKDVNNVLYDWTTSPPSSDYVWVGSCENTVNVVA 72
 Db 15 LTVFPLALVSQBGVLLEVKELSPNGFLGMWKEDSP--CKMFGISCDQKSKSVVG 73
 QY 73 LNLSDMLDGEISPAIDKLSLSDIRGNRLSGQIDEDGSSLQNLDSFVELSGDI 132
 Db 74 IDSSEGLVGFPSVVCNLQPKLVLSGDNNGISILPRNLSMCKQLQRLNLSQNLFEVGNL 133
 QY 133 PFSISKQLEQLILKNNOULGPIPTLSQIPNLKILDLAQNKLSGEIPRLIYVNEVLQY 192
 Db 134 PDRISLAELIEYLDLSSNNSSGSIIPAGIGKLPLOVNLCCNLNLERITPFLGSLNLQ 193
 QY 193 LGRGNLV--GNISPDLCQLTGLWYFDVRNNSLTGSIPEITGCTAFQVIDLSYQLTGE 251
 Db 194 LLLAVNFPAGVGPPELGKLAQLQNLWATSCNFGAIPDSIGNLSTLNLDSSNQLSGI 253
 QY 252 IIPPDIGL--QVATLSLQGNQSGKIPISVIGLMQALVLDLSGNLSSIPILGNLFT- 309
 Db 254 IIPAITKLNQIVQELYHNNLTGRI PENMANVLSLRHFDVSTNNLTGTPQLARLPLSS 313
 QY 310 -----EKLVLHNSNKLTSIPPELGNSKLAHYLELNDNLTHGI 347
 Db 314 LNFENNVLGTIPPAIGYSPILSLKLFNTNNLNGSLNSLCKPSGLQTLIDAGRLSCTL 373
 QY 348 PPELGKLTDLFDLVANNDLLEGPIPDHLSCTTNLSNVHGNKFSGITPRAFOKLESMTY 407
 Db 374 PPDLCCKGKQKQNTINFNNTFTGQLPLQYGACLSLQVRVISHNELMGQVPSSEFWGLPHVY 433
 QY 408 LNLSSNNIKSPI-----FVELSRIGNLDTLDSNNKINGII 443
 Db 434 LELSNKFEBSISSEIRNNAKMLALLISGNRPSGTLPEIGLVANLSDVSHQFTGPL 493

QY 444 PSSIGDLEHLLKNLNRNHTGVVPGDFGNLARSIMEIDLSNNDISGPIPEELNQLONIIL 503
 Db 494 PATLGSJNTKLSKXHLFQNGFSSGLTDILSWNBLTDLNLSNNFSGIPRELQELPLVLY 553
 QY 504 LRLNNNLTVNVSGLANCLSLTVLNVSHNNLVQDIPKNNNFSPSPDSFGNGLC--G 560
 Db 554 LDISVNLTEIPEPELGNLKLSNFSNLSDNQTGTIVSAFSL--FYKSSLMGNPGLSNDG 612
 QY 561 SWLNSPCHDSRRTRVRSISRATLGTAGLVLMLWLIAAC-----RPHNPPFLDGLS 615
 Db 613 LKGFKSCSDWENSGRKKCYSAWMLPRLPFLAGVIFVLGALTYRQYREYNKAKVND--L 670
 QY 616 DKPYTSTPKLVILHMMALHYEDIMRMTENLSKYLIGHGASSTYKCVLXNCKRPAI 675
 Db 671 WR--SNKSPWMLTTPHRLGFRYE---LDCIDEENVISGSGKYVKKATLNGETVAI 724
 QY 676 KRLYSH-NPQSMKO----FETLEMLSTIKRNLVSLQVSYSHLSGLLFTYLENGSL 729
 Db 725 KRLMNNNGAEGSTSCNDNGFKAEVETLGNIRHKNIVLMCCCVNDDSNLLVYEMPGSL 784
 QY 730 WDLHGPTKKKTLDMPTRLKIAVGAQGLAYLHHDSPRIIHRDVXSNLILDKLEARL 789
 Db 785 GDLHGP--KAGDLNWPTRYKIAVGAQGLAYLHHDVCPPIHRDVXSNLILDLADFGARV 843
 QY 790 TDFGIASLCSVSKSHTS---TYVNGTIGYIDPEYARTSLTEKSDVSYGIVLELLT 844
 Db 844 ADGLAK--VLSYKIGIDFMAIAGSYGIVAPEYATLKVNEKSDISYFGVLELLEVLT 900
 QY 845 RRYAV--DDESNLHHLIMST---GNNEVEMADPITSTC--KDLGVKKVFOALLC 886
 Db 901 GKQPVLDPEESKDVVMWVTRIEKQNDGLDILDSRWVDCPREEMAALKV---ALLVC 957
 QY 897 TKRQPNDRPTMHQVTRVL 914
 Db 958 TSAIPNRPMSRVLLEL 975

RESULT 9

US-10-101-464A-933
 ; Sequence 933, Application US/10101464A
 ; Patent No. 6768041
 ; GENERAL INFORMATION:
 ; APPLICANT: Strabala, Timothy
 ; APPLICANT: Nieuwenhuizen, Nicolaas
 ; APPLICANT: Higgins, Colleen M.
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells
 ; FILE REFERENCE: 11000.1020C2
 ; CURRENT APPLICATION NUMBER: US/10/101,464A
 ; PRIOR FILING DATE: 2002-03-18
 ; PRIOR APPLICATION NUMBER: 09/704,302
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/228,986
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/162,866
 ; PRIOR FILING DATE: 1999-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/00724
 ; NUMBER OF SEQ ID NOS: 989
 ; SOFTWARE: FaSeq for Windows Version 4.0
 ; SEQ ID NO 933
 ; LENGTH: 996
 ; TYPE: PRT
 ; ORGANISM: Pinus radiata
 US-10-101-464A-933

Query Match 26.6%; Score 1341.5; DB 2; Length 996;
 Best Local Similarity 35.4%; Pred. No. 1,6e-95;

Matches 346; Conservative 164; Mismatches 375; Indels 93; Gaps 20;

QY 13 LFCLSLVATVTSSEGATLLEIKSFKDVNNVLYDWTTSPPSSDYVWVGSCENTVNVVA 72
 Db 15 LTVFPLALVSQBGVLLEVKELSPNGFLGMWKEDSP--CKMFGISCDQKSKSVVG 73

Dh	15	LLVLEPLALTSVQEGVLLEVKKELSDPNGFGLCNMWRKAEDSP-CXMRGISCDQRSXSVG	73
Qy	73	LNLSLDNLDELGEISPAIGDKSLISIDLKGRNRLSGQIPDEIGDCSSYLQNLDSFNEISGDI	1322
Dh	74	IDLSSGGVGLGVPPSVVCNIPOLKNLSLGNNGNISIPRLNLSMCRQLORLMLQNLFPVGNL	1333
Qy	133	PFSSIKLKOBJEOLIKNNQOLIGIPFSTLSQIPULKILDLAQNKLSGEIPPLIYWNELVQY	1922
Dh	134	PDFISELAELETLDSNNFSGSIPGIGIKLPRLQVLNCLCNLLNETIPFPLGNLSNLQO	1933
Qy	193	LGLRGNMLV-GNISPDLCQLTGLMYPDVNRNLSLGSIPETIGNCTAFQVLDLSYNQLTGE	2511
Dh	194	LLAANPFAFGVIPPGLKTLAQNLMAINSNCFVGAIPDSIGNLSLUTNLDLSNQSGI	2533
Qy	252	IPFDIGFL-QVATLSIQGNQSGKIPSVIGLMQALAVLDSGULSGSIPPIIGNLTFT-	3099
Dh	254	IPEATTKNLQIVQIELDYHNHLTGRIPENNANILSLHFPDVSTIMNLNGITPEOLARPLSS	3133
Qy	310	-----EKLHNSKLTGSIIPPELGNNSKLYLELNNHLTGH	3477
Dh	314	LNLFENNLVGTIPEAIGYSPITLSEKLTFTNNLNGSIPSNLGRSGIQTLDIAGNRUSGTL	3737
Qy	348	PEELGKLTDFPLNVAANDLEGPIDPHLSSCTNLSLNVAHGNKFSGTTIPPAFOKLESMTY	4077
Dh	374	PPDLCKYKGLQTLNIFNNFTGQLPYQYGCJLSQVRISHNELMQGVESPFGMLPHVY	4333
Qy	408	LNLSNNNIKGP-----PVELSRIGNLDELDSLNNKINGIT	4433
Dh	434	LELSNNKKEGSSISEIRNAKNLSALLISGNRFSGTLPSEIGLVANLSVIDGSHNOFTGPL	4933
Qy	444	PSLSGDLLEHLKMNLSRNHITGVPEDPFGNLSIMEIDLSNNDISGPIPELNQNLIL	5033
Dh	494	PATLSLNLKLSKLHLPONQPSGSLTDLISNHELTDNLSSNPSGPIPELSELPVLT	5533
Qy	504	LRLENNNLTVNGVSLANCLSLTVLVNSHNLVGDIKPNNNFSPSPFIGNGLC--G	5600
Dh	554	LDLSVNALTGEIPEELGNLKNLSFNLSDNQLTGIVSARSL-SFYKSLMGNGLSDNG	6122
Qy	561	SWLNSPCHDSRRTVYVISRAAILGIAIGLVLLMYLIAAC-----RPNPPFLDGL	6155
Dh	613	LKGFSCSDMEMSGRKKCYSMWMLLPALPALGAVIFVLGALFYROYREYNKRAKVD--L	6707
Qy	616	DKPVYSPFVKLYILHNNMLAHYVEDIMRNTENSEKYIIGHGASFYVKCVLKNCKPVAI	6755
Dh	671	WR--SNKSPWMLTTHRLGFRFEY---ILDCIDEENVIGSGSGKYKATTLNGEIVAI	7244
Qy	676	KRLYSH-NPOSNKQ-----FETELEMLSSIKRHNLVSLQAYSLSHLGSLFYDLENGSL	7299
Dh	725	KRLMNGNAEGSTSCNDNGFKAEVETLGIRKHNIYKLMCCCVNDSNLLVLEYMPNGSL	7844
Qy	730	WDLHGPFYKTKTLDMDTRLKIAIYGAAGLAYLHDCSPRIHRDVYSSNLLDKDLBARL	7899
Dh	785	GDLHLGP-KAGDLMPTRYKIAIVGAAGLAYLHDCVPRIHRDVYSSNNILLDADGARY	8433
Qy	790	TDFGAKSLCVASKSTSTST---TYWAGTIGYIDPEAFARSRLREKSDVYSYGVILEILT	8444
Dh	844	ADFGIAK---VLOSTYKGIIDFMSAIGSAGYIAPETAYTLKVNKESDIYSFGVLLLEVY	9000
Qy	845	RRKAV--DDESNLHLIMSKT-----GNNEVEMEMADPIDTSTC--KOLGVKKFQFALIC	8966
Dh	901	GKQVPIQDFEESKDVVMVWRTRIEKQNDGLOIILDRVWVWDCREMAAVLVK---ALLC	9577
Qy	897	TKRQPNDRPTMHQVTRVL	9144
Dh	958	TSALPPIRPSMRKRVLELL	9755

RESULT 10
US-10-101-464A-914
; Sequence 914, Application US/10/01464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy

```

1  APPLICANT: Nieuwenhuizen, Nicolaas
2  APPLICANT: Higgins, Colleen M.
3  TITLE OF INVENTION: Compositions Isolated from Plant Cells
4  TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
5  FILE REFERENCE: 11000.1020c2
6  CURRENT APPLICATION NUMBER: US/10/101,464A
7  CURRENT FILING DATE: 2002-03-18
8  PRIOR APPLICATION NUMBER: 09/704,302
9  PRIOR FILING DATE: 2000-11-01
10 PRIOR APPLICATION NUMBER: 09/228,986
11 PRIOR FILING DATE: 1999-01-12
12 PRIOR APPLICATION NUMBER: 60/162,866
13 PRIOR FILING DATE: 1999-11-01
14 PRIOR APPLICATION NUMBER: PCT/US00/00724
15 PRIOR FILING DATE: 2000-01-11
16 NUMBER OF SEQ ID NOS: 989
17 SOFTWARE: FastSeq for Windows Version 4.0
18 SEQ ID NO 914
19 LENGTH: 998
20 TYPE: prt
21 ORGANISM: Eucalyptus grandis
22 US-10-101-464A-914

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Query Match	25.9%	Score 1305	DB 2	Length 998
Best Local Similarity	33.7%	Pred. No. 1.1e-92		
Matches 339	Conservative 163	Mismatches 382	Indels 122	Gaps 24
QY	VLAGFL-FCLSLVATVT-----SEEGATLLEIKKSFADYNNVLVDWTSPSSDYCWR	59		
DB	1 MFLSLTSLTLLLLAGAAMPALSLNQEGLYLHGATLSLDQSSLAAMDRAAP-CGMP	59		
QY	60 GVSCEMTENVVALNSDLNDGEISPAIGDKSLSIDLRGNRLSGQIPDEIGDCSSIQ	119		
DB	60 GVGCDRASGSVVSVDLSGANLGGPEPLLCRLPNTLPLFSFFNNISIT-SLPAGVASCRSLV	118		
QY	120 NLDSFNLSDGDIPEISIKLKQLEQLIKNNQLIPITSTSQIPNLKTLIDLAQNLSGE	179		
DB	119 HLDGQNLADLPASLADLPGLAYLDSANNFSGDIPASFCRFRLEVLSTLYNNLLDGA	178		
QY	180 IPRLIYMNVEVLYGLRGNNLV-GNISPDLCQLTLMYFDVNNSLTGSIPETIGNCTAF	238		
DB	179 IPGFLGNVSTLKMNLINISYNPAPGRIPPELGNLTNLVLEWLMECGLTGKIPESLGRKRL	238		
QY	239 QVLDLSTYQLTGELIPFDIGFLQ-VATLSLQGNQLSGKIPSYVGLMQALAVLDLSGNLSG	297		
DB	239 TDLLAFAYLELGGPIPSSTLEBSVQLELYNNSLTGLGELPAGLSKLTALRLDASMRLTG	298		
QY	298 SIPLILGNLF-----TEKTYLHNSKTLGSIIPPELGNMSKTH	334		
DB	299 TIPELTRLPLPSLNLVYNQSGELPASIAOSPNIENLRLFNKRLTGKLPKVLGQNAFLQ	358		
QY	335 YLELNDNHLTGHIPEPEKLTDLFDLVANNDLEGPIDHLSSTCNLSLVNHNKFSGT	394		
DB	359 YIDVSTNNFSGEIPASLCCANGELBELLIEMENFSQGPIDPALGRCCQLTRVRLGNRRLSGE	418		
QY	395 IPRAFQKLESTTYLNLSSNNIKGPIPVLSKRIQNLDTLDLSNNKINGIIPSSLGDEHLL	454		
DB	419 VPSSFQWGLPRVSLLELDLNKLSGPGEEIARASNLVSLSNEPFTGPKIGITIVRL	478		
QY	455 KMLNSRHNIITVVP-----GDFGLT-----RSIMEIDLSNNDISGP	490		
DB	479 DFGASENKLTSLPESLIINLQGLRLDRSNDLSEGLPSGRHMKKALNELDLADRNLSS	538		
QY	491 IPEELNQLNIILRLENNLTGAVGSLANCLSTVLNVSHNNLVGDIPIKNNFSFRSPD	550		
DB	539 IPAEIGGLSVLNYDLSGNQPSGKVPALQMLIKNLQNLSTYSLSGPLPMPFTKOMYK-N	597		
QY	551 SFIGNPGICGSWNLSPCH---DSKRTYRVVTSRPAIIGIALGCVITLMLVLAACRPHNP	607		
DB	598 SFLNPNGLCGEMKGLCNGGGEERNSGVWLLRSTFI--LAGLVFTIGV-----	644		
QY	608 PPLFDG-----SLDKPVTYSTPKLYVLHNNMALHVEDIMRMENLSEKYLIGHG	657		

Db 645 -----GWFMKXYSFKNAKRAIDKSKWTLMSPH---XLCFSED--EILDLDEBNVIGTG 694
 QY 658 ASSTVYCVLKNCKPVAIKRLY-----SHN-----PQSMKQFETELMSSIKHNLV 705
 Db 695 ASGKVYVVLSSGDAVAVKVKLMDGPRKSESHDEKBPVODDGDVAVKTLGKIRKNIV 754
 QY 706 SLOAYSLSHSGLLFYDYLENGSLMDLLHGPTKKKTLMDWTRLKIAVGAAGLAVLHHC 765
 Db 755 KWCSCSTRCKLVLVEYMGNSIGDILLHS-SKGGLDWPRYIAVDAABGLSYLHHC 813
 QY 766 SPRIHRDVKSNLIDKDLBARLTFGIASL-CVSKSHTS-TYVNGTGYIDPEYART 823
 Db 814 VPPVHVDVKSNNILDLADFGARVADFGVAKVVERTGKHGHSMSVIAAGCYIAPEYAYT 873
 QY 824 SRLTEKSDVYSYGVILLELITRRAVDESNLHLLI-----MSKTGNNEWEMADDDIT 877
 Db 874 LRNVEKSDYTSFGVLLLELVTRRRPVDEPGEKDLVWKVCTTLTQCKVDQVIT--DKLID 930
 QY 878 STCKDLGVKKVFQALLCTKRCQPNDRPTMHQVTRVLGSFMLSPO 923
 Db 931 SCFKE--DVCKVLNIGIGCTSPLEINPSMRVVKMLQETSAENAP 974

RESULT 11
 US-08-473-553A-6
 ; Sequence 6, Application US/08473553A
 ; Patent No. 5859338
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyerowitz, Elliot M.
 ; APPLICANT: Clark, Steven E.
 ; APPLICANT: Williams, Robert W.
 ; TITLE OF INVENTION: Plant Clavateal Nucleic Acids,
 ; TITLE OF INVENTION: Transformed Plants, and Proteins
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Teet, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/473,553A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Silva, Robin M.
 ; REGISTRATION NUMBER: 38,304
 ; REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 980 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-473-553A-6

Query Match 25.8%; Score 1300.5; DB 1; Length 980;
 Best Local Similarity 35.2%; Pred. No. 2.4e-92;
 Matches 348; Conservative 153; Mismatches 367; Indels 125; Gaps 27;
 QY 30 LLEIKKS-FKDVNNVLDWTTSPSSD-YCWRGVSCENVTFNVALNLSINDGEISPA 87

Db 31 LNLKSSMIGPKGKGLHDMWISSSPDAHCSFGVSCDD-DARVLSNVSTPFLGTISEB 89
 QY 88 IGLKSLISTDLRGNRLSGQIPDEIGDCSSLOWLDSFN-ELSGDIPFSISK-LKOLEQ 145
 Db 90 IGMVTHLVNLTLANFTGELPLEMKSLTSKALNLSNNGNLGTGTPGELTKMVDLEVL 149
 QY 146 ILKNNOLIGIPSTLSQIPNLKILDLAONKLSGEIPRLIYMEVLYOYGLRGNLVGNIS 205
 Db 150 DYNNNPNNGKLPRMEBELKLYLSPGNGFSGEIPESYVDIOSLEYLGLNGAGLSGKSP 209
 QY 206 PDLQCLTGL-----WFDVANNSLTSGIPETTGNCAFOYVLDLSYQVLTGEIPFDGLQ 260
 Db 210 AFLSRKLNLEMYIGY---NSYTGVPREFGGLTKLEILDVASCCTLTGGEIPTSLSNK 265
 QY 261 -VATLSIQNLQSGKIPSVIGLMOALAVLDLSGNLSGSPPI---IGNLTFPEKLYHS 316
 Db 266 HMTLTFHINNLGHIIPPELSGLVLSKSDLSINQLTGEIPQSFILGNITL---INLR 322
 QY 317 NKLTGSIIPPELGMSKLYH-----LELNDHNLGHIPELG 352
 Db 323 NNLYGQIPBAIGELPKLEVEFVWENNFTLQLPANLGRNGLKLDVSDNHLTGILPKDLC 382
 QY 353 KLTDLPDLVANNDLBGPIDPHLSCTNLNSLVNHGKRSCTIPRAFOKLESTYTLNLS 412
 Db 383 RGEKLEMLILSNPFPGPIPEELGKCKSLTKIRIVKNLNGVPAQFNLPLVTITIELTD 442
 QY 413 NNIKGPVPELS-----RIG--NLDTLDSNNKINGIIPESLGD 449
 Db 443 NPFSGELPVTMSGDVLDQIYLSNNWFSGEIPRAIGNFNLQTLFLDRNRKGIIPREIFE 502
 QY 450 LEHLKKNLSRNHITGVPGDFSNLRSIMEIDSNNDISGPIPEELNQLNITLLENN 509
 Db 503 LKHLRSINTANNITGGIPDISIRCSLTLSVDLSRRRINBEIKGINNVNLGTLSIGN 562
 QY 510 NLGNVGS-LANCLSLVLNVSHNMLVGDIPKNNNSRSPDSFIGNPGC-GSWNSPC 567
 Db 563 QLTGSIPGTGNNITSLTLDLSFNDLSGRVPLGQFLVFNETSFAGTYLCLPHRVSCTP 622
 QY 568 H-----DSRRTVVTSIRAAILGI-AIGGLVILMLVLIACRPHNPFPFLDGLSDKPVTY 621
 Db 623 RRGOTSDHNTALPSPSRIVYITIAAITGLILSVAIRONKKN-----QKSLAW 673
 QY 622 STPLVLHNMMLAHYEDIMRTEMLSEKXIIGHGASSTVYKCVLKNCKPVAIKLYSH 681
 Db 674 KLTAFQKLDKFS-----EDVL---ECKEENIIGKSGSIVYGMNNDVAIKSLVGR 725
 QY 682 NP-QSMKQFTELEMLSSIGHRLVLSIQAYSLHLSLFFDYLENGSLMDLLHGPTKK 740
 Db 726 GTGRSDHGFALIQTLGRIHRHIVRLGVANKDTNLLLEYEWPNGSLGELLHG-SKGG 784
 QY 741 TLMDPTRLKIAGAAGLAVLHHCSPRIHRDVKSNLILDKDLBARLTFGIASL-- 798
 Db 785 HLOMETRHRVAVPAKGLCYLHHCSPILHRDVKSNLILDDPFAHVADPGLAFVLD 844
 QY 799 -----CVSKSHSTYVNGTGYIDPEYARTSLTEKSDVYSYGVILLELITRKAAYD-- 851
 Db 845 GAASECWS-----IAGSYGIAPAYATLKVDEKSDVYSFGVVLLELITAGCKKPVGEFG 898
 QY 852 -----ESNLHLMSKTKGNNEWEMADDDITSTCKDLGVYKVFQALLCTKQPN 903
 Db 899 EGVDIYRWVNRTEEBETQPSDAIIVAILVDPRLG--YPLTSVIHVFKIAMVCBEBAA 956
 QY 904 RPTMHQVTRVLGSFMLSQPPAATDTSA 931
 Db 957 RPTMREYVH-----MLTNPCKSVANLIA 979

RESULT 12
 US-08-473-553A-2
 ; Sequence 2, Application US/08473553A
 ; Patent No. 5859338
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyerowitz, Elliot M.

APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-553A-2

Query Match 25.6%; Score 1293.5; DB 1; Length 985;
Best Local Similarity 35.1%; Pred. No. 8.5e-92;

Matches 347; Conservative 153; Mismatches 363; Indels 125; Gaps 27;

QY 30 LLEIKKS-FDVVNVVYDWTTPSPS-YCVMRGVSGENTFNVVALNLDLNDGEISPA 87
DB 36 LNLKSMWIGPKHGHDMHSSPDHSCFSCVSCDD-DARVSLNVSFTPLFGTISPE 94
QY 88 IGDLSKSLIDLRGNRLSGQIPDEIGDCSLQWLDLSPN-ELSGDIPFSISK-LKOLEOL 145
DB 95 IGLTTLVNLTLAANNFTGELPLEMKSLTSLKVLNLSNNGNLTGTFPEGLIKAMVDLEVL 154
QY 146 ILKNNGLIPETLSQIPNLKILDLAONKLSGEIRLIYMNENVLYQLGKNNLYGNIS 205
DB 155 DTYNNPNFGKLPKMBELKYLKLSFGNFSGEISYGDIOSLLELGLNGAGLSGKSP 214
QY 206 PDLQQLTG----WFDVARNNSLTGSIPETIGNCTAFQVLDLSYNQLTGEIPFDIGFLO 260
DB 215 AFLSRKLNREMYIGY---NSYTGAVREFGGLKELIDMASCTLICEITISLNK 270
QY 261 -VAISLQGNQSGKIPSVIGLMOALAVDLGNNLSGSTIPI--LGNLTTEKLYLHS 316
DB 271 HHTTFLHNNLTLGHIPPELSGLVSLKSLDLSINQLTGEIPQFIMGNITL--INLFR 327
QY 317 NKLTGSIPELGNMSKLTNY-----LELNDHNLGHIPPELG 352
DB 328 NNLVGOIPPAIGELPKLEVFVEWENNFTQLPMLNLRNGNLKLDVSDNHLTGLPKDLC 387
QY 353 KLTLDLFDLVVANNDEGPIDHLSCTNLSLVHGNKSGTIPRAFOKLESMTYLNLS 412
DB 388 RGRKLEMLILSNFPFGPIPEELGCKSLKIRIVNKLNGVTPALGPLVITIELND 447
QY 413 NNKGPVPELS-----RIG---NIDTIDLSNNKINGIIPSSLDG 449
DB 448 NFPSGELPVMTSGDVLDOYILSNMWFSGELIPAIIGNFPLQTLFDRNFRGNIPREIFE 507

QY 450 LEHLKNNLSRNHITGVPGDFGNLSIMEIDLSNNDISGPPEELNOLQNIILLRENN 509
DB 508 LKLSKRNISANNITGTIPDSISRCSTLISVDLSRRKINIEIKGINNVNGLTINSGN 567
QY 510 NLTVNGVS-LANCLSLTVLVNHNVLVDIPKXNNFSRPSDFIGNPGIC-GSWINSPC 567
DB 568 QLTGSIPTGIGNMTSLTTLDLSPNDLSGRVPLGQGLVFNETSPAGNTYLCPLHRSVSCP 627
QY 568 H-----DSRRTVAVSISRAILGI-AIGGLVILLMLVLAACRPHNPPPLDGLDPVY 621
DB 628 RPOGSDHNTALFSPSRVITVIAAITGLILISVAIRQNNKKN-----QKSLAW 678
QY 622 STEPLVILHNNMALHYVEDIMRMTENISEKIIIGHGASSVYCVKKNCKPAIKLYSH 681
DB 679 KLTAFQKLPDKS-----EDVL--ECLKEENITGKSGSGIVRGSPNNVDAIKLYGR 730
QY 682 NP-QSMKQFETELMULSIKRNVLVSLQVSLHSLGLFPYDLENGSLMDLLHPTKKK 740
DB 731 GTRSDHGFATIEIQTGRIRHRIHVLGVVANKDNTNLLYEXMPGSLGELLHG-SKGG 789
QY 741 TLDWDTRLKAYAGAGGLAYLHHDGSPRIIHRVKSNNILLDKDLARLTDGIAKSL- 798
DB 790 HLOMETRHRVAVAAKGLCYLHHDGSPRIIHRVKSNNILLSDFEAHVADFLAKFLVD 849
QY 799 -----CVSKSHTSTVYMGITGVTDPEYARTSRLTESDVSYSYIVLLELTRKAVDD-- 851
DB 850 GAASECMS-----IADSYGIAPRYATTLKXDESDVYSRGVALLBELAGKKPGBFG 903
QY 852 -----ESNLHLIMSKTGNNEVEMADPDITSTCKDLGVKKVFOALACTKROPND 903
DB 904 EGVDIVRWARNTEEBITQPSDAIVAIVDPRITG--YPLTSVIVHFKIAMCVBEBA 961
QY 904 RPTMQVTVKLSFMSLSEOPPAITDTSA 931
DB 962 RPTMREVVH-----MLTNPKSVANLIA 984

RESULT 13

US-08-473-553A-5
Sequence 5, Application US/08473553A
Patent No. 5859338

GENERAL INFORMATION:

APPLICANT: Meyerowitz, Elliot M.

APPLICANT: Williams, Robert W.

TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 999 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-473-553A-5

Query Match 25.6%; Score 1293; DB 1; Length 999;

Best Local Similarity 34.6%; Pred. No. 9.5e-92;

Matches 347; Conservative 160; Mismatches 385; Indels 112; Gaps 22;

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13 LFCLSLVATVTS-----EEGATLL-EIKKSFQVNNVLYDWTTPSSDYCVWRSVC 63
2 LYCLILLCLSSSTLYPSLSLNQDATTIRQAKLGSDPAQSSSDNNVTPCKMLGVSC 61
64 ENYTFNVVALNSDLNLDGEISPAIGDKSLISIDLRGNRLSGOI-PDEIGDCSSLNLD 122
62 D-ATSNVSVVDSLSFMLVGPSPSILCHLPISLHSLVYNSINGSLADDFPTCHNLISLD 120
123 LS-----FNEISGD-----IPPSISLTKQDEQLIKNNQLIGPIP 157
121 LSENLVGSIPKSLPFLPNLKFLIEISGNMISDTIPSSFGFRLLESNLNAGNLSGTIP 180
158 STLSQIENLKILDAONKLS-GEIPRLIYMNVEVQYGLRGNMIVGNISPDLCQTGLMY 216
181 ASLGNVTTLKEIKLALYVLPSPQIPSQLGNLTLEQVLMAGCNLVGPIPELSLSLTVN 240
217 FDVNNNSLTGSI-----PBTIGNCTAFOVLDISYNQLTGEI 252
241 LDFLNFQNLTSIPSMITQKTVEQIELFNNSFSGELPESMGMTTLKRFDSNNKLTGKI 300
253 PFDTGFIQVATLSIQGNQSGKISVIGLMQALAVLDLSGLSLSGSI-PRILGNLTFTKL 312
301 PDNLNLNLBESLNFENMLBEPLEPESITRSKTSLEKLFNNRLTGLVLPQSGANSPLQYV 360
313 YLHSNKLTGSIPLPBLGNMKSLLHYELNDNHLTGHIPELGKLTLPDLNVAANDLEGPIP 372
361 DLSVNRSGEIPAVVCGEKGLEYLLIDNSFSGEISNNLCKSKLTVRSLNNKLTSGQIP 420
373 DILSSCTNLNSLVNHNKFSGTIPPAFOKESMTYVLSNNIKGPIPELSRIGNLDL 432
421 HGFGLPRLSLLELSDNSFTGSIPTKTIIGAKNLNLRISKRFSGSIPNEIGSLNGIIEI 480
433 DLSNNKINGIIPSSLDLEHLKNNLSNNHITGVVPGDFGNLRISIMEIDSNNSIGPIP 492
481 SGAENDPSGEIPELSLVKQLSRDLSSKNQSGEIPRELKGMKNLNEINLNNHLSGEIP 540
493 EELNQLONIIILRLNNNLGTNVGSLANCLSLTVLVNASHNNLVGDIPIKNNFSRSPDSF 552
541 KEVQILPVLNLTDLSSNQSGEIPLELONLKTNLVNLNSYNHLSGKIPLVANKIYAHF-F 599
553 IGNFGCLGSWINSFCHDSRRTVAVSISPAIIGLIGLVIL--LMLVIAACRPHNPFF 610
600 IGNGLCAVD-LDGLCRKITRSGNIGYVWILLTIFLAGLVFVVGIVMFIACRKLRLA-- 656
611 LDGSLDRPVYSTKLVILHNNMALHYEDIMRMTENLSEKTIIGHGASSVYVCVLKNC 670
657 -----KSTTLAASKMSFH--KLHFSER--EIAQCLDERKNVIGFGSGKGYVVEYLRGG 705
671 KPAVAKRL-----YSHNPOSMKOFETLEMLSSIKRNLVSLQAYLSHLGLLF 720
706 EVAVAVKLINKSVKGGDEEYSSDSLNRDVFAPAEVETLGTIRKKSIVRLMCCSSGDDCKLLV 765
721 YDYLENGSLMDLHGPTK-KKTLDMWTRKTIAYGAQGLAYLHDCSPRIIHRDVKSSNI 779
766 YEYMPNCSLADVLTGDRKGVAVLGPBERLRIALDAEBGLSYLHHDVCVPIVHRDVKSSNI 825
780 LLDLDLEARLTDPGIAKSLCVSKSHT--STVYMGTTIGYIDPEYARTSRLNFKSNNVSYG 836
826 LLDSVDYGKIVADFGIAKVGQMSGSKTPPAMSGIASSCGYIAPEVYTLIRVKEKSDIISFG 885
837 IVLLELTTRRAKAVDESNIHL-----IMSGTGNNEVEMADPDITSTCKDLGVVKKVF 890

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886 VVLELVTKQKOPDSELDGDKMAKWCTALDKGCLPEVI---DPKDLKFXE--EISKYI 940
891 QALLLCTCKOPNDRPTMHQVTRVLGSPMLSE-----QPPATDTS 930
941 HIGLLCTSPPLNRPSPMRKV-----IMLOEVSQAVPSSPNTS 979

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RESULT 14

US-10-101-464A-900

Sequence 900, Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OR INVENTION: and their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 900

LENGTH: 1166

TYPE: PRT

ORGANISM: Pinus radiata

US-10-101-464A-900

Query Match 25.3%; Score 1275; DB 2; Length 1166;

Best Local Similarity 30.8%; Pred. No. 3e-90;

Matches 344; Conservative 170; Mismatches 342; Indels 260; Gaps 27;

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31 LEIKSFK----DVNNVLYDWTTPSSDYCVWRGVSCENVTRNVVALNLDNLGDEIS 85
41 IEALQAFKASLTYPDSHALNW--DFVANHVCMNVTGVCNPHKRLVSAIYNNSLQGTIP 99
86 PATGDLKSLISIDLRGRSLSGOI-PDEIG-----DCSS----- 117
100 PHIGNISFLGVNLTLNLSFGSIIIPNELGKURLKRLSKONQLISSIPEALKDCTSLRL 159
118 -----LQNLDSLFEELSGDIPPSISKQLQLEQLIKNNQLIGPIP 157
160 NLSHNNLTGTHIPSGLOGQLQNLKLSFNGLTKVPEPTFPCNSALLETLSGNSPLSGTIP 219
158 STLSQIPNLKILDAONKLSGEIP-----RLIYNEV-----LOY 192
220 SHLGMLARIKILISGRNQLSGGIPPSLNLCTELRGVLYENRLTGEIPWEIGAKLSKIEF 279
193 LGRGNLVGNISBDLCQLGLWYFDVRNNSLTGSIPEITIG----- 223
280 LSLGNOQSGIIPPSLNLCTELSELDELLENRLTGEIPWEIGAKLSKIEFSLGNOQSGG 339
234 -----NCTAFQVLDLSYNQLTGEIPDIG--FLQVATLSLQGNQSGKIPSYIGLMQAL 285
340 IIPSLNLCTELSELDELLENRLTGEIPWEIGAKLSKIEFSLGNOQSGGIPPSLNLCTEL 339
286 AVIDLSGNLSSGIPPLIGNL-----TFTEK----- 311
400 SELELDENSLTGGIPQSIGKRLIQDMDLDNNHLYSESEISFGALSNCTNLQWLSLSSN 459
312 -----LYHSNKLTSIIPPELGMSKLLHYELNDNHLTGHIPPELG 352
460 DLKGDLPGSIDRLSQNLILYILGGRNFTGKI PQBMNSLTGLILDLNDNLISGGLPSALG 519

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Search completed: September 2, 2006, 06:57:56
Job time : 56 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2006, 06:47:45 ; Search time 315 Seconds
(without alignments)
2866.080 Million cell updates/sec

Title: US-10-519-135-2
Perfect score: 5043
Sequence: 1 MALFRDIVLGFCLSLVA.....SASDAQFLRFQGVISONSE 976

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 segs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5043	100.0	976	2	Q42371_ARATH	Q42371 arabidopsis
2	3709	73.5	978	2	Q69SP5_ORYSA	Q69SP5 oryza sativ
3	3372.5	66.9	921	2	Q8W0U9_SORBI	Q8W0U9 sorghum bic
4	3200.5	63.5	980	2	Q65867_ORYSA	Q65867 oryza sativ
5	3113	61.7	999	2	Q7XB99_ORYSA	Q7XB99 oryza sativ
6	3089.5	61.3	967	2	Q6XAT2_ARATH	Q6XAT2 arabidopsis
7	3079.5	61.1	966	2	Q6XAT3_ARATH	Q6XAT3 arabidopsis
8	3059	60.7	932	2	Q9LVP7_ARATH	Q9LVP7 arabidopsis
9	2967.5	58.8	938	2	Q9LVB3_ARATH	Q9LVB3 arabidopsis
10	2306.5	45.7	719	2	Q84XU6_ELAGV	Q84XU6 elaeis guin
11	2299	45.6	441	2	Q56W23_ARATH	Q56W23 arabidopsis
12	1504.5	29.8	1124	2	Q49318_ARATH	Q49318 arabidopsis
13	1489	29.5	1102	2	Q9LVP0_ARATH	Q9LVP0 arabidopsis
14	1480.5	29.4	1109	2	Q6Y777_ORYSA	Q6Y777 oryza sativ
15	1464	29.0	1250	2	Q6L315_SORBI	Q6L315 sorghum dem
16	1454	28.8	1104	2	Q7F8X5_ORYSA	Q7F8X5 oryza sativ
17	1454	28.8	1104	2	Q7X817_ORYSA	Q7X817 oryza sativ
18	1446	28.7	1232	2	Q9SN91_ARATH	Q9SN91 arabidopsis
19	1442	28.6	1236	2	Q9FIZ3_ARATH	Q9FIZ3 arabidopsis
20	1441	28.6	1109	1	RPK1_IPONT	RPK1 ipomoea nil
21	1427.5	28.3	1029	2	Q7XZM7_ORYSA	Q7XZM7 oryza sativ
22	1412.5	28.0	1133	2	Q9SH12_ARATH	Q9SH12 arabidopsis
23	1410.5	28.0	1003	2	Q49545_ARATH	Q49545 arabidopsis
24	1410.5	28.0	1008	2	Q9LXZ6_ORYSA	Q9LXZ6 oryza sativ
25	1409	27.9	1072	2	Q69X93_ORYSA	Q69X93 oryza sativ
26	1407.5	27.9	1098	2	Q7XHS7_ORYSA	Q7XHS7 oryza sativ
27	1407.5	27.9	1098	2	Q8W5K7_ORYSA	Q8W5K7 oryza sativ
28	1401	27.8	1012	2	Q9LXZ4_ORYSA	Q9LXZ4 oryza sativ
29	1400	27.8	1123	2	Q8GZ71_ORYSA	Q8GZ71 oryza sativ
30	1399.5	27.8	1030	2	Q8H037_ORYSA	Q8H037 oryza sativ
31	1397.5	27.7	392	2	Q6ZG67_ORYSA	Q6ZG67 oryza sativ

32	1397	27.7	1123	2	Q9SSL9_ARATH	Q9SSL9 arabidopsis
33	1396	27.7	1023	2	Q6ZLK5_ORYSA	Q6ZLK5 oryza sativ
34	1393	27.6	1012	2	Q9LXZ5_ORYSA	Q9LXZ5 glycine max
35	1391	27.6	1123	2	Q8L740_ARATH	Q8L740 arabidopsis
36	1383	27.3	1274	2	Q6ZAB5_ORYSA	Q6ZAB5 oryza sativ
37	1378	27.3	1274	2	Q6L155_ORYSA	Q6L155 oryza sativ
38	1368.5	27.1	1002	2	Q9M221_ARATH	Q9M221 arabidopsis
39	1367.5	27.1	992	2	Q65440_ARATH	Q65440 arabidopsis
40	1367	27.1	1112	2	Q6ZAB7_ORYSA	Q6ZAB7 oryza sativ
41	1366.5	27.1	1040	2	Q6Z8Y3_ORYSA	Q6Z8Y3 oryza sativ
42	1365.5	27.1	1192	1	EX5_ARATH	EX5 arabidopsis
43	1352.5	26.8	1041	2	Q9F115_ARATH	Q9F115 arabidopsis
44	1352	26.8	1117	2	Q5VQM7_ORYSA	Q5VQM7 oryza sativ
45	1345.5	26.7	1120	2	Q84RP5_ARATH	Q84RP5 arabidopsis

ALIGNMENTS

RESULT 1
ID Q42371_ARATH PRELIMINARY; PRT; 976 AA.
AC Q42371;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Putative receptor-like protein kinase, ERCTA (Putative receptor
DE protein kinase, ERCTA).
GN Name=ERCTA; OrderedLocNames=At2g26330;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; eusteroide II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SPRAIN=ecotype Columbia;
RX MEDLINE=96206819; PubMed=8624444; DOI=10.1105/ltpc.8.4.735;
RA Torii K.U., Mitsukawa N., Oosumi T., Matsura Y., Yokoyama R.,
RA Whittier R.F., Kameda Y.;
RT "The Arabidopsis ERCTA gene encodes a putative receptor protein
RT kinase with extracellular leucine-rich repeats.";
RL Plant Cell 8:735-746(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Skyes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.W., Quach H.L., Toriumi M., Ju G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawal J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shimizu P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonCommercial license
CC
CC EMBL: U47029; AAC49302.1; -; mRNA.
CC EMBL: DB3257; BAA11869.1; -; Genomic DNA.
CC EMBL: AY035110; AAK5615.1; -; mRNA.
CC EMBL: AC004484; AAC14518.1; -; Genomic DNA.

DR PIR; B84659; B84659.
 DR HSSP; P36897; 1IAS.
 DR GenomeReviews; CT845783_GR; ATG263330.
 DR TAIR; Atg26330; -
 DR GO; GO:0005739; C:mitochondrion; IDA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_pln.
 DR InterPro; IPR003591; LRR_typ.
 DR InterPro; IPR013210; LRRNT_2.
 DR InterPro; IPR008271; Prot_Kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00560; LRRNT_2; 1.
 DR Pfam; PF00563; LRRNT_2; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding;
 KW Receptor; Repeat; Serine/threonine-protein kinase; transferase.
 SQ SEQUENCE 976 AA; 107334 MW; 0E51D46A4B94C8D CRC64;

Query Match 100.0%; Score 5043; DB 2; Length 976;
 Best Local Similarity 100.0%; Pred. No. 9 6e-272;

Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALFRDIVLLGFLFCLSLVATVTSEEGATLLEIKKSRFDVNNVLYDMTTPSSSDYCVWG 60
 DB 1 MALFRDIVLLGFLFCLSLVATVTSEEGATLLEIKKSRFDVNNVLYDMTTPSSSDYCVWG 60
 QY 61 VSCGNVFNVAVALNSDLNLDGEISPAIGDKSLISIDLRNRLSGQIPDEIGCSSLQN 120
 DB 61 VSCGNVFNVAVALNSDLNLDGEISPAIGDKSLISIDLRNRLSGQIPDEIGCSSLQN 120
 QY 121 LDISFNLSGDIPRSISKQLKQLEQILKNNQLIPFSTLSQIPNLKILDLAOKLSGEI 180
 DB 121 LDISFNLSGDIPRSISKQLKQLEQILKNNQLIPFSTLSQIPNLKILDLAOKLSGEI 180
 QY 121 LDISFNLSGDIPRSISKQLKQLEQILKNNQLIPFSTLSQIPNLKILDLAOKLSGEI 180
 DB 121 LDISFNLSGDIPRSISKQLKQLEQILKNNQLIPFSTLSQIPNLKILDLAOKLSGEI 180
 QY 181 PRLIYNEVLQYGLRGNNLVGNISPDLCQITGLWYFDVNNVLTGSIPTETGCTAFQV 240
 DB 181 PRLIYNEVLQYGLRGNNLVGNISPDLCQITGLWYFDVNNVLTGSIPTETGCTAFQV 240
 QY 181 PRLIYNEVLQYGLRGNNLVGNISPDLCQITGLWYFDVNNVLTGSIPTETGCTAFQV 240
 DB 181 PRLIYNEVLQYGLRGNNLVGNISPDLCQITGLWYFDVNNVLTGSIPTETGCTAFQV 240
 QY 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
 DB 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
 QY 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
 DB 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
 QY 301 PILGNLFTFEKLYHSNKLGTSGIPPELGNNSKLHYLEINDHLLTGHIPEELGKLTDLFDL 360
 DB 301 PILGNLFTFEKLYHSNKLGTSGIPPELGNNSKLHYLEINDHLLTGHIPEELGKLTDLFDL 360
 QY 301 PILGNLFTFEKLYHSNKLGTSGIPPELGNNSKLHYLEINDHLLTGHIPEELGKLTDLFDL 360
 DB 301 PILGNLFTFEKLYHSNKLGTSGIPPELGNNSKLHYLEINDHLLTGHIPEELGKLTDLFDL 360
 QY 361 NVANNIDEGPIPDHLSGCTNLSINLVHGNKSGTIPRAFOKLEBMTYLNISNNIKAPIP 420
 DB 361 NVANNIDEGPIPDHLSGCTNLSINLVHGNKSGTIPRAFOKLEBMTYLNISNNIKAPIP 420
 QY 361 NVANNIDEGPIPDHLSGCTNLSINLVHGNKSGTIPRAFOKLEBMTYLNISNNIKAPIP 420
 DB 361 NVANNIDEGPIPDHLSGCTNLSINLVHGNKSGTIPRAFOKLEBMTYLNISNNIKAPIP 420
 QY 421 VELSRINLDTLDSNNKINGIIPSSIGDLPHLLKMLSRHITGVVPGDGNRSTMEI 480
 DB 421 VELSRINLDTLDSNNKINGIIPSSIGDLPHLLKMLSRHITGVVPGDGNRSTMEI 480
 QY 421 VELSRINLDTLDSNNKINGIIPSSIGDLPHLLKMLSRHITGVVPGDGNRSTMEI 480
 DB 421 VELSRINLDTLDSNNKINGIIPSSIGDLPHLLKMLSRHITGVVPGDGNRSTMEI 480
 QY 481 DLSNNDISGPIPEELNQLQNIILRLENNLLTGAVSGLANCLSTLVNVSHNNLVGDIPIK 540
 DB 481 DLSNNDISGPIPEELNQLQNIILRLENNLLTGAVSGLANCLSTLVNVSHNNLVGDIPIK 540
 QY 481 DLSNNDISGPIPEELNQLQNIILRLENNLLTGAVSGLANCLSTLVNVSHNNLVGDIPIK 540
 DB 481 DLSNNDISGPIPEELNQLQNIILRLENNLLTGAVSGLANCLSTLVNVSHNNLVGDIPIK 540
 QY 541 NNNFSRSPSPSFIGNPGICGSMWNSPCHDSRTYRVASISRAAIIIGIAGIVILLAVLIA 600
 DB 541 NNNFSRSPSPSFIGNPGICGSMWNSPCHDSRTYRVASISRAAIIIGIAGIVILLAVLIA 600
 QY 541 NNNFSRSPSPSFIGNPGICGSMWNSPCHDSRTYRVASISRAAIIIGIAGIVILLAVLIA 600
 DB 541 NNNFSRSPSPSFIGNPGICGSMWNSPCHDSRTYRVASISRAAIIIGIAGIVILLAVLIA 600
 QY 601 ACRPHNPPPLDGLDKPVYTYSTPKLYIILHNNMLHYVEDIMRMTENLSEKYIIIGHGASS 660
 DB 601 ACRPHNPPPLDGLDKPVYTYSTPKLYIILHNNMLHYVEDIMRMTENLSEKYIIIGHGASS 660
 QY 601 ACRPHNPPPLDGLDKPVYTYSTPKLYIILHNNMLHYVEDIMRMTENLSEKYIIIGHGASS 660
 DB 601 ACRPHNPPPLDGLDKPVYTYSTPKLYIILHNNMLHYVEDIMRMTENLSEKYIIIGHGASS 660

QY 661 TVYKCVLKNCKPAVKRLYSHNPQSMKOPETELEMSSIKGRNLVSLQAVSLSHLSGLLF 720
 DB 661 TVYKCVLKNCKPAVKRLYSHNPQSMKOPETELEMSSIKGRNLVSLQAVSLSHLSGLLF 720
 QY 721 YDYLENGSLMDLHGPKPKKTLDMWTRLKAYGAAGLALVHHDSPRIIHRVYKSSNLL 780
 DB 721 YDYLENGSLMDLHGPKPKKTLDMWTRLKAYGAAGLALVHHDSPRIIHRVYKSSNLL 780
 QY 781 LDLDLEARLTDPGIAXSLCYSKGHTSYVMGTIGYIDPEYARTSRLTSEKSDVSYGIVLL 840
 DB 781 LDLDLEARLTDPGIAXSLCYSKGHTSYVMGTIGYIDPEYARTSRLTSEKSDVSYGIVLL 840
 QY 841 ELLTRRAVDDESNNLHLLIMSKGNNEVEMADPDITSTCKDLGVYKVFQALACTKQ 900
 DB 841 ELLTRRAVDDESNNLHLLIMSKGNNEVEMADPDITSTCKDLGVYKVFQALACTKQ 900
 QY 901 PNDPPTMHQYTRVLGSMLESEPPAATDTSATLAGSCYDEYANLKTTPHVNCSMSASD 960
 DB 901 PNDPPTMHQYTRVLGSMLESEPPAATDTSATLAGSCYDEYANLKTTPHVNCSMSASD 960
 QY 961 AOLFLRFGVISONSE 976
 DB 961 AOLFLRFGVISONSE 976

RESULT 2
 069SP5_ORYSA PRELIMINARY; PRT; 978 AA.

AC 069SP5;
 DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2004, sequence version 1.
 DT 21-FEB-2006, entry version 15.
 DE Putative receptor protein kinase.
 GN Name=OSJNB0016019.39;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
 OC Euharicotidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa japonbare (GAJ) genomic DNA, chromosome 6, BAC
 clone:OSJNB0016019."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC EMBL; AP004991; BAD35990.1; -; Genomic DNA.

DR Gramene; O69SP5;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_pln.
 DR InterPro; IPR003591; LRR_typ.
 DR InterPro; IPR013210; LRRNT_2.
 DR InterPro; IPR008271; Prot_Kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00560; LRR_1; 19.
 DR Pfam; PF00569; Pkinase; 1.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; kinase; leucine-rich repeat; Nucleotide-binding;
 KW Receptor; Receptor; Serine/threonine-protein kinase; transferase.
 SQ SEQUENCE 978 AA; 106746 MW; 9F0485366B705BD2 CRC64;

Query Match 73.5%; Score 3709; DB 2; Length 978;
 Best Local Similarity 73.6%; Pred. No. 1,5e-197;
 Matches 713; Conservative 100; Mismatches 148; Indels 8; Gaps 4;

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13 LFCLSAVATVSEAGATLLEIKKSFKDYNVLYDWTTPSSDYCVWGVSCENTFENVA 72
13 LVAALLVAVAVADDGSLLEIKKSFYRVNDVLYDMA--GDGYCSWGVLCNDVTFVAA 69
73 LNSLDNLDEISPAIGDKLSLSDKGRKLSQIPDEIGDSSGLONLSPNELSGDI 132
70 LNLGSLNLGGEISPAVGRKLGIVSIDKNSLGGQIPDEIGDSSSLKTLDFSNLSDGI 129
133 PFESIKLKOLEQLKKNQOLIGPISPTLSQIPNLKIDLQNKLSGEIPRLIYWEVLYQY 192
130 PFESVSKLKIESILKKNQOLIGVIPSSTLSQIPNLKIDLQNKLSGEIPRLIYWEVLYQY 189
193 LGLRNNLVGNISPDLCQLTGLWYFDVRNNSLTGSIPEITGNCTAFQVLDLSTNLTGEI 252
190 LGLRNNLVGNISPDLCQLTGLWYFDVRNNSLTGSIPEITGNCTAFQVLDLSTNLTGEI 249
253 PPIGIFQVATLSLQGNQLSGKIPSVGLMQALAVLDLGNLSGSIPEPLIGLNTFEKL 312
250 PFNIGIFQVATLSLQGNQLSGKIPSVGLMQALAVLDLSTNLTGSIPEPLIGLNTFEKL 309
313 YLHNSNKLTSIPPELGNMSKLYLELNDNLGHIPELGLKLDLPLIYANNNDLSEPIP 372
310 YMGANKLTGIPPELGNMSKLYLELNDNLGHIPELGLKLDLPLIYANNNDLSEPIP 369
373 DHLSSCTNLNSLVHGNKFSGITIPRAFOKLESMTYLNLSSNNIKGPIPELISIGLNDLT 432
370 DNISSCVNLNSFAYAGRLNGTIPPSLHKLESMTYLNLSSNNIKGPIPELISIGLNDLT 429
433 DLSNNKINGIIPBSLGDLEHLKKNLSRHHITGVPGDFGNLSINEIDLSNNDISGPIP 492
430 DLSNNKINGIIPBSLGDLEHLKKNLSRHHITGVPGDFGNLSINEIDLSNNDISGPIP 489
493 BELNOLQNIILALENNNLTVGNVGLANCLSTVYLVNNSHNLVGDIPKNNNSPESDSF 552
490 BELNOLQNIILALENNNLTVGNVGLANCLSTVYLVNNSHNLVGDIPKNNNSPESDSF 549
553 IGNPGLCGSWLNSPCHDSRRTVVISRAAIIIGAIIGLVIILMVLIACRPHNPPEFLD 612
550 LGNPGLCGYWLSSCSHGHQKPLISKAILIGAVGLVILMLIIVAVCRPHSPVFKD 609
613 GSLDKVVTYSTPKLVILHNNMALHYEDIMRMTENUSEKTYIGHGASTYKCVLXNCKP 672
610 VSVSKFVSNNPPLKLVILHNNMALHYEDIMRMTENUSEKTYIGHGASTYKCVLXNCKP 669
673 VAKRLYSHNPOGKOFETELMSSIKHRLNLSLAQVLSHSGSLFYVLYNGSLMDL 732
670 VAKRLYSHNPOGKOFETELMSSIKHRLNLSLAQVLSHSGSLFYVLYNGSLMDL 729
733 LH-GPTKKKTLDMDTRKLIAVGAAGLAVLHHDSPRIIRHDVKSNIILDKXLEALTD 791
730 LHGGPTKKKTLDMDTRKLIAVGAAGLAVLHHDSPRIIRHDVKSNIILDKXLEALTD 789
792 FGIAXSLCVSKSHSTYVMGTIGYIDVARTSRRLTEKSDVSYGYVLELLTRRAVDD 851
790 FGIAXSLCVSKSHSTYVMGTIGYIDVARTSRRLTEKSDVSYGYVLELLTRRAVDD 849
852 ESNLHLIMKKTGNNEMKADPDITSTCDLGVKVVQFQALICTROGNDSPTHMQVT 911
850 ESNLHLIMKKTGNNEMKADPDITSTCDLGVKVVQFQALICTROGNDSPTHMQVT 909
912 RVLGSEFMLSQPPAATDTSA---TLAGSCVDEYANIKTSHSVNCSGMS--ASDAQFLRF 967

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Db 910 RVLDCLVRPDPPEKSAQOQLMPQRPAPVPSYINIEVSLRGTSVLSCANSCTSDAEFLFK 969
 QY 968 GOVISONSE 976
 Db 970 GEVISONTE 978

RESULT 3
 O8W09_SORBI
 ID O8W09_SORBI PRELIMINARY; PRT; 921 AA.
 AC O8W09;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 21-FEB-2006, entry version 24.
 DE Putative receptor protein kinase.
 GN Name=SB35P03.1;
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 OX NCBI_TaxID=4558;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15466289; DOI=10.1101/gr.2332504;
 RA Swigonova Z., Lai J., Ma J., Ramakrishna W., Liaca V., Bennetzen J.L.,
 Messing J.;
 RT "Close split of sorghum and maize genome progenitors."
 RL Genome Res. 14:1916-1923(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15466290; DOI=10.1101/gr.2701104;
 RA Lai J., Ma J., Swigonova Z., Ramakrishna W., Linton E., Liaca V.,
 Tanyolac B., Park Y.J., Jeong O.Y., Bennetzen J.L., Messing J.;
 RT "Gene loss and movement in the maize genome."
 RL Genome Res. 14:1924-1931(2004).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Park Y.-J., Ramakrishna W., Sanmiguel P., Emberton J., Bennetzen J.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Liaca V., Young S., Kovchok S., Messing J.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC
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 CC
 CC EMBL: AF466199; AAL68842.1; -; Genomic_DNA.
 DR Gramene; O8W09;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001611; IPR.
 DR InterPro; IPR007090; IPR_pln.
 DR InterPro; IPR003591; IPR_tyr.
 DR InterPro; IPR013210; IPRNT 2.
 DR InterPro; IPR007719; Prot_Kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00560; IRR.1; 17.
 DR Pfam; PF00569; kinase.1.
 DR Pfam; PF07714; kinase_Tyr.1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase.1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KM ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding;
 KM Receptor; Repeat; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 921 AA; 100740 MW; FECCD22F874E463 CRC64;

Query Match 66.9%; Score 3372.5; DB 2; Length 921;

Best Local Similarity 68.4%; Pred. No. 7,3e-179;

Matches 666; Conservative 96; Mismatches 141; Indels 71; Gaps 8;

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QY 13 LFCSLVATYSEGGATLLEIKSFKDVNNVLYMTTSPSSDYCVWNGVSEENTENVVA 72
DB 9 LVALLVAVAVADGATLVETIKSFRRVGNVLYMA--GDYCSMGVGLCDNVTFAVA 65
QY 73 LNTSLDLDEISPAIDGLKSLSIDRGNRLSGQIPDEIDCGSSLONLDSFNEISGDI 132
DB 66 LNTSLDLDEISPAISVSLKSLVSDIKSLNLSQIPDEIDCGSSLKRLDPSFNNLGD 125
QY 133 PFSISKLEQELILKNNLIGPISLISQIPNLKILDLAONKLSGEIPRLIYNEVLYQ 192
DB 126 PFSISKLEHNLILKNNLIGPISLISQIPNLKILDLAONKLTGEIPRLIYNEVLYQ 185
QY 193 LGLRGNLVGNISDLCQLTGLWFPDVRNNSLTGSIPEITGNCFAFOVLDSTYNQLTGEI 252
DB 186 L-----DVKNNSLTGVIPDTIGNCTSFVLDSTYNRFTGP 221
QY 253 PFIDGFOVATLSLQGNLQSGKIPSVIGLMQALAVLDISGNTLGSIPILIGNLTFTK 312
DB 222 PFNIGFOVATLSLQGNLQSGKIPSVIGLMQALAVLDSTYNQLTGEIPISLIGNLTFTK 281
QY 313 YLHNSKLTGSIPELGNMSKLYLHLDNHLTGHIPELGLTDLFDLVANNDLEGP 372
DB 282 YIQGNKLTGSIPELGNMSKLYLHLDNHLTGHIPELGLTDLFDLVANNDLEGP 341
QY 373 DHLSSCTNLSLNGHKKFSGTIPRAFOKLESMYILNLSNNIGPPELISRGINDTL 432
DB 342 DNLSSCTNLSLNGHKKFSGTIPRAFOKLESMYILNLSNNIGPPELISRGINDTL 401
QY 433 DLSNNKINGTIPSSLDGHEHLKNNLSRNHTGVVPGFGNLRISIMEIDLSNNDISGP 492
DB 402 DLSNNKINGTIPSSLDGHEHLKNNLSRNHTGVVPGFGNLRISIMEIDLSNNDISGP 461
QY 493 EELNQLONILRLLENNLITGNVSLANCLSLTVLVNLSHNLVGDIPKNNNSPSPSP 552
DB 462 OELEMLQNMLM-----LNVSYNNLAGVADVANNFTFSPSPSF 498
QY 553 IGNNGLGSMNLNSCHSRKTRVRSISRAALIGLIVLLMVLIACRPHNPPPLD 612
DB 499 LGNNGLGSMNLNSCHSRKTRVRSISRAALIGLIVLLMVLIACRPHNPPPKD 558
QY 613 GSLDKPTVSTPKLVILHMMNALHYEDIMTENTLSEKYLIGHGASTYKCYLKNCKP 672
DB 559 VTYSKPRNAPPKVILHMMNALHYEDIMTENTLSEKYLIGHGASTYKCYLKNCKP 618
QY 673 VAIKRLYSNPQSKQFETELMSSLIKHRLVSLQVLSLHGLSLFYDLENGSLMDL 732
DB 619 VAIKRLVYAHYPOSKEFETELTGSIKHRLVSLQVLSLHGLSLFYDMEGCSLMDV 678
QY 733 LH-GPTKKKTLDMVTRKIAVGAAGLAVLHDCSPRIIRHDVSSNILLDKDLAALT 791
DB 679 LHGGSSKKKLDWETRLRLAAGLAVLHDCSPRIIRHDVSSNILLDKDLAALT 738
QY 792 FGIASLCSVSKSHSTYVMGTIGYIDPEYARTSLRTEKSDVY-----SYGVLLELTR 846
DB 739 FGIASLCSVSKSHSTYVMGTIGYIDPEYARTSLRTEKSDVYRMLHMSAG----- 788
QY 847 KAVVDESNNLHLLIMSKTGNNEVMEMADPITSTCKDLGVKKVYFQALLCTKRPND 906
DB 789 -AADWQASAGORITSLTASNEVMDVTDPIGDTCKDGEVKKLQALLCTKRPND 847
QY 907 MHQVTRVLGSPMLSEOPP---AATDTATLAGSCYVDEYANLKTTPHAYNC-SSMSADAQ 962
DB 848 MHEVVRVLDCLVNPDPPPKSAHQLPPSPAVPSYINEYVSLRGTGALSCANSTSTSDAE 907

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QY 963 LFLRFGVVISONS 976
 DB 908 LFLRFGVVISONS 921

Query Match 63.5%; Score 3200.5; DB 2; Length 980;

Best Local Similarity 65.8%; Pred. No. 2.9e-169;

Matches 624; Conservative 140; Mismatches 178; Indels 11; Gaps 7;

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QY 26 EGATLEIKSFKDVNNVLYMTTSPSSDYCVWNGVSEENTENVVA 85
DB 35 EGATLEIKSFKDVNNVLYMTTSPSSDYCVWNGVSEENTENVVA 92

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QY	86	PAIGGLKSLSTLDIGENRRLSGQIPDEBIGCCSSLONLDSNENLSGPIPSISKLKOLEQ	145
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QY	146	ILKNNQLIGPIPSTLSQIPNLKILDLAOKNLGSEIPRLIYMNVEVLYLGIRGNLLVGNIS	205
Db	153	ILKNNQLIGPIPSTLSQIPNLKILDLAOKNLGSDIRLLIYMNVEVLYLGIRGNLSLGTLS	212
QY	206	PDLCOLTGLWYFDVNRNLSLSPETIGNCTAFQVLDLSYNQLTGEIPDIFGLQVATLS	265
Db	213	PDMCOLTGLWYFDVNRNLTGTRIPESIGNCTSEIIDI SYNQISGEIPYNIIGLQVATLS	272
QY	266	LOGNOLSGTIPESVIGLQMLAVLDLSGNLLSGSIPRIIGNLTTREKLYLHNSLGTSP	325
Db	273	LOGNRLTGKIPROVIGLQMLAVLDLSENLVGPISPIIGNLSTGKLYLHGNKLTGVIPP	332
QY	326	ELGNNSKLHYLELNDNHLRGHIPPETLGKLTDLFDLVANNNDLGGPIPDHLSGCTNLSLN	385
Db	333	ELGNNSKLSLYLOLNDNLVGTIPAEIGKLEBELFELMANNLLOGPIIPANISCTALANKFN	392
QY	386	VHGNKFSGTIPPAFOKLESMYTLNLSNNIKGPIPVELSRIGNLDTLDSNNKINGIIPS	445
Db	393	VYGNKLTNGSIPAGFOKLESLTYTLNLSNNPKNGIPSELGHIINLDTLDSLYNFSGVPVA	452
QY	446	SLGLDEHLIKNLSRNHITGVYPGDFGNRSIMEIDLSSNDISGPIPEELNQLQNIILLR	505
Db	453	TIGDEHLEHLEMLSKNHLDPGPAEFGNLRSVQVIMSNNSNLSGSLPEELGQLQNDLSLI	512
QY	506	LENNNLTVNV-GLSANCSTLVLYNHNHNLVGGIPKNNNPSRSPSPSFGNPGLCGSMWN	564
Db	513	LNNNLVGEIIPQOLNCSFLNNLNLSYNLSGHNVPAAKNFSKFPMSFLGNPLLHYQQD	572
QY	565	SPCHDSRRTRVRSISRPAALIGLIGLVLLMWLIAACRPHNPPEPLDGLDKPVTVSTP	624
Db	573	SSCGSHSQ-RNISKETALACIIGPIIILCVLLAIYKTNQOPLVKS-DKPV-QGRP	629
QY	625	KLVLILHNNMNLHVYEDIMKMTENLSSEKTIIGHGASVTYKCVLKNCKPVAIKLYSHNPQ	684
Db	630	KLVLVQMMALHTFYEDIMKLTENLSSEKTIIGHGASVTYKCELSGKALIAVKRLYSQYNH	689
QY	685	SMKOFETELMSSIKHRLVLSLQAVSLSHLSGLFYDVLNENSLMDLHGPKKXTLDW	744
Db	690	SLRETELETTGSIHRHNVSLHGFSLSPHGWLIFYDVNENSLMDLHGPKKVKLW	749
QY	745	DTRLIYAGAAGLAVYLHHDSCPRILHRPVKSSNILLDKDLARLTDFGIASLCSKSH	804
Db	750	DTRLRIYAGAAGLAVYLHHDCHPRILHRPVKSSNILLDERFEHLSDFGIAKVPASAKSH	809
QY	805	TSTYVMGTIGYIDPEYARTSRLTESKDVSYSGYIVLLELTLRRKAVDSESNLHILMSKTG	864
Db	810	ASTYVIGTIGYIDPEYARTSRLTENKSDVSYSGYIVLLELTLTKKAVDNESNLHQILSKAD	869
QY	865	NNEVEMADPDITSTCKDLGVYKKAFFOLALLCTKROPNDRPYHQAOTRVLGSMISE--Q	922
Db	870	DNTWEADVSESVCTDGMGLVRKAFQALLCTKRPSDRPTMHEARVAVLSLLPVSAMT	929
QY	923	PPAATDTASTLLAGSCVDEYANILKTHSVNCSMSASDQLPLRFQVITSNS	975
Db	930	TPKTYVYSRLASTITTA--ADMRGHDTVTDIGNSSSDDEQFVRFESVLSKHT	979
RESULT 5			
Q7XB99_ORYSA			
ID	Q7XB99_ORYSA	PRELIMINARY; PRT; 999 AA.	
AC	Q7XB99;		
DT	01-OCT-2003,	integrated into UniProtKB/TrEMBL.	
DT	01-OCT-2003,	sequence version 1.	
DT	21-FEB-2006,	entry version 15.	
DE	Transmembrane protein kinase.		
GN	Name=PK3;		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade;		

OC	Enharptoidaeae: Oryzaeae; Oryza.
OX	NCBI_TaxID=339477;
RN	(1)
RP	NUCLEOTIDE SEQUENCE.
RA	Yao Q., Peng R., Xiong A.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NonDerivs license
CC	-----
DR	EMBL: AY32474; AAC01160.1; -, mRNA.
DR	Girameine; Q7X899; -.
DR	GO: GO:0016021; C: Integral to membrane; IEA.
DR	GO: GO:0005524; F: ATP binding; IEA.
DR	GO: GO:0000166; F: nucleotide binding; IEA.
DR	GO: GO:0004674; F: protein serine/threonine kinase activity; IEA.
DR	GO: GO:0016740; F: transferase activity; IEA.
DR	GO: GO:0006468; P: protein amino acid phosphorylation; IEA.
DR	InterPro: IPR001611; LRR.
DR	InterPro: IPR007090; LRR p1n.
DR	InterPro: IPR003591; LRR typ.
DR	InterPro: IPR013210; LRRNT 2.
DR	InterPro: IPR000719; Prot Kinase.
DR	InterPro: IPR008271; Ser Thr_pkin_AS.
DR	InterPro: IPR002290; Ser Thr_pkinase.
DR	InterPro: IPR001245; Tyr_pkinase.
DR	Pfam: PF00560; LRR 1; 18.
DR	Pfam: PF00069; Pkinase; 1.
DR	PRINTS: PR00019; LEORICHRPT.
DR	ProDom: PD000001; Prot_kinase; 1.
DR	PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE: PS00114; PROTEIN KINASE DOM; 1.
DR	PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW	ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding; Repeat;
KW	Serine/threonine-protein kinase; transferase; transmembrane.
SO	SEQUENCE 999 AA; 109036 MW; F0F8BD3D70917E03 CRC64;
QY	Query Match: 61.7%; Score 3113; DB 2; Length 999;
QY	Best Local Similarity: 63.1%; Pred. No. 2.2e-164;
QY	Matches 618; Conservative 135; Mismatches 182; Indels 44; Gaps 9;
DB	26 EGATLLEIKKSFKDVNNVLYDMTTPSSPDYCVWRGVSCEVTFNVVALNLSIDLNDGEIS 85
DB	35 EGMALMGKXGFGNAALVDM--DGADHCHAMRGVTCDNASFVALLNLSNMLGGEIS 92
QY	86 PAIDDLKSLSLIDLRNRLSGQIPDEIGDCSSLONLDSLSENLSGDIPFSISKIKOLEQL 145
DB	93 PAIPELKNLQGVDDKGNKLTQGIPEDEIGDCISLKYLDLSGNLALGDIPIFSISKIOLLEEL 152
QY	146 ILKNNQLIGPIPSLTSGQIPNLKIILDAONKLSGSIPIILYWNELQYLGIRGNLVGNIS 205
DB	153 ILKNNQLTGPPIPSLTSGQIPNLKIILDAQNOLGTGDIPIILYWNELQYLGIRGNLVTGLS 212
QY	206 PDLQQLTGLMVFYDRNNLSLTGSIPEITGNCATPAQVLDLSYNOLGELIPFDIGFQVATLS 265
DB	213 PDMQQLTGLMVFYDRGNLNLGTIPESIGNCTSPFILDISTNQISGELIPYINIGFQVATLS 272
QY	266 LQGNQLSGKIPSVIQLMOALAVLDLSGNLLSGSIPIILGNLTTEKLYLHNSKLTGSIPP 325
DB	273 LQGNRLTGKIPDVIGLMOALAVLDLSSENLVGPIPSILGNLSYGKLYLHGKLTGVIYP 332
QY	326 ELGNMSTLHYLELNDNLHTGHIPELGLKTLDPILYANNDLSBPITDHLSSCTNLNLSN 385
DB	333 ELGNMSTKLSYQLNDNLVGTIPAEIQLKEELFELIYANNLQGPISANTSSCTALNKPEN 392
QY	386 VHGNKFSGGTIPRAFOKLESMTYLLSSNNIKGPIPEVLSRIGNDITDLSNNKINGIIPS 445
DB	393 VYGNKLGSIIPAGQOKLESILTLYLLSSNNRKGNIPSLGHIINDITDLSYNESGGVPA 452
QY	446 SLGGLLEHLKNNLSRNHITGVVPDPEGNLRSIMEIDLSNNDISGPIPEELNQLONTILLR 505

Dh 453 TIGDLEHLLELNLSKNHLDGFPVPAEFGNLSVQYIDMSNNLSGSLPELIGQLONLDSLI 512
Qy 506 LENNNLTGVN-GSLANCLSLTVLVNHNHVGDI PKNNFSRSPD----- 550
Db 513 LNNNLVGEIIPAOLANCFSL-----NNLAFQEFVIQOFIWTCPDGKELLETPNGKHL 565
Qy 551 -----SFIGNPGLCGSLWLNPCDHSRRTRVVSISRAAILGAIAGVILLMLV 598
Db 566 ISDONQYINHKCSPLGNPLLHVVCQDSCGSHQ-RVNISKTAIACILIGFILLCVLL 624
Qy 599 IAACRPNPPEFLDGLDKPVYTSIPKVLIIHNMALHVEDIRKMTENSEKYLIGHGA 658
Db 625 LAIYKTKQPPPLVYKGS-DKEV-QGPVKVLQDMALHTYEDIRKLTENLSEKYLIGYGA 682
Qy 659 SSTYKCVLKNCKRVAIKRLYSHNPQSMKOPETELEMSSIKHNLVSLQAVSLSHGSL 718
Db 683 SSTYKCVLKNCKRVAIKRLYSHNPQSMKOPETELEMSSIKHNLVSLQAVSLSHGSL 742
Qy 719 LFYDYLNGSLMDLHGPRTKKTLDMDTRLKIAYGAQGLAYLHSDSPRIHRDVXSN 778
Db 743 LFYDYMNGSLMDLHGPRTKKTLDMDTRLKIAYGAQGLAYLHSDSPRIHRDVXSN 802
Qy 779 ILDDKDIPEARLTDFGIAKSLCVSKSHSTYVMGTIGYIDPEYARTSLTEKSDVSYGIV 838
Db 803 ILDDENEFAHLSDFGIAKCVPSAKSHASTYVLTGTYIDPEYARTSLTEKSDVSYGIV 862
Qy 839 LLELLTRKAVDSDSNLHILMSKTGNNEWMEMADPITSTCXDLGVYKVFQALILCTK 898
Db 863 LLELLTRKAVDSDSNLHILMSKTGNNEWMEMADPITSTCXDLGVYKVFQALILCTK 922
Qy 899 ROPNDRPTMHQVTRVLSFMLE--OPPAATDTSATLAGSCYVDENALTKPHSNSSM 956
Db 923 RHPEDRPTMHQVTRVLSFMLE--OPPAATDTSATLAGSCYVDENALTKPHSNSSM 979
Qy 957 SASDPAQLPLRFGVYISONS 975
Db 980 SSSDEQMFVRFGEVYSKHT 998

RESULT 6

Q6XAT2_ARATH PRELIMINARY; PRT; 967 AA.
AC Q6XAT2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 13.
DE ERECTA-like kinase 2.
GN Name=ERL2;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
NP NUCLEOTIDE SEQUENCE.
RP PubMed=14985254; DOI=10.1242/dev.01028;
RA Shpak B.D., Berthiaume C.T., Hill E.J., Torii K.U.;
RT "Synergistic interaction of three ERECTA-family receptor-like kinases
controls Arabidopsis organ growth and flower development by promoting
cell proliferation.";
RL Development 131:1491-1501(2004).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
CC EMBL: AY244746; AAP69764.1; -; mRNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
PR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro: IPR001611; LRR.
DR InterPro: IPR007090; LRR_p1n.
DR InterPro: IPR003591; LRR_typ.
DR InterPro: IPR013210; LRRNT_2.
DR InterPro: IPR0007219; Prot_Kinase.
DR InterPro: IPR008271; Ser_thr_kin_AS.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00560; LRR_1; 18.
DR Pfam: PF00069; Kinase; 1.
DR PRINTS: PR00019; LEURICHRPT.
DR ProDom: PD000001; Prot_Kinase; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding; Repeat;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 967 AA; 106680 MW; 90096C7B67CE852C CRC64;

Query Match 61.3%; Score 3089.5; DB 2; Length 967;
Best Local Similarity 62.2%; Pred. No. 4,3e-163;
Matches 605; Conservative 134; Mismatches 211; Indels 23; Gaps 6;

Qy 11 GLEFCLSLV-----ATTSEGAITLLETKSFQDVNNVLYDWTSPSSDYCVNRGVSC 63
Db 9 GLFFCLGMVVFMLGSGVSPMNEGKALMAIKAFSVNANMLDMDDVHNHDFCSMRGVFC 68
Qy 64 ENTENVVALNLSDLNLDGEISPAIGDLKSLISIDLRGNLSGQIPDEIGDCSSLQNL 123
Db 69 DNVSANVSNLNLNLNGEISSALGDMNLQSIDLGNLGQIPDEINCVSLAYVDF 128
Qy 124 SFNELSGDIPFSISKQLEQLILKNNQLGIPSTLSQIPNLKILDLAQNKLSGEIPRL 183
Db 129 STNLRFEDIPFSISKQLEFNLKNNQLGPIPATLTQIPNLKILDLAQNQLTGEIPRL 188
Qy 184 IYNNVLYQYGLGNNLVGNISPDLCQLTGLMTFVDNRANSLTGISERTGNCTAFQVLD 243
Db 189 LYNNVLYQYGLGNNLVGNISPDLCQLTGLMTFVDNRANSLTGISERTGNCTAFQVLD 248
Qy 244 SYNQLTGEIPFDIGFLOVATLSLQGNLSGKIPSVIGLMOALAVLDLSGNLSGIPRL 303
Db 249 SYNQLTGEIYNNIGFLOVATLSLQGNLKTIRIEVIGLMOALAVLDLSGNLSGIPRL 308
Qy 304 GNLTFTEKLYLHGNKLTGSIPELGNMSKLYLDELNDNLHGIPELGLTDLFDLNV 363
Db 309 GNLSTFKLYLHGNKLTGQIPELGNMSRSLYQLNDNELVGIPELGLTDLFDLNV 368
Qy 364 NNDLEGPIDPHLSSCTNLSNLNHNKFKSGTIPRAQKLESMTYLLNLSNNIGPIPEL 423
Db 369 NNDLVGIPENISSCALNPFNHNKFLSGAVPLERFNLGSLTYLLNLSNPSFGKIPAE 428
Qy 424 SRIGNLDTLDSNNKINGIIPSSIGDLEHLKNNLSNNHTGVVPGDFGNLSIMEIDL 483
Db 429 GHIINLDTLDSNNNSGSIPLTLGDLEHLILNLSRNLNGTLPAEFGNLSRIQIIDS 488
Qy 484 NNDISGPIPELNQNLNIIILRLNENNLTVN-GSLANCLSLTVLVNHNHVGDIIPKN 542
Db 489 ENFLAGVITPELQQLQNLNLIINNKKIHGKIPEQLNCFSLANLNISFNLSGIIIPMK 548
Qy 543 NFRSFPDSFTGNPGLCGSLWLNPCDHSRRTRVVSISRAAILGAIAGVILLMLVIAAC 602
Db 549 NFRSFPASFPFGNPFGLCGNMGVSGICGSLPKQSV-FRRVAVICMVVIGFILLIMIFAVY 607
Qy 603 RPNHPPEFLDGLDKPVYTSIPKVLIIHNMALHVEDIRKMTENSEKYLIGHGASSTV 662
Db 608 KSKQKQKVLKSGSKQ--ESTKLVIHMDALHTPDIKRVENDEKIIIGYGASSTV 665
Qy 663 YKCVLKNCKRVAIKRLYSHNPQSMKOPETELEMSSIKHNLVSLQAVSLSHGSLFLYD 722
Db 666 YKCTSKSRDIAIKRIYQYPSNFRRETELETIGSRHNNIVSLHGVALSPGNLLFYD 725
Qy 723 YLENGSLMDLHGPRTKKTLDMDTRLKIAYGAQGLAYLHSDSPRIHRDVXSNLLD 782

Db	726	YMNCSLMDLHNPGRKKVYLDWETRLKAYAGAOGLAFLHHDCTPRLIHHDKSNNLLD	765
Qy	783	KDLEARLTDPGIAKSLCVSKSHSTYYWGTTGIDYIDPEYARTSRLTESDVSYSVGIALL	842
Db	786	GNEEARLSFGIAKSLIPATKYASTYVLCTIGYIDPEYARTSRLTNEKSDIYSFGIVLLEL	845
Qy	843	LTPRRKAVDESNLHHLINSGKTNNMEMADDDISTCKDGVYKKVYFQALLCTKQPN	902
Db	846	LTKKKAVDNEANLHQMLTISKADNNTVMEAVDNEAVSTCMDSGHIKTFQALLCTKKNPL	905
Qy	903	DREPTMQVRYLGSFMISSQPPAATDTSATLTAAGSCYDVEYANLKTPTHSVNCSSASDAQ	962
Db	906	ERTMTQEVSRVLLSLVPPSP-----KKLPSPAKVQGEGERRSHSDTIT-----PQ	963
Qy	963	LFLRFGQVSIQNS 975	
Db	954	WFVQFREDISKSS 966	

RESULT 7

ID	ORGANISM	PRELIMINARY	PRT	966 AA
AC	OS Arabidopsis thaliana (Mouse-ear cress)			
DT	05-JUL-2004, integrated into UniProtKB/TrEMBL			
DT	05-JUL-2004, sequence version 1			
DT	07-MAR-2006, entry version 14			
DE	ERECTA-like kinase 1.			
GN	Name=ERL1			
OS	Arabidopsis thaliana (Mouse-ear cress)			
OC	Eumariophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
OC	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	NOCLCOTIDE SEQUENCE.			
RX	PubMed=14985254; DOI=10.1242/dev.01028;			
RA	Shpak E.D., Berthiaume C.T., Hill E.J., Torii K.U.;			
RT	"Synectogenic interaction of three ERECTA-family receptor-like kinases			
RT	controls Arabidopsis organ growth and flower development by promoting			
RT	cell proliferation.";			
RL	Development 131:1491-1501(2004).			
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC				
DR	EMBL: AY244745; AAP69763.1; -. mRNA.			
DR	GenomeReviews; BA000015.GR; AT5G62230.			
DR	GO: GO:0005524; F:ATP binding; IEA.			
DR	GO: GO:0000166; F:nucleotide binding; IEA.			
DR	GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO: GO:0016740; F:transferase activity; IEA.			
DR	GO: GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro: IPR001611; LRR.			
DR	InterPro: IPR007090; LRR_p1n.			
DR	InterPro: IPR003591; LRR_CYP.			
DR	InterPro: IPR013210; LRRNT_2.			
DR	InterPro: IPR000719; Prot_Kinase.			
DR	InterPro: IPR008271; Ser_Thr_Pkin_AS.			
DR	InterPro: IPR002290; Ser_Thr_Kinase.			
DR	InterPro: IPR001245; Tyr_kinase.			
DR	Pfam: PF00560; LRR_1; 19.			
DR	Pfam: PF08263; LRRNT_2; 1.			
DR	Pfam: PF00063; Kinase; 1.			
DR	PRINTS: PR00019; LEURICHRPT.			
DR	ProDom: PD000001; Prot_Kinase; 1.			
DR	PROSITE: PS00107; PROTEIN KINASE ATP; UNKOWN_1.			
DR	PROSITE: PS0011; PROTEIN KINASE DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
DR	ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding; Repeat;			
DR	Serine/threonine-protein kinase; Transferase.			
DR	SEQUENCE 966 AA; 106401 MW; 2B63CF9693338D95 CRC64;			
DR	SEQUENCE 966 AA; 106401 MW; 2B63CF9693338D95 CRC64;			

Query Match	61.1%;	Score 3079.5;	DB 2;	Length 966;
Best Local Similarity	62.7%;	Pred. No. 1.5e-162;		
Matches 608;	Conservative 140;	Mismatches 205;	Indels 17;	Gaps 6;

QY	7	1VLIGFLCJLSVATVTSBEGATLLEIKKSKVDVNNVLYDMTTPSPSSDYCYWRGVCENV	66
Db	12	LAWGFM--VGVASANNNEGKALMAIKGSFSNNLVNMLDMDVDHNSDLCSWRVCFCNV	69
QY	67	TENVVANTLSDUNJEDGEISPAIGDKSLSTJDRKGNLSGOIPDEIGDCSSLOMDLSFN	126
Db	70	SYVSVLSLSSNLGGEISPAIGDRNDQSSIDLOGNKLAGOIPBEIGNCASVYLDLSEN	129
QY	127	ELASGDIPEFSIKLQOLBKNNQLIGPIESTLSQIPNKLIDLAONKLSGEIPRLIYW	186
Db	130	LLYGDIPFSIKLQOLETINKNNQOLGVPVATLTQIPNKRDLAGNHLGIESIRLLYW	189
QY	187	NEVVOYIGLRNNLVGNISPDLCOLGMYADVGNNSVLTGISEPTIGNCAFOYLDLSYN	246
Db	190	NEVVOYIGLRNNLVLTSSDMCCOLTGMVFDVGNLVTGIPESIGNCISFOYLDLSYN	249
QY	247	QLTGEIPEFDIGFOVATLSLOGNQLSKISPSVILMOALAVLDLSGNLSGSIPIIGNL	306
Db	250	QITGEIPIPNICFOVATLSLOGNRLTGRIPVIGLOALAVLDLSDBEIVGPIPIIGNL	309
QY	307	TFTKLYLHNSKLTGSIPELGNNSKLYHVELNDNHLTGHIPELGLKTDLPDINVANN	366
Db	310	SFTKLYLHGMLTGPIPELGNNSRSLYLOLANNKLVGTIPPELGLKEQLEFELTANSR	369
QY	367	LEGPIPHLSCTMNLNHNHGNKFSCTIPAPQKESMTYLNLSNNIKSIPIVELSRI	426
Db	370	LVGPIPSNISCCALNOPVHGNLSSIPAFENLSSLYTLNLSNNFKKIPVELECHI	429
QY	427	GNLDTLDSLNNKINGIIPSSLGDELHKLKNLSRNHTTGVVPGDFGNLRSMEDLSND	486
Db	430	INDKRLDLSGNNSFGSIPLTGLDLEHLLINTLSNHLSCQAPAFGNLRSLQMDIVSPNL	489
QY	487	ISGPIPEBLONQNIILRLENNLTGVN-GLSANCISLYLVANSNNLVODIPKNNFS	545
Db	490	LSGVIPELGOLOMNLNLIINNNTLHKKIPDOLNCFEVLNVLANSFNNLSGIVPMKXFS	549
QY	546	RFSPDFIGNGLCGSWNPSCHDSRRTRVYSIRAAIILGAIGLVILMLVLAACRPH	605
Db	550	RFAASAFGNNDYLOGNWVGSI CGPLPS-RV-FSRGALICIVLAVITLLCMIFLAVYKSM	607
QY	606	NPPELDGSDLPVYTSPPKLVILHMMNALHYVEDINRMENISEKYLIGHGASVYYKC	665
Db	608	QOKKILGSSKQ--AEGJTKLVILHMDMAIHTPDIMRVENINLEKFIIGVAGASTYYKC	665
QY	666	VLKACCPEVALIKRLYSNHPQSKQOFELEMLSSIKHRLVSLQAYSLSHGLSLFPDYLE	725
Db	666	ALKSRPAIRLRLNOQPHNLRFEFETELETIGSIRHRNIVSLHGYALSPTGNLLFYDME	725
QY	726	NGSLMDLLHGHTKKKTLDMPTRLKIAVGAOGLAYLHHDCSPRIIHRDVKSSNILLDKL	785
Db	726	NGSLMDLLHSGLKVKYKLGMETRLKIANGAOGLAYLHDCIPRLIIMHDIKSSNILLDBNF	785
QY	786	EARLTDGIAKSLCVSKSHSTSVYMGITGYIDPEYARTSRLLTEKSDVSYGIVILLELIR	845
Db	786	EAHLSDGIAKSIIPASKTHASTVYLGTGYIDPEYARTSRINEKSDIYSFGIVILLELITG	845
QY	846	RKAVDDSSNLHLLIMSKTGNNEVNMADPDLTSCXKLGVYKVFOLALLCTKQOPNDR	905
Db	846	KKAVDNEANHLQLLISTADNDTVNEADPEVYVCMOLGHRKRFOLALLCTKKNPIERP	905
QY	906	TMHOVTEVLGFSFMLEOPAPATDTSATVLACSVCYDEVANUKTPHSVNCSSMSASDAQFL	965
Db	906	TMLEVSRLVLSLVSLO-----VAKKLPJLDSHTKXKLOQNEVNRPDADAQOWFV	955
QY	966	RFGOVISONS 975	
Db	956	QFREVISKSS 965	

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RESULT 8
Q9LYP7_ARATH PRELIMINARY; PRT; 932 AA.
ID Q9LYP7_ARATH
AC Q9LYP7
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 28.
DE Receptor-like protein kinase.
DE Name=At5g07180; OrderedLocustNames=At5g07180;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -| CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -| SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AL163652; CAB87274.1; -; Genomic_DNA.
DR PIR; T48489; T48489.
DR TAIR; At5g07180; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_Pln.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR013210; LRRNT_2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00060; LRR_1; 18.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding;
KM Receptor; Repeat; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 932 AA; 102776 MW; F288A6F66C9FA4 CRC64;

Query Match 60.7%; Score 3059; DB 2; Length 932;
Best Local Similarity 63.1%; Pred. No. 2e-161;
Matches 597; Conservative 131; Mismatches 202; Indels 16; Gaps 5;

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QY 211 LTGLWYFDVRRNNSLTGSIPEITIGCTAFQVLDLSYNQLTGTEIPFDIGLQVATLSQNG 270
DB 181 LTGLWYFDVRRNNSLTGSIPEITIGCTAFQVLDLSYNQLTGTEIPFDIGLQVATLSQNG 240
QY 271 LSGKISVIGLMOALAVLDLSGSLGSGIPPIIGNTTFTEKLYASHNKLGTSPPELGNM 330
DB 241 LTGRIVEVIGLMOALAVLDLSGSLGSGIPPIIGNTTFTEKLYASHNKLGTSPPELGNM 300
QY 331 SKLHYELNDNHTGHIPELGLTDFDLNVANNDLEGPDPHLSSTCTNLNSLVHGNK 390
DB 301 SRLSTYQLNDNLNVLGKIPPELGLTDFDLNVANNDLEGPDPHLSSTCTNLNSLVHGNK 360
QY 391 FSGTIPRAFOKLSMTYLYLSSNNIKGPIPELSRIGMTDPTLDSNNKINGIIPSSLDGI 450
DB 361 LSGAVPLEFRNLGLTYLYLSSNIFKGIPELGLTDFDLNVANNDLEGPDPHLSSTCTNLNSLVHGNK 420
QY 451 EHLKRNLSNHTTGVVPPDQGLRISIMEIDLSNNDISGPIPELMOLONIILLRLENN 510
DB 421 EHLIINLSNHTLGLTDFDLNVANNDLEGPDPHLSSTCTNLNSLVHGNK 480
QY 511 LTGNV-GSLANCLSTVLYVSHNHLVGDIPKNNNFRSPDSFIGNPLGSLNSPCHD 569
DB 481 IHGKIPDQLTNCSTLANLNSFNMLSGIIPMKNTFRFPASFGNPFILGNWVSGICG 540
QY 570 SRRTRVYSISRAALIGLIGVILLMLVLIACRPHNPPFLDGLDKPVYSTPKLVIL 629
DB 541 SLRKSQV-FTRVAVICWVLGFTILCMIFLAVYKSKQKPFVLKSGSKOP--EGSTKLVLII 597
QY 630 HMMALHLYVDIIRMTENLSKTIIGHGASTYYKCVLKNCKRVALIKRLYSHNPKQK 669
DB 598 HMDMAHTFPDIDIRVTEENDEKTIIGHGASTYYKCVLKNCKRVALIKRLYSHNPKQK 667
QY 690 ETELEMSSIKHRLNLSLQVSLSHGSLTFYDLENGSLMDLHGPTKKTLDMDTRLK 749
DB 658 ETELETIGSRHNIYSLHGYALSPGNLFLFYMENGLMDLHGPTKKTLDMDTRLK 717
QY 750 IAYGAAQGLAYLHHDSPRIIRHDKVSSNITLDDKLEARITDFGIKSLCVSKSHSTYV 809
DB 718 IAYGAAQGLAYLHHDSPRIIRHDKVSSNITLDDKLEARITDFGIKSLCVSKSHSTYV 777
QY 810 MGTIGYIDPEYARTSLTEKSDVYSGIVLELTTRKAVDSDSHHILMSTGNNEWM 869
DB 778 LGTIGYIDPEYARTSLTEKSDVYSGIVLELTTRKAVDSDSHHILMSTGNNEWM 837
QY 870 EMADPDITSTCKDLGVKVFQALALCTKQKQPNDRPTMHQVTRVLGSMLEQPPATDT 929
DB 838 EAYDAEVSVCNDSGHKKTFOALALCTKRNPLERPTMGVSRVLLSLVSPPP----- 891
QY 930 SATLAGSCYVDEVYANLKTPHSVNCCSMASDAQFLRFQGVISQNS 975
DB 892 -KLLPSPAKQVEGEERESHSDTTT-----PQMFQVREDISKSS 931

RESULT 9
Q9LYB3_ARATH PRELIMINARY; PRT; 938 AA.
ID Q9LYB3_ARATH
AC Q9LYB3
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 28.
DE Receptor-like protein kinase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20181125; Pubmed=10718197; DOI=10.1093/dnares/7.1.31;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence

```


DR Pfam; PF00560; LRR_1; 10.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding; Receptor;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 719 AA; 79689 MW; 38A5F547FAC6FD02 CRC64;

Query Match 45.7%; Score 2306.5; DB 2; Length 719;
 Best Local Similarity 63.5%; Pred. No. 1e-119;
 Matches 466; Conservative 93; Mismatches 150; Indels 25; Gaps 9;

QY 251 EIPPDIFLOVATISLOGNLSKIPSVIGLMQALVLDLSGNLSSTIPPIIGNLTFTE 310
 DB 1 EIPVNIQFLOVATISLOGNRLTKIPVIGLMQALVLDLSGNLSSTIPPIIGNLSTYTG 60
 QY 311 KLYHSNKLGSIPPELGNNSKLHYELNDNLGHIPPELGLTDFDLVANNDEGP 370
 DB 61 KLYHGNKLGPPELGNNKTLSTYLDNDKLVGTIPALGKLELPELANNLEGP 120
 QY 371 IPEHLSSCTNLNSLVHGNKFSGTIPPAFOKLESMTYLNSSNNIKGPIPELSRIGNLD 430
 DB 121 IPQVISTCTALNKNFVHGNRLNGSIPIQFOKLESITLYLNFSNNFKGKPELGRINLD 180
 QY 431 TLDLSNNKINGIIPSSIGDLEHLKNNLSRHNGVPGDPGNRSIMEIDLSNNDISGP 490
 DB 181 TLDLSNNHFGSPIDSGIDLEHLELNLNRNNLNGPTEGNGRSQOTIDISTNKLSPQ 240
 QY 491 IPEELNQLNIILRLNENNLTVNGV-SLANCLSLTYLVNHNVLVDIPKNNNFSRSP 549
 DB 241 IPEELGVQITDITLIANNNDYIGIPVQLTNCFSLSSLNLSFNNFSDVPLSKNFSPQ 300
 QY 550 DSFTGNFGCGSWNSPCHDSRRTRVVISRAAIIIGLGLVILLVLAACRPNNPP 609
 DB 301 ESFTGNFMLCGNWLSSCGODLHSGKYTISRAAVVCITLGSMLVAIYKSSQPKQ 360
 QY 610 FLGSLDKPVTYSPKLVILHNNMALHVPEIDIMEMTNLSKYYIIGHASSTVYKCVLKN 669
 DB 361 FIKGS--NRTVQGPVKLVLRMDAIIHYEDIMKTNLSKYYIIGHASSTVYKCVLKN 418
 QY 670 CKPAIAIKLYSHNPOSMAKOFETELEMSSIKRNIVLSQAVSLSHLSGLFYDYLENGSL 729
 DB 419 SKPIAIKRLISQYVHNHHEFELETFIGSIRNRVLVSLHGSISPHGNLIFYDYMENGSL 478
 QY 730 WDLHGFTKKKTLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKSSNILLDKOLEARL 789
 DB 479 WDLHGFSKKVKLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKSSNILLDENFEARL 538
 QY 790 TDEGIAASLCVSKSHSTVYMGITGYIDPEYARTSLTEKSDVSYGVILLELTRKAV 849
 DB 539 SDEGIAACIPAKTHASTYVLTGYIDPEYARTSLRNKSDVSYGVILELLETRKAV 598
 QY 850 DDESNLHLHLSKTKGNNEVMADPDTSTCKDGLGVKKVFOALLCTKSPNDPTMHQ 909
 DB 599 DNGSNLHQLILSKADNDTWEAVDFEVRSPAWMG-CQKAFQOLA-ICAQR--SPRPIMHE 654
 QY 910 VTRYLGSFM-----LSEQPPAATTSATLAGSCYVDEYANLKTSHSVNCSMSASDA 961
 DB 655 VAVRLVSLLEVPSPSLKPLVPOKP--MDYAHYLAAGPDV---KIKRTHDN---SSSDG 704
 QY 962 QLFARFGQVSONS 975
 DB 705 QMFURFGEVISKNT 718

RESULT 11
 ID Q6WZ3_ARATH PRELIMINARY; PRT; 441 AA.
 AC Q6WZ3;
 Q6WZ3;

DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Putative receptor-like protein kinase (Fragment).
 GN Name=At2g26330.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxId=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tsuchioka Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
 RA Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
 RA Kobayashi M., Toyota A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinzaki K.;
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC -----
 DR EMBL; AK221866; BAD94220.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_Thr_kin AS.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 441 AA; 49058 MW; 3E2696FC5B9CF796 CRC64;

Query Match 45.6%; Score 2299; DB 2; Length 441;
 Best Local Similarity 100.0%; Pred. No. 1.4e-119;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 GDIPKNNNFSRSPDSFTGNPGICGSWLNSPCHDSRRTRVVISRAAIIIGLGLVILL 595
 DB 1 GDIPKNNNFSRSPDSFTGNPGICGSWLNSPCHDSRRTRVVISRAAIIIGLGLVILL 60
 QY 596 MVLIACRPNNPPPIDGLSDKPVYSTPRLVILHNNMALHVVEDIMRMTENISEKYYIG 655
 DB 61 MVLIACRPNNPPPIDGLSDKPVYSTPRLVILHNNMALHVVEDIMRMTENISEKYYIG 120
 QY 656 HGASSTVYKCVLKNCKPVAIKRLYSHNPOSMAKOFETELEMSSIKRNIVLSQAVSLSHL 715
 DB 121 HGASSTVYKCVLKNCKPVAIKRLYSHNPOSMAKOFETELEMSSIKRNIVLSQAVSLSHL 180
 QY 716 GSILFDYILENGSLMDLHGPTKKKTLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKV 775
 DB 181 GSILFDYILENGSLMDLHGPTKKKTLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKV 240
 QY 776 SSNILLDKOLEARLTDPGIAKSLCVSKSHSTVYMGITGYIDPEYARTSLTEKSDVSY 835
 DB 241 SSNILLDKOLEARLTDPGIAKSLCVSKSHSTVYMGITGYIDPEYARTSLTEKSDVSY 300
 QY 836 GIVLELLETRKAVVDESNLHLHLSKTKGNNEVMADPDTSTCKDGLGVKKVFOALL 895
 DB 301 GIVLELLETRKAVVDESNLHLHLSKTKGNNEVMADPDTSTCKDGLGVKKVFOALL 360
 QY 896 CTRKQPNDRPTMHQVTRYLGSFMLSQPPAATTSATLAGSCYVDEYANLKTSHSVNCS 955

Db 361 CTRKQPRMTQVTRKVLSPMLSEQPPATDTSATLASCYVDEVANLKTSPHVNCS 420

QY 956 MSASDAQFLRFGQVISONSE 976

Db 421 MSASDAQFLRFGQVISONSE 441

RESULT 12

049318 ARATH PRELIMINARY; PRT; 1124 AA.

AC 049318 ARATH

DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.

DT 01-JUN-1998, sequence version 1.

DT 21-FEB-2006, entry version 33.

DE Putative receptor-like protein kinase.

GN OrderedLocustNames=At2g33170;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.

OC NCBI_TaxID=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Rounsley S.D., Ketchum K.A., Lin X., Crosby M.L., Brandon R.C., Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R., Venter J.C.;

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL [2]

RP NUCLEOTIDE SEQUENCE.

RA Town C.D., Kaul S.;

RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

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CC EMBL; AC002334; AAC04906.1; -; Genomic_DNA.

DR PIR; B84742; B84742.

DR HSSP; P36897; 11AS.

DR TAIR; At2g33170; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0000166; F:nucleotide binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR007090; LRR_Pln.

DR InterPro; IPR003591; LRR_Typ.

DR InterPro; IPR013210; LRR_2.

DR InterPro; IPR000719; Prot_Kinase.

DR InterPro; IPR008271; Ser_Thr_Pkin_AS.

DR InterPro; IPR002290; Ser_Thr_Pkinase.

DR InterPro; IPR001245; Tyr_Pkinase.

DR Pfam; PF00560; LRR_1; 20.

DR Pfam; PF00069; Kinase; 1.

DR PRINTS; PR00019; LEUCINCHPT.

DR ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding; Receptor; Repeat; Serine/threonine-protein kinase; Transferase.

SEQUENCE 1124 Aa; 123723 MW; 53010CD25966777 CRC64;

Query Match 29.8%; Score 1504.5; DB 2; Length 1124;

Best Local Similarity 33.8%; Pred. No. 7.5e-75;

Matches 383; Conservative 172; Mismatches 340; Indels 237; Gaps 29;

QY 8 VILGFLCISLVATVTFSE---EGATLLERK-KSFQVNVNVLVDWTSSSDYCVKRGVS 62

Db 15 MFGVGLFLTLTLVW-TSESLSNDGFLLELKNKGFDQSLNRLNMGIDETP-CNMIGVN 72

QY 63 CENV-----TENVVALNSIDLNDGEISPAIGDKLSIDLGRNRSQGPDEIGDC 115

Db 73 CSSQSSSSSSSSSLVVTSLDSSNMNLGIVSPSIGLVNLVNLAVNALTGDIPREIGNC 132

QY 116 SSLQNLDSFNEISGDIPIPSISKXQ-----LEQLILKNQ 151

Db 133 SKLEVMFLNNQGGSIPEINKLSQLRSPNLCNNKSGLPPEIGDLYNLELVAYTN 192

QY 152 LIGPIESTL-----SQIP-----NLKIIDLAKNLSGEIIPR----- 182

Db 193 LTFPLPRSLGNLKLTPFPAQNDPFGNIPTEIGKLNKLGLAQNFTSGELPKELGML 252

QY 183 -----LIYNE-----VLQYLGKGNLVGNISPDLCQLTGLWYFDVRNNS 223

Db 253 VKLQEVILWQNKPSGFI PKDIGNLTLETTLATYGNLGVPIPEIGNMKSLKKLYIQNQ 312

QY 224 LNSIPEITGNCAFOVLDSTYQLTGEIPEIDGL-QVATLSQNGQSGKIPSYIGLM 282

Db 313 LNSTIPEKELSKVMEIDFSENLISGEIPELSKISERLVLFQNKLTGLIIPNELSKL 372

QY 283 QALAVDLGSLNLSGSIPIPLIGNLTPEKLYHSNKLTSIPELGNMKSGLHYLEINDN 342

Db 373 RNIAKLDLSINSLTGP1PPGFQNLTSRQQLFHNLSGVIPQGLGYSPFWVVDSENG 432

QY 343 LTGHIPP-----ELGKL 354

Db 433 LSGKIPPIQCGSNLILNLGNSRIRGNIPGVLRCKSLQLRVGNRLTGQFPTELCKL 492

QY 355 TDLFDLVANNDLEGIIPHLSSCTNLNSLVNHNKFSGTIPPAFOKLSMITYLNSNN 414

Db 493 VNLSAIELOPNRPSGGLPPEIGTCQKQLRIHLAANFSSNLPELSKLNLYFNVSNS 552

QY 415 IKGP1VELSRIGNDITLPSNNKINGIIPSSIGDLEHLIKMNLNHNITGVVPGFGNL 474

Db 553 LSGPISEIANKMQLRLSRNSFGISLPPELISHLQELIRLSNRNSGNIPTITGNL 612

QY 475 RSIMEI-----DLSNNDISGPIPEELNQLNIILLENN 509

Db 613 THLTQLQMGNLFSGSIPQGLSLSLQIAMNLSYNDPFGSEIPEELGNLHLMYLSLNN 672

QY 510 NLTVN-GLANCLSTVLNVSHNNLVGDIPEKNNFSRSPDSFGNPGLCGSLMNS--P 566

Db 673 HLSGEIPTFENSLISLGNFNSNNLTGQLPHTQIFQNNMTLTSFLGNKLCGGHLSGCP 732

QY 567 CHD-----SRRTVRSIRALIGIIVILLMLI-----AACRDP 605

Db 733 SHSMPHISLKAAGSRRGRITII-----IVSVYIGISLILIAIVHFLNVPVETAPYVH 788

QY 606 NPPEFLDGLDKPVYVSTPEKVLILHNNMALHYVEDIMRTENLSEKYIIGHGASSTVYKC 665

Db 789 DKEPFQES-----DIYFVK-----ERFTVKDILEATKGFHDSYIVGRACGVYKA 836

QY 666 VLKNCKPAIKRLYS-----HNPQMKQFETELMSSIGHRLVLSQAVSLSLGS- 717

Db 837 VMPGKTIIVAKKLESREGNNNSNTDNSFRAEITLTCKIRHNRIVRLYSPCY-HQGSN 895

QY 718 --LLEFDYENSGIMDLHGPTKKKTLMDWDTLKTAYGAAGLAVYHHCSPRIITHRDV 775

Db 896 SNLLLEYMSRSLGLLHG-GKSHSMDPTFPALGABGLAVYHHCCKRIIHRDK 954

QY 776 SSNILLDKLEARLNDFGIAKSLCVSKSHTSTYWGTTIGYIDPEVARTSLTEKSDVSY 835

Db 955 SNNILIDENFEHVDGFLAKYIDMPLSSVAVAGSYVIAPFVAYTMKVTEKKDIFYSF 1014

QY 836 GIVLELLTRRAV---DDESNL---HLLIMSTGNNEVMADPDITSTCKD--LGV 885

Db 1015 GVLLLELLTGKAPVPLEQGDGLATWTRNHI-----RDSLSTSEIIDPYLTKEVDVILNH 1070

QY 886 VKKVQALCTKRPQNPRTMHOYT-----RVLSGFMISEQPPA 926

Db 1071 MTTVTKIAYLCTKSSPSDRPTMRREVVLMLIESGRAGKVIYSTGSDLPFA 1122

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RESULT 13
Q9LVPO_ARATH PRELIMINARY; PRT; 1102 AA.
ID Q9LVPO_ARATH
AC Q9LVPO1
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 27.
DE Receptor-like protein kinase.
GN OrderedLocNames=At5g63930;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
OX RN
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=2018115; PubMed=10718197; DOI=10.1093/dnares/7.1.31;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RA "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Ref.7,31-63(2000).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC
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CC
EMBL: AB019227; BAA96896.1; -; Genomic_DNA.
DR TAIR; At5g63930; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:000668; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_pln.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR013210; LRRNT_2.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 16.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding;
KW Receptor; Repeat; Serine/threonine-protein kinase; Transferase.
SQ
SEQUENCE 1102 AA, 120477 MW, 6CDF852ADD32D54D CRC64;

Query Match 29.5%; Score 1489; DB 2; Length 1102;
Best Local Similarity 35.0%; Pred. No. 5.3e-74;
Matches 397; Conservative 168; Mismatches 350; Indels 218; Gaps 32;

QY 3 LPRDIYLGLFCLSLVATYTSR-----RCATLLFETKSKFKDQVNVVLYWMTSPSSDYC 56
DB 1 MVEKEMKLAVFPSLLILILISFTTGTLNEGQYLLETKSKFKVAKONLRLWNNSNDSP-C 59
QY 57 VNRGVSCENVTFN--VVALNLSDLNLGEGISPAIGDKLSLIDLRGNRLSGQIPDEIGD 114
DB 60 GNTGWGWSNVSSDPYLSNLSSMWLSGKSPISGIVHLKQDLSTVNGLSGRIKREIGN 119
QY 115 CSSLQNLDSFNFELSGDIPFSISKLKQLEQLIKNNQLPIPIP-----STLSQ----- 162
DB 120 CSSLEILKLNNGPDEIIPVEIGKLVLENIILYNNRISGSLPVEIGNLISLSQLVLYSN 179
QY 163 -----IPNK-----IIIDLQNKLSGEIPR----- 182
DB 180 NISGQLPRSIGNLKRLTFRPAGQNMISGSLPSEIGGCSLVMLGLAQNLGSLPEIKM 239
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QY 183 -----LIYW-NEV-----LQYGLRGNNLVGNISPDLCQLTGLMYPDVRNN 222
DB 240 LKLSQVILMEBNSFGFIPREISNCTSLFTLALYKQLVGPIPKELGDLQSLSEFLVLYEN 299
QY 223 SLTGSIPETIGNCTAQAQVLDLSTNQLTGEIPEDIGLQ--VAITSLQGNQSGKIPVIGL 281
DB 300 GLNGTIPREIGNSVYIEIDFSENALTGEIPLETGNIIEGLLELYLPENQLTGTPVPELST 359
QY 282 MQALAVALDLSGNLSSGIPPIIGNLFTFEKLYHNSKLTGSIIPPEIGNSKLHYLELNDN 341
DB 360 LKNLSKLDISNALTPPIPLGFGYLGMLQLFQNSLSGTIPPKLGWYSDLVNLDMSDN 419
QY 342 HLTHGIPPEIGKLTDFDNLVANNDLGPIPHLLSSC----- 378
DB 420 HSGRIPSYLCSHSNMIIINLGTNNLSGNIPTGITTCKTLVQLRLARNLVGRFPENLCK 479
QY 379 -TYNLSLVNHNKFKSGTIR-----AFQKLE-----SMTYNLSSN 413
DB 480 QVNVTVAIIEGQNRFRGSIPIREVGNCALQRLQADNGFTGELPREIGMLSQDGLNISN 539
QY 414 NIKGPIPEVL-----SRIGN--LDTLDSNNKINGIIPESLGD 449
DB 540 KLTVGEVPSSEIFNCKMLQRLDMCCNNPSGTLPSVEGSLYQLELLKLSNNLSGTTIPALGN 599
QY 450 LERHLKMNLSRNHITGVDPDQGNLRSI-MEIDLSNNDISGPIPEELNQLQNIILRLEN 508
DB 600 LSRTELQNGNLFNGSIPRELISLTGLQIALNLSYNKLTGEIPPELSVLMLEFLLNN 659
QY 509 NNITGNV-GSLANCLSLTVLVNNSHNVLVDIPKNNNFSFSPDSFGNGGLCGSWLN--- 564
DB 660 NNLISGEIPSSFANLSLLQYNFSYNSLTGPILRLNISM---SSFIGNEGGLCGPPLNOCI 716
QY 565 --SPGDSRRYVRSISRA-----AIGIAIGGLVILMLVI-----AACRPHNP 607
DB 717 QTPRPAPSGSTGKPGGMRSSKIATTAAYIGGYSMLILYVLMRPPRYTASSAQDQ 776
QY 608 PPEFLDGLDKPVYTSPTKLVILMMNALHYEDIMKMTENLSEKYLIIHGASSTYKCVL 667
DB 777 PS--EWSLSD--IYFPFK-----EGFTPDQVLVATDNFDES FVVGAGCAGTVKAVL 823
QY 668 KNCKPVALIKRLYS-----HNPSMKPFETLEMLSSIKRNLVSLQAYLSLHSG--LLEY 721
DB 824 PACYTLAVYKKLASNHGKNNVNDNSFRAEILTGINIRNRNLYKLGK-CNQGSLVLLY 882
QY 722 DYLENGSLMDLHGPPKKKTLMDWTBLKIAYGAAQGLAVLHDCSPRIIHRDVKSSNILL 781
DB 883 EYMPKSLSGEILHDPs--CNLDMSKRFKALGAAGLAVLHDDCKRIRIHRDICKSNNILL 940
QY 782 DKDLERLTDPGIAKSLCVSKSHTSTYVNGTIGYIDPEYARTSRLTEKSDVYSYGIVLE 841
DB 941 DMFEHAVDQFGIAKVIDMPSKSMGALIGSYGIAPYATMKVTEKSDIYSYGIVLE 1000
QY 842 LLTR--KAVDDESULHLHLSKTNNEVMEADDDITSTCKDLGVK---KVPDLALL 895
DB 1001 LLLGKAPVGPITDGGGVVWVRSYI-RRDALSSGVLDARLTLEDERIVHMLTVLIALL 1059
QY 896 CTKRQPNDRPTMNVQTVRVLSFMLSQPPAATPTSATLAGSCYVDREYANKTP 948
DB 1060 CTSVSVAPRSMQVVLMLIESERSEGEQEHDT-----EELTQTTP 1102

RESULT 14
Q6YT77_ORYSA PRELIMINARY; PRT; 1109 AA.
ID Q6YT77_ORYSA
AC Q6YT77
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, entry version 14.
DE Putative LRR receptor-like kinase.
GN Name=BJ364A02.24;
OS Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta;
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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Erihartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa n Japonbare (GA3) genomic DNA, chromosome 7, BAC
 clone:B1364A02."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 CC EMBL: AP006163; BAC84715.1; -; Genomic DNA.
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 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR007090; LRR typ.
 DR InterPro: IPR003591; LRR typ.
 DR InterPro: IPR000719; LRRNT 2.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
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 DR Pfam: PF00560; LRR_1; 21.
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 DR PRINTS: PR00019; LEURICHRPT.
 DR ProDom: PD000001; Proc kinase; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
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 DT 05-JUL-2004, sequence version 1.
 DT 21-FEB-2006, entry version 15.
 DE Putative receptor-like protein kinase.
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 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 OX NCBI_TaxID=50514;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R., Liu J., Zaborsky J., Tallon L., Wirtz U., Wei F., Kuang H.,
 Zhang P., Wang X., Marano M.R., Baker B.;
 RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2006, 18:19:15 ; Search time 381 Seconds
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Scoring table: IDENTITY NUC
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Searched: 2281053 seqs, 824500224 residues

Total number of hits satisfying chosen parameters: 4562106

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3176	100.0	3191	US-11-056-355B-46415	Sequence 46415, A
3	3176	100.0	3191	US-11-056-355B-48174	Sequence 48174, A
4	1691.4	53.3	3705	US-11-216-545-1706	Sequence 1706, Ap
5	1343.8	42.3	3673	US-10-449-902-23703	Sequence 23703, A
6	1117.6	35.2	2901	US-10-519-135-9	Sequence 9, Appl1
7	1074.6	33.8	2751	US-10-519-135-7	Sequence 7, Appl1
8	1050.8	33.1	2766	US-10-519-135-5	Sequence 5, Appl1
9	1035.2	32.6	3000	US-10-519-135-3	Sequence 3, Appl1
10	1022.2	29.2	2614	US-11-218-905-13435	Sequence 13435, A
11	935.2	22.4	1712	US-10-519-135-44	Sequence 44, Appl1
12	901.2	28.4	2315	US-10-519-135-44	Sequence 44, Appl1
13	714.2	22.5	1714	US-11-218-905-14406	Sequence 14406, A
14	552.4	17.4	1688	US-10-449-902-2426	Sequence 2426, Ap
15	530.8	16.7	1273	US-10-519-135-21	Sequence 21, Appl1
16	488.6	15.4	1346	US-10-519-135-19	Sequence 19, Appl1
17	484.6	15.3	1514	US-11-218-905-421	Sequence 421, App
18	480.6	15.1	1394	US-11-056-355B-4048	Sequence 4048, Ap
19	467.8	14.7	1881	US-10-449-902-6920	Sequence 6920, Ap
20	413.8	13.0	1305	US-10-519-135-422	Sequence 422, App
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25	269.8	8.5	556	US-10-519-135-42	Sequence 42, Appl1
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36	209.6	6.6	429	US-10-519-135-41	Sequence 41, Appl1
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40	203.2	6.4	3725	US-10-519-135-9197	Sequence 9197, Ap
41	200	6.3	1704	US-11-056-355B-70586	Sequence 70586, A
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43	192	6.0	3658	US-11-174-307B-1667	Sequence 1667, Ap
44	192	6.0	3658	US-11-056-355B-83028	Sequence 83028, A
45	191.8	6.0	3754	US-10-519-135-4748	Sequence 4748, Ap

ALIGNMENTS

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; Sequence 1, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU P53339
; PRIOR FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3176
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana ERECTA allele
US-10-519-135-1

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Best Local Similarity 100.0%; Pred. No. 0;
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DB 3061 GTTAGAAATTAATGATGCTCATGATTAAGTATTAATGACGCTTATTAATTAAGCAAG 3120
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QY 3121 TGTGTGTGTGATATGCTCTTCAAGCTGACCTTAGACTTCTATTAAGTTCTTGCC 3176
|||
DB 3121 TGTGTGTGTGATATGCTCTTCAAGCTGACCTTAGACTTCTATTAAGTTCTTGCC 3176
|||

RESULT 2
US-11-056-355B-46415
; Sequence 46415, Application US//11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 46415
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(3191)
; OTHER INFORMATION: Ceres Seq. ID no. 13578685
; NAME/KEY: misc feature
; LOCATION: (1)-(3191)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14316144

OTHER INFORMATION: as cited in SEQ ID NO 52397
US-11-056-355B-46415

Query Match 100.0%; Score 3176; DB 9; Length 3191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCTTCATGAGAGCTGGAAGCTTTTAAGATATCTTAAAGCAAGCGATTTTA 60
|||
DB 1 GTTCTCTTCATGAGAGCTGGAAGCTTTTAAGATATCTTAAAGCAAGCGATTTTA 60
|||
QY 61 AGACTGTGTGAGAAATGAGCTCTGTTAGATATGTTCTTCTGGTTTCTCTTC 120
|||
DB 61 AGACTGTGTGAGAAATGAGCTCTGTTAGATATGTTCTTCTGGTTTCTCTTC 120
|||
QY 121 CTGAGACTATGATGCTATGCTGACCTTCAAGAGAGGAGCAAGCTTCTGAGATTAAGA 180
|||
DB 121 CTGAGACTATGATGCTATGCTGACCTTCAAGAGAGGAGCAAGCTTCTGAGATTAAGA 180
|||
QY 181 GTCAATCAAGATGAGCAATGTTCTTATGATGATGAGCAACTTCACTTCTCGGATTA 240
|||
DB 181 GTCAATCAAGATGAGCAATGTTCTTATGATGATGAGCAACTTCACTTCTCGGATTA 240
|||
QY 241 TTGCTGTGAGAGAGTGTCTTGTGAAATGTCACTTCAATGTTGCTCTTAATT 300
|||
DB 241 TTGCTGTGAGAGAGTGTCTTGTGAAATGTCACTTCAATGTTGCTCTTAATT 300
|||
QY 301 GTCAATTTGAATCTTGTATGAGAGAAATCTCACTGCTTATGAGATCTCAAGCTCTT 360
|||
DB 301 GTCAATTTGAATCTTGTATGAGAGAAATCTCACTGCTTATGAGATCTCAAGCTCTT 360
|||
QY 361 GTCAATTTGAATCTTGTATGAGAGAAATCTCACTGCTTATGAGATCTCAAGCTCTT 360
|||
DB 361 GTCAATTTGAATCTTGTATGAGAGAAATCTCACTGCTTATGAGATCTCAAGCTCTT 360
|||
QY 421 TTCTTCTTGAACAACTTGAACCTTATCTTCAATGATTAAGTGTGATACCGTTTC 480
|||
DB 421 TTCTTCTTGAACAACTTGAACCTTATCTTCAATGATTAAGTGTGATACCGTTTC 480
|||
QY 481 GATTTGAAAGTTGAGCAACTTGAAGAGCTGATCTGAAAGATTAACCAATTGATAGACC 540
|||
DB 481 GATTTGAAAGTTGAGCAACTTGAAGAGCTGATCTGAAAGATTAACCAATTGATAGACC 540
|||
QY 541 GATCCCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 600
|||
DB 541 GATCCCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 600
|||
QY 601 ACTCAGTGTGAGATACCAAGCTTATTTATGGAATGAAGTTCTTCAATCTTGGGTT 660
|||
DB 601 ACTCAGTGTGAGATACCAAGCTTATTTATGGAATGAAGTTCTTCAATCTTGGGTT 660
|||
QY 661 GCGAGGAAACAACTTATGCTGTAACATTTCTCAGATTTGTGCACTGATCTGTTG 720
|||
DB 661 GCGAGGAAACAACTTATGCTGTAACATTTCTCAGATTTGTGCACTGATCTGTTG 720
|||
QY 721 GATTTTGAAGTAAGAAACAAAGTTGACGTGATTAACCTGAGACATGAGAAATGG 780
|||
DB 721 GATTTTGAAGTAAGAAACAAAGTTGACGTGATTAACCTGAGACATGAGAAATGG 780
|||
QY 781 CACTGCTTCCAGGTTTGTGACCTTGTCTTCAATCACTAATGATGATCCCTTTTGA 840
|||
DB 781 CACTGCTTCCAGGTTTGTGACCTTGTCTTCAATCACTAATGATGATCCCTTTTGA 840
|||
QY 841 CATCGGCTTCTGCAAGTTGCAACATTTATGATGCAAGCAATCACTCTGAGGAAGAT 900
|||
DB 841 CATCGGCTTCTGCAAGTTGCAACATTTATGATGCAAGCAATCACTCTGAGGAAGAT 900
|||
QY 901 TCCATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
|||
DB 901 TCCATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
|||
QY 961 GAGTGATCTATTCCTGATTCGGAATCTTCACTTCACTTCACTTCACTTCACTTCACTT 1020
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Db	961	GAGTGGATCTATTTCTCCGATTCTCGGAAATCTTAATCTTACCCGAAATATGTAATTGGCA	1020
Qy	1021	CAGTAAACAAGCTGACTGGTCAATTCGACCTGAGCTGGGAAACAATGTCMAAATCCATTA	1080
Db	1021	CAGTAAACAAGCTGACTGGTCAATTCGACCTGAGCTGGGAAACAATGTCMAAATCCATTA	1080
Qy	1081	CCTGGAATCAATGATTAATCATCTTACGGGTCATATACCACCAAGCTTGGGAAAGCTTAC	1140
Db	1081	CCTGGAATCAATGATTAATCATCTTACGGGTCATATACCACCAAGCTTGGGAAAGCTTAC	1140
Qy	1141	TGACTGTGTTGATCTCGAATGTGGGCCAACAATGATGTGGAGAGACCTTAATACCTGATCT	1200
Db	1141	TGACTGTGTTGATCTCGAATGTGGGCCAACAATGATGTGGAGAGACCTTAATACCTGATCT	1200
Qy	1201	GAGCTCTTGCACAAAATCTTAAACAGCTTAAATGTTTCATGGGAAACAAGTTTAACTGGCACTAT	1260
Db	1201	GAGCTCTTGCACAAAATCTTAAACAGCTTAAATGTTTCATGGGAAACAAGTTTAACTGGCACTAT	1260
Qy	1261	ACCCGAGCATTTCAAAGCTAGAAAGTATGATCTTAATCTGTCCAGCAACAATAT	1320
Db	1261	ACCCGAGCATTTCAAAGCTAGAAAGTATGATCTTAATCTGTCCAGCAACAATAT	1320
Qy	1321	CAAGGTCCAATCCCGGTGAGCTATCTCGTATCGGTAACTTAGTAATTTGATGATCTTTC	1380
Dp	1321	CAAGGTCCAATCCCGGTGAGCTATCTCGTATCGGTAACTTAGTAATTTGATGATCTTTC	1380
Qy	1381	CAACAACAAGATTAATGGAATCATTCCTTCCTCCCTGGGTGATTTGGAGCATCTTCTCAA	1440
Db	1381	CAACAACAAGATTAATGGAATCATTCCTTCCTCCCTGGGTGATTTGGAGCATCTTCTCAA	1440
Qy	1441	GATGAACCTTGAGTAGAAATCATATATACCTGTGTAGTCTCCAGGCGACTTTGGAAATCTAAG	1500
Db	1441	GATGAACCTTGAGTAGAAATCATATATACCTGTGTAGTCTCCAGGCGACTTTGGAAATCTAAG	1500
Qy	1501	AAGCATCTATGGAATAATGATCTTTCAAATAATGATATCTCTGGCCAAATTCAGAGAGAGCT	1560
Db	1501	AAGCATCTATGGAATAATGATCTTTCAAATAATGATATCTCTGGCCAAATTCAGAGAGAGCT	1560
Qy	1561	TAAACAATTAACAAGACATTAATTTTCTGAGACTGGGAAATAATACTGACTGGTAATGT	1620
Db	1561	TAAACAATTAACAAGACATTAATTTTCTGAGACTGGGAAATAATACTGACTGGTAATGT	1620
Qy	1621	TGGTTCATTAGCCAACTGTCTTCAGTCTCACTGTATTTGAATGATATCTCAACAACCTCGT	1680
Db	1621	TGGTTCATTAGCCAACTGTCTTCAGTCTCACTGTATTTGAATGATATCTCAACAACCTCGT	1680
Qy	1681	AGGTGATATCCCTTAAGAACATTAATCTTCAAGATTTTCAACAAGACCTTCATTGGGAA	1740
Db	1681	AGGTGATATCCCTTAAGAACATTAATCTTCAAGATTTTCAACAAGACCTTCATTGGGAA	1740
Qy	1741	TCTCTGCTCTTTGCGGTAGTGGCTAAACTCAACCGTGTATGATTTCTGTGMACTGTACG	1800
Db	1741	TCTCTGCTCTTTGCGGTAGTGGCTAAACTCAACCGTGTATGATTTCTGTGMACTGTACG	1800
Qy	1801	AGTGTCAATCTCTTAGAGCACTAATCTTGGAAATAGCTAATTTGGGGGACTTGTGATCTTCT	1860
Db	1801	AGTGTCAATCTCTTAGAGCACTAATCTTGGAAATAGCTAATTTGGGGGACTTGTGATCTTCT	1860
Qy	1861	CATGCTCTTAATAGCAGCTGTGCGCAACCGCATTAATCTCTCTCTTTCTTGAATGATCACT	1920
Db	1861	CATGCTCTTAATAGCAGCTGTGCGCAACCGCATTAATCTCTCTCTTTCTTGAATGATCACT	1920
Qy	1921	TGACAAACAAGTAATCTTAATTTGACACCGGAGCTCGTCAATCTTCAATATGMAAATGGCACT	1980
Db	1921	TGACAAACAAGTAATCTTAATTTGACACCGGAGCTCGTCAATCTTCAATATGMAAATGGCACT	1980
Qy	1981	CCACGCTTTACAGATATCATGAGATGACAGAGATCTAAGTGGAGAGTATCATTTGG	2040
Db	1981	CCACGCTTTACAGATATCATGAGATGACAGAGATCTAAGTGGAGAGTATCATTTGG	2040
Qy	2041	GCACGGAGCATACAGCACTGTATACAAATGTGTTTTGAAGATTTGTAACCGGTGGCAT	2100
Db	2041	GCACGGAGCATACAGCACTGTATACAAATGTGTTTTGAAGATTTGTAACCGGTGGCAT	2100

QY	2101	TAA	GCGCTT	ACTCT	CAC	CAACCC	CACAGT	CAATG	AAACAGT	TTG	AAACAGAACT	CGAGAT	2160	
Db	2101	TAA	GCGGCTT	ACTCT	CAC	CAACCC	CACAGT	CAATG	AAACAGT	TTG	AAACAGAACT	CGAGAT	2160	
QY	2161	GCT	AGTAGT	CAAC	CAAGCA	CAGAAAT	CTGTG	AGCC	CTAC	AGGCT	TAT	CCCTCT	CACTT	2220
Db	2161	GCT	AGTAGT	CAAC	CAAGCA	CAGAAAT	CTGTG	AGCC	CTAC	AGGCT	TAT	CCCTCT	CACTT	2220
QY	2221	GGG	GAGTCTT	CTGTCT	CTATG	ACTAT	TTTGG	AAATG	TGTAG	CCCTCT	TGGGAT	CTTTCAT	TGG	2280
Db	2221	GGG	GAGTCTT	CTGTCT	CTATG	ACTAT	TTTGG	AAATG	TGTAG	CCCTCT	TGGGAT	CTTTCAT	TGG	2280
QY	2281	CCCT	ACGA	AAAAA	AGACTCTT	GAT	TGGG	ACAC	CGGCTT	TAAG	ATG	CATATG	TGC	2340
Db	2281	CCCT	ACGA	AAAAA	AGACTCTT	GAT	TGGG	ACAC	CGGCTT	TAAG	ATG	CATATG	TGC	2340
QY	2341	ACA	AGTTAG	CTT	ATCTA	CA	CCATG	ACG	TGTG	CCAA	GGATCAT	TAC	AGAC	2400
Db	2341	ACA	AGTTAG	CTT	ATCTA	CA	CCATG	ACG	TGTG	CCAA	GGATCAT	TAC	AGAC	2400
QY	2401	GTC	GCCAA	CATTCT	CTT	GSA	CAAA	AGACTT	AGGCTCTT	TG	ACAT	TTT	TGAA	2460
Db	2401	GTC	GCCAA	CATTCT	CTT	GSA	CAAA	AGACTT	AGGCTCTT	TG	ACAT	TTT	TGAA	2460
QY	2461	GA	AAAGCTT	TGTGT	GTCA	AAAGTCA	CAATCTT	CA	CTTAC	CTTAC	TGATG	GGC	ACAT	2520
Db	2461	GA	AAAGCTT	TGTGT	GTCA	AAAGTCA	CAATCTT	CA	CTTAC	CTTAC	TGATG	GGC	ACAT	2520
QY	2521	CAT	TAACCC	CGAGT	ATGCT	CGAC	CTTAC	AGGCTC	ACTG	AGAAAT	CCGATG	CTAC	AGTTA	2580
Db	2521	CAT	TAACCC	CGAGT	ATGCT	CGAC	CTTAC	AGGCTC	ACTG	AGAAAT	CCGATG	CTAC	AGTTA	2580
QY	2581	TGG	ATAGCTT	CTTCTT	TGAGT	TTTAA	CCCGA	AGAAAGCC	GTGAT	GAC	CAATCC	ATCT	2640	
Db	2581	TGG	ATAGCTT	CTTCTT	TGAGT	TTTAA	CCCGA	AGAAAGCC	GTGAT	GAC	CAATCC	ATCT	2640	
QY	2641	CC	ACCATCT	GAT	TAATGT	CA	AAAGCG	GGGA	CAATGA	AGTGA	GAATGG	CAGATCC	AGA	2700
Db	2641	CC	ACCATCT	GAT	TAATGT	CA	AAAGCG	GGGA	CAATGA	AGTGA	GAATGG	CAGATCC	AGA	2700
QY	2701	CAT	CACTG	ACG	TGTAA	AGATCT	CGGTGT	GGTGA	AAAGTTT	TCC	ACTGG	CACTCTT	2760	
Db	2701	CAT	CACTG	ACG	TGTAA	AGATCT	CGGTGT	GGTGA	AAAGTTT	TCC	ACTGG	CACTCTT	2760	
QY	2761	AT	GCA	CAAA	AGAC	CGCA	TGATG	CA	CCCAAT	GAC	CAAGT	ACTG	CTGT	2820
Db	2761	AT	GCA	CAAA	AGAC	CGCA	TGATG	CA	CCCAAT	GAC	CAAGT	ACTG	CTGT	2820
QY	2821	CAG	TTT	TATG	CTAT	CGGA	CAAC	CACTG	CTG	GACTG	ACAC	CGTGC	TGG	2880
Db	2821	CAG	TTT	TATG	CTAT	CGGA	CAAC	CACTG	CTG	GACTG	ACAC	CGTGC	TGG	2880
QY	2881	TT	CGTG	CTAC	CGT	CA	TGATG	CAAA	TCTCA	AGATCT	CTCT	CAAT	TGCT	2940
Db	2881	TT	CGTG	CTAC	CGT	CA	TGATG	CAAA	TCTCA	AGATCT	CTCT	CAAT	TGCT	2940
QY	2941	CAT	GAGT	GTCTT	GAT	GTG	CTCA	CTGTTT	CTT	CGGTT	TG	GA	CAAGT	3000
Db	2941	CAT	GAGT	GTCTT	GAT	GTG	CTCA	CTGTTT	CTT	CGGTT	TG	GA	CAAGT	3000
QY	3001	TG	AGTAG	TTTTT	CGTT	AG	AGGA	GAACTTT	AAACGG	TATCTTTT	CGTT	CGT	TAA	3060
Db	3001	TG	AGTAG	TTTTT	CGTT	AG	AGGA	GAACTTT	AAACGG	TATCTTTT	CGTT	CGT	TAA	3060
QY	3061	GTT	AGAAAA	TTAAT	ATG	TCTCAT	GT	TAAAG	TAAT	TG	CACTG	CTTAT	TAT	3120
Db	3061	GTT	AGAAAA	TTAAT	ATG	TCTCAT	GT	TAAAG	TAAT	TG	CACTG	CTTAT	TAT	3120
QY	3121	TGT	G	GTG	GTG	TAAT	ATG	CTT	CAG	ACTG	GC	ACTT	TA	3176
Db	3121	TGT	G	GTG	GTG	TAAT	ATG	CTT	CAG	ACTG	GC	ACTT	TA	3176

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RESULT 3
US-11-056-355B-48174
; Sequence 48174, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polyptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48174
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3191)
; OTHER INFORMATION: Ceres Seq. ID no. 13578685
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3191)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14316144
; OTHER INFORMATION: as cited in SEQ ID NO 52397
US-11-056-355B-48174

Query Match      100.0%; Score 3176; DB 9; Length 3191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 541 GATCCCTTCAACACTTTACAGATCCAAACCTGAAAAATCTGGACTTGGCAGAAATA 600
Qy 601 ACTCAGTGTGAATATCCAGACTTATTTATCTGGAATGAAGTCTTCAGATCTTGGGT 660
Db 601 ACTCAGTGTGAATATCCAGACTTATTTATCTGGAATGAAGTCTTCAGATCTTGGGT 660
Qy 661 GCGAGAAACAACCTTGTGCGTAACTTTCTCCAGATTTGTGCACTGACTGCTTTG 720
Db 661 GCGAGAAACAACCTTGTGCGTAACTTTCTCCAGATTTGTGCACTGACTGCTTTG 720
Qy 721 GATATTTGAGTAAGAAACAAGTTGACTGTGATATACCTGAGCGATAGAAATG 780
Db 721 GATATTTGAGTAAGAAACAAGTTGACTGTGATATACCTGAGCGATAGAAATG 780
Qy 781 CACTGCTTCAGATTTTGGACTTTGCTCTCAATACGCTAACCTGGAGATCCCTTTG 840
Db 781 CACTGCTTCAGATTTTGGACTTTGCTCTCAATACGCTAACCTGGAGATCCCTTTG 840
Qy 841 CATCGCTTCGCAAGTTGCAATATCATTTGCAAGGCAATCACTCTGGGAAGAT 900
Db 841 CATCGCTTCGCAAGTTGCAATATCATTTGCAAGGCAATCACTCTGGGAAGAT 900
Qy 901 TCCATCAGTATGATCTCATGCAAGCCCTTGCACTTATAGTGAAGCACTTGT 960
Db 901 TCCATCAGTATGATGATCTCATGCAAGCCCTTGCACTTATAGTGAAGCACTTGT 960
Qy 961 GAGTGCATCTATTCCTCCGATTTCTCGGAATCTTACTTTACCGAATAATTTGAT 1020
Db 961 GAGTGCATCTATTCCTCCGATTTCTCGGAATCTTACTTTACCGAATAATTTGAT 1020
Qy 1021 CAGTAACAAGCTGAGTGTCAATTCACCTGAGCTTGGAAACATGCAAACTCCAT 1080
Db 1021 CAGTAACAAGCTGAGTGTCAATTCACCTGAGCTTGGAAACATGCAAACTCCAT 1080
Qy 1081 CTTGGAATCTCAATGATATCATCTCAAGGATCATATACCAAGAGCTGGAACTTAC 1140
Db 1081 CTTGGAATCTCAATGATATCATCTCAAGGATCATATACCAAGAGCTGGAACTTAC 1140
Qy 1141 TGAATGTTGATCTGAATGTGGCAACAATGATCTGGAAAGCACTATACCTATCT 1200
Db 1141 TGAATGTTGATCTGAATGTGGCAACAATGATCTGGAAAGCACTATACCTATCT 1200
Qy 1201 GAGCTCTTGCAAAATCTAAACAGCTTAAATGTTCAATGGAAACAAGTTAGTGCAT 1260
Db 1201 GAGCTCTTGCAAAATCTAAACAGCTTAAATGTTCAATGGAAACAAGTTAGTGCAT 1260
Qy 1261 ACCCGAGCAATTCAAAGCTAGAAAGTATGACTTACCTTATCTGTCGAAACAATAT 1320
Db 1261 ACCCGAGCAATTCAAAGCTAGAAAGTATGACTTACCTTATCTGTCGAAACAATAT 1320
Qy 1321 CAAAGTCCAAATCCGGTGAAGTATCTGATACGATTAATGATATGATGATCTTTC 1380
Db 1321 CAAAGTCCAAATCCGGTGAAGTATCTGATACGATTAATGATATGATGATCTTTC 1380
Qy 1381 CAACAACAAGATTAATGGAATCATCTCTTCTCCCTGGGATTTGGAGACCTTCCAA 1440
Db 1381 CAACAACAAGATTAATGGAATCATCTCTTCTCCCTGGGATTTGGAGACCTTCCAA 1440
Qy 1441 GATGAACCTGAGTGAATCATATACTGATGATTCAGAGGCACTTTGGAATCTAAG 1500
Db 1441 GATGAACCTGAGTGAATCATATACTGATGATTCAGAGGCACTTTGGAATCTAAG 1500
Qy 1501 AAGCATCATGGAATATGATCTTCAATATATGATATCTGAGGCAATTCGAAAGGCT 1560
Db 1501 AAGCATCATGGAATATGATCTTCAATATATGATATCTGAGGCAATTCGAAAGGCT 1560
Qy 1561 TAACCAATTAACAAGATATTTGCTGAGACTGAGAAATTAATACCTGATGATGT 1620
Db 1561 TAACCAATTAACAAGATATTTGCTGAGACTGAGAAATTAATACCTGATGATGT 1620
Qy 1621 TGGTCAATTAAGCAACTGTCTCACTGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 TGGTCAATTAAGCAACTGTCTCACTGATGATGATGATGATGATGATGATGATGAT 1680
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1681 AGGTATATCCCTAAGAACATACTCTCAAGATTTTACAGACAGCTTCATTTGGCAA 1740
1681 AGGTATATCCCTAAGAACATACTCTCAAGATTTTACAGACAGCTTCATTTGGCAA 1740
1741 TCCTGTCTTTGGCGGATTTGGCTAACTCAACGCTGTCATGATTTCTGTCGAACCTGACG 1800
1741 TCCTGTCTTTGGCGGATTTGGCTAACTCAACGCTGTCATGATTTCTGTCGAACCTGACG 1800
1801 AGGTCAATCTTATAGACAGATATCTTGGATATGCTATTTGGGGGACCTTGGATCCCTCT 1860
1801 AGGTCAATCTTATAGACAGATATCTTGGATATGCTATTTGGGGGACCTTGGATCCCTCT 1860
1861 CATGTCTTAAATAGACAGCTTGGCGACCGCATTAATCTCTCTCTTTCTTGTATGATCACT 1920
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1921 TGACAAACCGATTAATTTGACACCGAAGCTGTCATCTTGTATGAAATGACGACCT 1980
1921 TGACAAACCGATTAATTTGACACCGAAGCTGTCATCTTGTATGAAATGACGACCT 1980
1981 CCAAGTTTACGAGATATCATAGAAATGACAGAAATCTAAAGTAAAGTATATCATTTGG 2040
1981 CCAAGTTTACGAGATATCATAGAAATGACAGAAATCTAAAGTAAAGTATATCATTTGG 2040
2041 GCAAGGAGATCAAGACCTGATTAATGATGTTTGAAGATTTGTAACCGGTTGGAT 2100
2041 GCAAGGAGATCAAGACCTGATTAATGATGTTTGAAGATTTGTAACCGGTTGGAT 2100
2101 TAAGCGCTTTACTCTCAACCAAGTCAATGATAAAGATTTGAAACAGAACTCGAGAT 2160
2101 TAAGCGCTTTACTCTCAACCAAGTCAATGATAAAGATTTGAAACAGAACTCGAGAT 2160
2161 GCTAAGTATGATCAAGACAGAAATCTTGTAGGCTCAAGCTTATTCCTCTCTCACTT 2220
2161 GCTAAGTATGATCAAGACAGAAATCTTGTAGGCTCAAGCTTATTCCTCTCTCACTT 2220
2221 GGGGAGCTTCTGTTCTATGACTATTTGAAATGATGAGCTCTGGGATCTTCTTCAAGG 2280
2221 GGGGAGCTTCTGTTCTATGACTATTTGAAATGATGAGCTCTGGGATCTTCTTCAAGG 2280
2281 CCTTACGAAAGAAAGACTCTTATTTGGGACACCGGCTTAAATGATGATGATGACG 2340
2281 CCTTACGAAAGAAAGACTCTTATTTGGGACACCGGCTTAAATGATGATGATGACG 2340
2341 ACAAGTTTATGCTATCTACACCATGACTGATGACCAAGGATCTTACAGAGAGCTGAA 2400
2341 ACAAGTTTATGCTATCTACACCATGACTGATGACCAAGGATCTTACAGAGAGCTGAA 2400
2401 GTGCTCCAAATCTCTTGGACAAAGCTTATGAGGCTGTTTGAAGATTTTGGATATAGC 2460
2401 GTGCTCCAAATCTCTTGGACAAAGCTTATGAGGCTGTTTGAAGATTTTGGATATAGC 2460
2461 GAAAAAGCTTGTGTGTCAAAAGTCAATCTTCACTTATGCTATGAGGACAGATAGGTTA 2520
2461 GAAAAAGCTTGTGTGTCAAAAGTCAATCTTCACTTATGCTATGAGGACAGATAGGTTA 2520
2521 CATAGACCCCGAGATGCTGCACTTCAAGGCTCACTGAGAAATCCCATGCTTCAAGTTA 2580
2521 CATAGACCCCGAGATGCTGCACTTCAAGGCTCACTGAGAAATCCCATGCTTCAAGTTA 2580
2581 TGAATATGCTCTTCTTGAATTTTAAACCGAAGAAAGCCGTTGATGACGATCCAAATCT 2640
2581 TGAATATGCTCTTCTTGAATTTTAAACCGAAGAAAGCCGTTGATGACGATCCAAATCT 2640
2641 CCACCATCTGATTAATGTCAAAGACGGGAAACATGAAATGATGAAATGGCATATCCAGA 2700
2641 CCACCATCTGATTAATGTCAAAGACGGGAAACATGAAATGATGAAATGGCATATCCAGA 2700
2701 CATCATATGACGATGTAAGATCTCGGATGATGTAAGAAAGTTTCCAACTGGGACTCT 2760
2701 CATCATATGACGATGTAAGATCTCGGATGATGTAAGAAAGTTTCCAACTGGGACTCT 2760

2761 ATGCACCAAAAAGACAGCCGATGATGCAACCAATGACACAGAGTACTGCTGCG 2820
2761 ATGCACCAAAAAGACAGCCGATGATGCAACCAATGACACAGAGTACTGCTGCG 2820
2821 CAGTTTATGCTATTCGGAACAAACCACTGCTGAGCTGACAGCTCAGCCGCTGCTGG 2880
2821 CAGTTTATGCTATTCGGAACAAACCACTGCTGAGCTGACAGCTCAGCCGCTGCTGG 2880
2881 TTGCTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
2881 TTGCTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
2941 CATGATGCTTCTGATGCTCACTGTTCTTGGGATGATGATGATGATGATGATGATGATG 3000
2941 CATGATGCTTCTGATGCTCACTGTTCTTGGGATGATGATGATGATGATGATGATGATG 3000
3001 TGAGTATGTTTGTGATGAGGAGAAATCTTAAACGATATCTTTCGTTGCGTTAAGCT 3060
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3061 GTTAAAGAAATTAATGCTCATGTAAGATTAATGATGATGATGATGATGATGATGATG 3120
3061 GTTAAAGAAATTAATGCTCATGTAAGATTAATGATGATGATGATGATGATGATGATG 3120
3121 TGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3176
3121 TGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3176

RESULT 4
US-11-216-545-1706
Sequence 1706, Application US/11216545
Publication No. US20060135758A1
GENERAL INFORMATION:
APPLICANT: MONSANTO Technology, LLC
APPLICANT: McLeod, Paul L
APPLICANT: tao, Nengbing
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
NUMBER OF SEQ ID NOS: 8783
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1706
LENGTH: 3705
ORGANISM: Glycine max
Query Match 53.3%; Score 1691.4; DB 8; Length 3705;
Best Local Similarity 74.2%; Pired. No. 0;
Matches 2204; Conservative 0; Mismatches 731; Indels 34; Gaps 4;

68 GTGAGAAATGAGCTGTTTGAAGATATGTTCTTCTGTTGCTTCTGTTGAGC 127
505 GTTGCACCTATGACATTTGCAATTTGAGAGTCTTATTTCTTGTCTTATTTGTTGAG- 553
128 TTAGTACTACTGTGACTTCAAGAGAGGACAAAGTCTGAGATTTAAGAGTCAATTC 187
564 --TGTCAATCTGTGAAATCTGATGATGAGCAACGTTTGAAGATTAAGAGTCAATTC 621
188 AAAGATGTGAACAATGTTCTTATGATGATGATGATGATGATGATGATGATGATGATG 247
622 AGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 661
248 TGAAGAGTGTGCTGTTGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 307
682 TGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 741

308 TTGAATCTTGATGAGAAATCTCACCTGCTATTGGAGATCTCAGAGCTCTCTTGCAATT 367
742 TTGAATCTTGATGAGAAATCTCACCTGCTATTGGAGAAATCTCACAGTTGCTCTTAAT 801
368 GATCTGAGAGATATC-GCTTGTCTGCAAAATCCCTGATGAGATTTGTAAGTCTTCTC 426
802 GACCTCAGAGAAAAACAGGTTATCAGGGCAGATACCCGATGAGATGTGTGACTGCTTCC 861
427 TTTGCAAAACTTGACTTATCTCTCAATGATTAAGTGTGACATACCGTTTTCGATTTCC 486
862 TTTTAAAGAACCTGGACTTATCATTTAATGAAATTAGAGGGATTAACCATTTTCTATTTC 921
487 GAAGTTGAAGCAACTTGAGCAG-----CTGATCTGAAGATAACCAATT 531
922 TAAGTTCAAAACAGATGAGAAATCTGCTCGGAGAAATCTGATTTTGAAGAACCAATT 981
532 GATAGAGCCGATCCCTTCAACATTTGACAGATTCCAACCTGAAATTTGACCTTGGC 591
982 GATTTGACCAATTCCTTCAACTTTGCTCAGATTCTGATTTGAAGATTCTAGACTGGC 1041
592 ACAGAAATAAATCAGTGTGATGATACCAAGACTTATTTACGAAATGAAGTTCTTCAGTA 651
1042 TCAAAATAAATCTTAGCGAGAAATACCAAGCTTATTAATTGAAACGAAGTTTGCATA 1101
652 TCTTGGGTGCGAGAAACAACCTTAGTCGGTAACATTTCTCAGATTGTGTCAACTGAC 711
1102 TCTAGGCTTAGAGAGAAACATTTGGTTGCTCACTACACAGACATGTGCCAGTTAAC 1161
712 TGTGCTTTGGTATTTTGTACGTAAAGAACACAGTTTGTACGTATTAACCTGAGACAT 771
1162 TGGGCTGTGGTATTTTGTATGTAGAGAAACATTAAGCTGACAGAAATTCACAGAACAT 1221
772 AGGAAATGTGACAGCTCTTCCAGTTTGGACTTGTCTCAATATGACTTAAGTGTGAT 831
1222 AGGCAATTTGATGCTCTTCCAGGTCTTGAATTAATCTTACCAACCACTTAATGAGAT 1281
832 CCTTTTGAACATGGGCTCTCCGCAAGTTGCAACATTAATCTTGAAGAGCAATCACTCTC 891
1282 ACCATTCATATTTGATTTCTTGCAAGTAGAACATTTTCTTGCAAGCAATTAATCTCTC 1341
892 TGGAAAGATTCATCACTGATTTGTCTCATGCAAGCCCTTGCAGTCTTATGATCTAAGTGG 951
1342 TGGACATATTCACCGGTGATCGGTCTCATGCAAGCACTTGCTGTCTTAGCTTGAAGCTG 1401
952 CAATCTGTGATGATGATCTATCTCCGATTTCTGGAATCTTACTTACCCAGAAAT 1011
1402 CAATCTGTGATGATGATGATCTCTCTATCTTGGGAAATTTGACAGAAAAAT 1461
1012 GATTTGCAAGTAAACAGCTGATGCTTCAATTCACCTGAGCTTGGAAACATGTCAA 1071
1462 GTTACTTGATGAGAAACAGCTGATGCTTCAATTCACCCCGAGAGCTTGGAAATATGTCAA 1521
1072 ACTCATTTACCTGAACTCAATGATTAATCTCAAGGATCATATACCAACAGAGCTTGG 1131
1522 GCTTCACTATTTGGAATGATGATTAATCAATTTAAGGACATATCCCGCCGAGCTTGG 1581
1132 GAAGCTTACGACTTGTGTTGATCTGATGTGGCCAAATGATCTGGAAGAGACTTAATCC 1191
1582 AAAGCTTACGATCTGTTTGAATTAATGTGCTAAACAAATCTCAAGGGGCAATTC 1641
1192 TGATCATCTGAGCTCTTGACCAATCTAAACAGCTTAATGTTCAATGGAACAGTTAG 1251
1642 TAGTAACTTAGCTCATGTAAATCTCAACAGCTTAATGTGATGCAACAGTTGAA 1701
1252 TGGCACTATAACCCGAGCAATTTCAAAAGCTAAGAAAGTATGACTTAATCTTGTCCAG 1311
1702 TGGATCAATTCCTCTTGTGAGAGCTTGGAGAGATGACCTTTGATCTTTCTTC 1761
1312 CAACATATTAAGAGTCCATCCCGGTTGAGCTATCTGATGTGTAACCTTAATATAT 1371
1762 CAACATCTTCAGGGGCAATTCCAATTAAGAACTGTCCGGAATTTGGCAATTTGATAT 1821
1372 GGATCTTTCCAGCAACAAATTAATGGAATCATTTCTTCCCTTGGTATTTGAGCA 1431

1822 GGATATTTCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1881
1432 TCTTCTCAAGATGAACTTGAATGAAATCATATTAATCTGTGATGCTCAGGCACTTTGG 1491
1882 TCTTCTCAAGATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1941
1492 AAATCTTAAGAAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1551
1942 AAATCTTAAGAAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2001
1552 AGAAGAGCTTAACCAATTAACAAATTAATTTGCTGAGACTGGAATAATTAATTAATTAATTAAT 1611
2002 TGATGAACCTTAGCAGCTTCAAAACATGATATCTTGAGACTTGAATAATTAATTAATTAATTAAT 2061
1612 TGGTATGTTGTTTCAATTAACCACTGTCTCAGCTCAGTATGATGATGATGATGATGATGATGAT 1671
2062 TGGCGATGTGGCATCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2121
1672 CAACCTGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1731
2122 CAACCTATTTGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2181
1732 CATTTGCAATCTGTGCTTGTGCGGTAGTTGGCTAACTCACCCGTGATGATTTCTGCTG 1791
2182 CATTTGCAATCTGTGCTTGTGCGGTAGTTGGCTAACTCACCCGTGATGATTTCTGCTGCTG 2241
1792 AACTGATGAGTCAATCTCTAAGAGACTATTTCTGGAATTAATTAATTAATTAATTAATTAAT 1851
2242 TTCAGAGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2301
1852 GATCTTCTCATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1911
2302 GATCTTCTCATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2361
1912 TGGATCACTTGAACAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1971
2362 TGGATCACTTGAACAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2421
1972 CATGCACTTCACGCTTATTAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2031
2422 TATGCACTTCACGCTTATTAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2481
2032 TATCACTTGGGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2091
2482 TATCACTTGGGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2541
2092 GGTTCGATTAAGCGGCTTACTCTCAACCAACAGTCAATGAACAGTTTGAACAG 2151
2542 GTTTCGATTAAGCGGCTTACTCTCAACCAACAGTCAATGAACAGTTTGAACAG 2601
2152 ACTGAGATGCTAAGTATGATCAACAGCAAGAAATCTTGGAGCTTCAAGCTTATTCCT 2211
2602 ACTTGAAGAGCTTGGAGATCAACAGCAAGAAATCTTGGAGCTTCAAGCTTATTCCT 2661
2212 CTCTCACTTGGGAGAGCTTCTGTTATGATTAATTTGAAATTAATTAATTAATTAATTAATTAAT 2271
2662 GTTCCATTAAGGAGCTTCTGTTATGATTAATTTGAAATTAATTAATTAATTAATTAATTAATTAAT 2721
2272 TCTTCACTGAGCTTCAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2331
2722 TCTTCACTGAGCTTCAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2781
2332 TGGTGAAGCAACAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2391
2782 TGGAGCAAGCAACAGGCTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2841
2392 AGAGTGAAGTGTGCAACATCTCTTGAACAAAGCTTAAGAGCTTGTGACAGTTT 2451
2842 AGATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2501
2452 TGGATTAAGGAAAGCTTGTGTGTCAAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2511

Db	2902	TGGCATTGGCCAAAAGTCTCTGCGCCCTCAAAGTCCACTTCTACTTACATATATGGGAC	2961
Qy	2512	GATAGGTTACATAGACCCCGAGTATGTCGCACTTCACGGCTCACTGAGAAATCGATGT	2571
Db	2962	AATTGGCTATATPAGACCTCGAGTATGTAGAACTTCACGCTCTCACTGAGAAAGTCTGATGT	3021
Qy	2572	CTACAGTTATGGAATATGTCCTTCTTGAAGTTGTAAACCGAAGGAAAGCCGTTGATGACGA	2631
Db	3022	GTAACAGTTACGATATGTTTTACTTGAAGTTGTAACTGAAAGGAAAGCTGTTGACAAATGA	3081
Qy	2632	ATCCAAATCCACCACTGATATATGTCAAAGCGGGGAAACAATGAAGTATGGAATGGC	2692
Db	3082	ATCCAACTCCACCACTGATATTTTGTCCAGAGGCACAACTAGCATGATGAGAAACGT	3141
Qy	2692	AGATCCAGACATCACATGACGCTGTAAAGATCTCGTGTGTGAGAAAGTTTCCAACT	2751
Db	3142	TGATTCAGACATTACTGCGACATGGAAGACCTAGAGACTGTAAAAAGTTTATCAGCT	3201
Qy	2752	GGCACTCCTATGACCAAAAGACAGCCGATATGATGACCCCAATGACCAAGTGATCTGG	2811
Db	3202	TGCTCTATTTATGACAAAGAGGACGACGCTGATAGGCCGACAAATGACGAAAGTGACAG	3261
Qy	2812	TGTTTCTGGGCAAGTTTATGCTATC-----GGAAACACCACTGCTGCGCAC	2856
Db	3262	TGTACTCGGAAAGCCTTGTGCTGTCAAAACCCCAACCAAGCACTAGTGACTACCAAC	3321
Qy	2857	TGACACGTCAGACGACGCTGGCTGGTCTGTGCTGATGATGATGTGCAAAATCTCAAGAC	2916
Db	3322	TGCTTCCAAATCCATCTGCGCAAAAGTCCATGCTACGTGATGATGATGTGCAAACTTCAGAC	3381
Qy	2917	TCTCTATTTCTGTCAATGCTCTTCCATGAGTGTCTGATGCTCAACTGTTCTTCGGTT	2976
Db	3382	TCCACACTTGGTGAACGTGCCCTGTCAATGAGCACCTCAATGCTCAACTCTTCTTCAGATT	3441
Qy	2977	TGACAAAGTTATTTCTCAAAACGATGAGT	3005
Db	3442	TGGAGAGTAAATCTCTCAAAACAGTGAAT	3470

RESULT 5
US-10-449-902-23703
; Sequence 23703, Application US/10449902
; Publication No. US20060123505A1

APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205Y1-US
 CURRENT APPLICATION NUMBER: US/10/449,902
 PRIOR FILING DATE: 2003-05-29
 PRIOR APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: JP 2002-383870
 PRIOR FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 23703
 LENGTH: 3673
 TYPE: DNA
 ORGANISM: *Oryza sativa*
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AK073793
 DATABASE ENTRY DATE: 2001-12-06
 US-10-449-902-23703

	Query Match	42.3%	Score 1343.8	DB 6	Length 3673
	Best Local Similarity	67.6%	Pred. No. 0		
	Matches 1969	Conservative 0	Mismatches 917	Indels 25	Gaps 5
Oy	112 TCCTCTTCGCTTGAGCTTAGTAGCTACTGTGACTTCAGAGAGGAGCAACCTTGCTGGA	171			

D	407	TCCTGTCGGCGCTCCTGCTCGTCGCGCCGTCGCCGTTGCCGATGATGGGTGCAGCGCTGCTGGA	466
Q	172	GATTAAAGAGTCATTCAAAGATGTGAACAATGTTCTTTATGACTGCAACAATTCACCTTC	231
D	467	GATCAAGAGTCCTTCCGCAATGTGACAACGATCTGTAAGATTGGCCGGCGGCG-----	521
Q	232	TTGCGATTATGTGTCTCGAGAGGTGTGTCTTGGAAGAAATGTCACTTCAATGTTGTTGC	291
D	522	---GACTTACGTCTCGGGCGCGCGCTCTGTGGACAAAGTCACTTTCGCGCTGCGCGC	577
Q	292	TCTTAATTTTGCATATTGGAATCTTGATGTGAGAAATCTCACTGCTATTTGAGATCTCAA	351
D	578	GCTACACCTATCCGGGCTCAACTCTGGAGGCGAGATCTCTCCGGCGGTGGAGTTGAA	637
Q	352	GAGTCTCTTGCAATTGATCTGCCAGGTAATCGCTTCTGCACAAAATCCCTGATGAGAT	411
D	638	GGGATCGTCTCGATTGACTGAAGTGGAATGGGCTGTCTGGGCGAGATCCCTGATGAGAT	697
Q	412	TGTGACTGTCTTCTTTGCAAACTTAGACTTATCCTTCAATGAAATTAAGTGTGAT	471
D	698	TGGGATTTGTTCACTACATAAAATCTCGAATTTGTCTTCAATGCTTGGATGGGGCAT	757
Q	472	ACCGTTTTCGATTTCGAATTTGAAGCAACTTGACACGTGATTTGGAAGATACCAATT	531
D	758	TCCGTTCTCAATATCGAAGCTGGAAGCACTTGAAGCTTGATATTTGAAGAACCAACAAT	817
Q	532	GATAGGACCGATCCCTTCAACACTTTTCAAGATTTCCAAACCTGAAAATTCGACTTGGC	591
D	818	GATGGAGTGATCCCATCAACGGCTCTCAGACTCCAAATTTGAAGATTTTGGACTTGGC	877
Q	592	ACAGATTAATCTCAGTGTGAGATACCAAGCTTATTTACTGGAATGAAGTTCTTCACTA	651
D	878	ACAGAACAACTGATGTGAGAGATACCAAGCTGATATTTGGAACAGAGTTCTTCAATA	937
Q	652	TCTTGGGTGGAGAGAAACAATTAATGCGGTAATTTCCAGATTTGTGTCAACAGAC	711
D	938	CTTGGGATTAACGGGTATATATTTGAAGGACAGATCTCCCGAGATATATGCCAGTTGAC	997
Q	712	TGCTCTTTGGATTTTGAAGTAAGAAACAACAGTTTACTGTGATTAACCTGAGACGAT	771
D	998	TGGGCTTTTGTGACTTATGACGTAAAGAACACAGCTTATGCGGCCGATACAGAAACAT	1057
Q	772	AGGAATTCGACTGCTTCCAGTTTGGACTGTGCTCTACATCAGCTAACTGTGTGAT	831
D	1058	TGGAGACGTGAACAAGTTTCAAGCTTGGATTTGTCTTCAATATMACTTTCTGATCAAT	1117
Q	832	CCCTTTTGACATGGGCTCTCTCGAAGTTGGAACAATTCATTTGGAAGGCAATCAACTGC	891
D	1118	TCTCTTCAACATGGGTTTCTTCAAGATTGTACACTATCTTTGGAAGGAACATGTTTAC	1177
Q	892	TGGAGATTCATCAGTGAATGGTCTCATGCAAGCCCTTGACGCTTGAATCTTAAGTGG	951
D	1178	TGGTCATATTCATCAATTAATTTGACATTTAGCAGGCTCTGCGTGTACTGATCTGAATTA	1237
Q	952	CAACTTGTGATGATCTATTCCTCCGATTTCTGGAAATCTTACTTACCGGAATTT	1011
D	1238	CAACCAATTTGCTGTGCTTATTCATCGATACTGGAATTTAAATTAATCACTGGAAGCT	1297
Q	1012	GTAATTCACAGTAACAGCTGACTGGTCAATTTCCACCTGAGCTTGGAAACATGTCAA	1071
D	1298	GTAATATCAAGGCATATGATTAAACAGGTCCAAATCACTGAGCTTGGAAATATGTCAAC	1357
Q	1072	ACTCATTTACCTGGAACTCATATGATATCATATCTCAGGGCTATTTACACACAGAGCTTGG	1131
D	1358	CTTTCATTTACTAGAACTTAACATATATCAACTTAGGGGGTCACTTCTCCAGAGTTGG	1417
Q	1132	GAACTTACTGACTTGTGTTGATCTGAATGTGGCCAAATGATCTGGAAGACCTATACC	1191
D	1418	AAAGCTAAAGGGTATTTGACTTAAACCTTGCAAAACAACAATTTGAAGTCCAAATCCC	1477
Q	1192	TGATCATCTGAGCTCTTGCACAAAATCTAAACAGTTTAAATGTTTATGTGGAACAAGTTTGA	1251
D	1478	TGATTAATATAGCTCATGTGTGATCTCAATAGCTTCAATGCTTATGTGCAACAATTTAA	1537

QY 1252 TGGCACTATATCCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGTCAG 1311
 DB 1538 TGGGACCATTCCTCTTCATTTGCAATTAAGTATGAGCATGCTTAATTTGATTTGTATC 1597
 QY 1312 CAACATATCAAAAGTCCAAATCCCGGTGAGCTATCTGTATGGTAACTTATGATTAAT 1371
 DB 1598 AAATTTCTAAGTGTCTAATCTTATTTGAGCTATGAGAAATCAAAATTTGACACCTT 1657
 QY 1372 GGAATCTTCAACAACAAGAAATATGATATCTCTTCTCTCTCTCTCTCTCTCTCTCTCT 1431
 DB 1658 GGAATTTACCTGTAAACATGATTAATCTGAGCCCAATTCATCAACATTTGGAGTTGAGCA 1717
 QY 1432 TCTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1491
 DB 1718 TCTATTTAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1777
 QY 1492 AAATCTAAGAGATCAATGAGAAATGATCTTCAAAATGATATCTCTGAGCCCAATTC 1551
 DB 1778 CAATTTGAGAGATCAATGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1837
 QY 1552 AGAAGACTTAACCAATTAACAAGAAATATTTTGTGAGACTGAGAAATTAATTAATCTG 1611
 DB 1838 TCAAGAACTGGAATGCTGCAAAATCTGATGTTGTTAAATCTCAAAACAAACAATTAAC 1897
 QY 1612 TGGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1671
 DB 1898 TGGGAGTGTCTCTTCACTGATGAACTGCTCTGAGCTCAATATCTTAATATGATCTTA 1957
 QY 1672 CAACCTGTAGTGTATATCCCTTAAGAAATTAATCTTCAAGATTTTCAACAGACCTT 1731
 DB 1958 TAATTTGGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2017
 QY 1732 CATTTGAAATCTGCTGTTTGGCGTATGCTTAATCTCAACCGTGTATGATTTCTGCTG 1791
 DB 2018 TTTGGGTAATCCAGAGACTTGTGTATATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2077
 QY 1792 AACTGTACGAGTGTCAATCTCTAGAGAGCTATCTTGAATAGCTATGAGGAGCTTGT 1851
 DB 2078 TCAACAGAAACCAATATCTCAAAAGCTGCAATCTTGAATTTGCGTGGGTGGCTTGT 2137
 QY 1852 GATCTTCTGATGCTTAAATAGACGCTTCCGACCGCATATCTCTCTCTCTCTCTCTCT 1911
 DB 2138 TATCTCTGATATCTTATGAGGCTGTCAGGCTCATATGTCACCTGTTTCAAGA 2197
 QY 1912 TGAATCACTTGAACAAACAGTAATTTGACACCGAGAGCTGCTATCTCTCATATGAA 1971
 DB 2198 TGTCTCTGTAGCAAAACAGTGAAGCAATGTCCCCCAAGCTGGTTATCTTCAATAGAA 2257
 QY 1972 CATGGCACTGACGTTTACGAGGATATGAGAAATGAGAAATGAGAAATGAGAAATGAG 2031
 DB 2258 CTTTTCCCTCTTGTATACGAGGATATAGCATGACTGAAACCTGAGTGAAGTGA 2117
 QY 2032 TATCATTTGGCAGGAGCATCAAGCACTGTATCAAAATGTTTGAAGATTTGAAC 2091
 DB 2318 CATCATTTGGGTAGGAGCATCCAGCAAGT-TATTAATGTTTTCGAAGAACCGCAAC 2376
 QY 2092 GGTGGCATTAAGCGGCTTATCTCTCAACCAACAGTCAATGAACAGTTTGAACAGA 2151
 DB 2377 AGTGGAGTAAAGGATATATGCCCCATATCCACAGAGCTTCAAGGAATTTGAACATGA 2436
 QY 2152 ACTGAGATGCTAATGATGATCAAGCAAGAAATCTTGTAGGCTTCAAGCTTATTCCT 2211
 DB 2437 GCTTGAAGCTGTGATGATCAAAACCGGAATCTAGTCAAGCTTCAAGAAATTTCTCT 2496
 QY 2212 TCTTCACTTGGGAGTCTTGTCTATATGATATTTGAAATGTTAGCCTTGGAGATCT 2271
 DB 2497 ATCTCCGTTGGAATCTTCTCTTACGATTAATGAAATGGAAGCCTCTGGAGATGT 2556
 QY 2272 TCTTCAAT---GGCCCTAAGAAAGAAAGAAAGCTTGTATGAGGAGCAACGGCTTAAAGATAGC 2328
 DB 2557 TTTGCAAGAGGTCACATTAAGAAAGAAAGAAAGCTTGTATGAGGAAAGCTGTCTACGAATTCG 2616

QY 2329 ATATGTGACAGCAAGGTTTAGCTTATCTACACCATGATGATGATGATGATGATGATGATG 2388
 DB 2617 TCTAAGTGGCGCCCAAGGCTTGTATCTTATCATGATGATGATGATGATGATGATGATG 2676
 QY 2389 CAGAGAGTGAAGTGTCTCAACATCTCTTGAACAAAGACTTGAAGGCTGTTTGAACAGA 2448
 DB 2677 CAGGAGTGTGAATTAACAAATATATCTCTGATTAAGATTAAGAGGACATCTTAACAGA 2736
 QY 2449 TTTTGAATAGCGAAAGCTGT 2508
 DB 2737 CTTTGGATTTGCTAAGGTTTGT 2796
 QY 2509 CAGCATAGTTTAAATAGACCCCAAGATGCTCCCACTTCAAGGCTCACTGAAGAAATCCGA 2568
 DB 2797 AACTATGGCTATATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 2856
 QY 2569 TGTCTCAAGTTATGAAATAGTCTCTTGTGATTTGTTAAACCCGAAGAAACCGTTGATGA 2628
 DB 2857 TGTCTACAGCTATGAGCATTTGTTGTTGTTGATGCTGATGATGATGATGATGATGATGATG 2916
 QY 2629 CGATCCATCTCCACATCTGATATATGATCAAGAGCGGGAAACATGATGATGATGATGAT 2688
 DB 2917 CGAGTGAATCTCCATCACTGATCTTGTCAAAAGACGGCTTAACATGCTGTGTGAGAC 2976
 QY 2689 GGCAGATCCAGATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2748
 DB 2977 AGTCGACCCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3036
 QY 2749 ACTGGCACTCTTATGACCAAAAGACAGCCGAATGATGATGATGATGATGATGATGATG 2808
 DB 3037 GCTGGCGCTCTTGTGACCAAGAGACCAATCGGATCGGATCGGATCGGATCGGATCGGATCG 3096
 QY 2809 TCGTGTCTCGGAGTTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 2859
 DB 3097 GCGGCTCTGAGTCTGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 3156
 QY 2860 CAGCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2919
 DB 3157 CATGCCGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3216
 QY 2920 TCAATCTGCAATGCTC---TTCATGAGTCTTGTGATGCTCAACTGTTTCTTGGTT 2976
 DB 3217 CAGCGTCTCTCTGCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3276
 QY 2977 TGGCAAGTTATTTCTCAAGACGATGATG 3007
 DB 3277 TGGCAGGTCATTTCTCAAGAACAGAGTAG 3307

RESULT 6

US-10-519-135-9
 ; Sequence 9, Application US/10519135
 ; Publication No. US20060137041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Australian National University
 ; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT
 ; FILE REFERENCE: 94948/MRO
 ; CURRENT APPLICATION NUMBER: US/10/519,135
 ; PRIOR FILING DATE: 2004-12-22
 ; PRIOR APPLICATION NUMBER: AU PS3339
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 2901
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana ERECA homolog
 US-10-519-135-9
 Query Match 35.2%; Score 1117.6; DB 6; Length 2901;
 Best Local Similarity 64.0%; Pred. No. 0;
 Matches 1741; Conservative 0; Mismatches 964; Indels 15; Gaps 3;

131 GTAGCTACGTGACCTTCAGAGGAGGAGCAACGTTGCTGAGATTAAGATCATTCAAA 190
64 GTTGCTTCGGCTATGAAACAAGAGGAAAGCTGTGATGGCATTAAGAGCTCTTTACG 123
191 GATGTGAACAATGTTCTTTATGACTGCAACATTCACCTTCTTGAGATTAATGTGTGG 250
124 AACCTAGTAATATGCTTTGGATTGGGACGATGTTCACAAACAGTGAATCTGTGTTGG 183
251 AGAGGTGTCTGTGAAAAATGTACCTTCATGTGTGTCTTAATTTGTGCAATTTG 310
184 CGAGGTGTTTTCTGCAACAACGTTAGCTACCTGCTGTCTCTGAAATTTGTCAGCTG 243
311 AATCTTAGAGAAATCTCACTGCTATTGAGATCTCAAGAGCTCTTGTCATTTGAT 370
244 AATCTTGAGGGAGATATCTCCAGCTATTGAGACCTACGGAATTTGCATCAATAGAC 303
371 CTGCGAGTAATCGCTGTGTGCAACAATCCCTGATGAGATTTGTGACTGTTCTTTG 430
304 TTGCAAGTAATAAATAAGAGGTCAAAATTCAGATGAGATTGGAACGTGCTTCTCT 363
431 CAAAATTAACCTTATCTCTCAATGAATTAAGTGTGACATACGCTTTTGGATTGCAAG 490
364 GTTATCTGATTTGTCCGAAATCTGTATATGAGACATACTTTCTCAATCTTAA 423
491 TTGAAGCACTTGAGCAGCTGATCTGAGAAATAACCAATTGAGAGCCGATCCCTTCA 550
424 CTCAGAGAGCTTGAACCTGGAATCTGAATCTGAAGAACATACGCTACAGGCTCTGTACAGCA 483
551 ACACTTTCACAGATTCGAAACCTGAAAAATCTGAGCTTGGCAGAAATTAACCTCAGTGT 610
484 ACCCTAACCCAGATTCGAAACCTTAAGAGCTTATGATCTGTGCAATCACTTAACGGGT 543
611 GAATTAACAGACTTATTTACTGGAATGAAGTCTTCAGTATCTTGGGTTGCCAGAAAC 670
544 GAGATATCGAGATTGCTTACTGGAATGAAGTATTGAGATATCTTGAATTAACGAGGAAT 603
671 AACTTACGCTAACATTTCTCCAGATTTTGTGCACTGACTGCTCTTGGTATTTTGAC 730
604 ATGTGACTGGAACGTTATCTTCTGATATGTGTACGCTAACCCGTTGTGTGATCTTTGAT 663
731 GTAAGAAACAACAGTTTGACTGTAGTAATCTGAGACGATGAGAAATTTGACGCTTC 790
664 GTGAGAGAAATATCTTAACCTGGAACCATCCGAGAGCAATCGAAATTTGACAAAGCTTT 723
791 CAGGTTTGGACTGTCTTACATCACTGATACGTGTGAGATCCCTTTGACATGTGCTTC 850
724 CAATCTGAGCATATCTTATTAATCAGATTAACAGAGAGATTCCTTCAATATGCGCTTC 783
851 CTGCAAGTTGCAACATTAATCACTTGAAGGCAATCACTCTGGAAGATTCATCAGTG 910
784 CTCGAACTGTCTACTGTCTCACTTCAGAGAAACAGATTTGACGGGTAGAAATTTCCGAAAGTT 843
911 ATTGCTCATGCAAGCCCTTGCAGTCTTAGATCTAAGTGGCACTTGTGAGTGATCT 970
844 ATTGCTTAATGCAAGGCTTGTGCTGTTTGGATTGAGTGAATGAGCTTGTGTGCT 903
971 ATTCTCCGATTTCTGGAAATCTTAATTTCAACGAGAAATTTGATTTGACAGTAACAAG 1030
904 ATCCCAACCGAATCTTGGCAATCTCTCAATTAACGGAAGATTTGATCTCCATGAGCAATATG 963
1031 CTGAGCTGTTCAATTCACCGAGCTTGGAAACAGTCAAAACCTTCATTCCTGGAAGCTC 1090
964 CTCACCTGTCAATCCCTCTGAGCTTGGGAATATGTCAAGCTCTCAAGTATTTGACAGCTA 1023
1091 AATGATTAATCATCTCAGGGTCATATAACCAAGAGCTTGGGAAGCTTAATGACTTGT 1150
1024 AAGACAAATAAATCAATGAGGAATATTCACCTGAGCTTGGAAAGCTGAGCAATTTGTT 1083
1151 GATCTGAATGTGGCAACATGATCTGAGAGACCTTATCCTGATCATCTGAGCTTTGCG 1210
1084 GAACTGAATCTTGCACCAACACCGTTTATGAGGGCCCATACCATCAACATTAATGATCATGT 1143

1211 ACAATCTAACAACAGCTTAATATGTTCAATGGACAAAGTTTAGTGCACTATACCAGCA 1270
1144 GCAGCCTTGAATCAATTAATGTTCAATGGACCTCTGAGTGATCTATTTCCATGGCG 1203
1271 TTTCAAAAGCTAAGAAATGATGACTTACCTTAATCTGTCCAGCAACAATATCAAGGTCCA 1330
1204 TTTGCAATCTCGGAGCTTGAATCTGAAATCTTTCGTGCAACAATTTCAAGGAGAAA 1263
1331 ATCCCGTTGAGCTATCTGATCGGTAATCTGATGATACATTTGATCTTTCCAAACAAG 1390
1264 ATACCACTTGAAGCTTGAACATTAATCAATCTTGACAAACATGATCTGTGCGCAATAC 1323
1391 ATAAATGAATCATCTCTCTCTCTGATTTGAGAGCATCTTCAAGATGAACCTTG 1450
1324 TTCTCAGGGCTATTAACATTAACGCTTGGGACTTGAACACCTTCAATTAATAATCTT 1383
1451 AGTAAGAAATATTAATCTGTGATGTTCCAGGGGACTTTGGAATCTAAGAACATCATG 1510
1384 AGCAGAAACCATCTTATGATGCAATTAACCTGAGAGTTGGGAACCTTGCAACCATTCAG 1443
1511 GAAATGATCTTCAAAATTAATGATATCTGAGCCCAATTCAGAGAGCTTAACAATTA 1570
1444 ATGATTTGATATATTAATTAATCTGCTCTCCGAGTTATTTCACTGAATTTGGCCATTTG 1503
1571 CAGAACATTAATTTTGTGAGACTGGAATAATTAATTAACCTGATATGTT---GGTTCA 1627
1504 CAGATTTTAATCTTAAATTAATTAATGAACAACAACAGCTTATGGAATAATTCAGATCAG 1563
1628 TTAGCCACTGTCTCAGCTCACTGATTAATGATATCTCATTAACAACCTGATAGTGTAT 1687
1564 CTTAACGAATCGCTTCACTCTGTGCAATCTGAATGTCTCTTCAACAATCTCTCGGAGTA 1623
1688 ATCCCTAAGAACAAATTAATCTCTCAAGATTTTCAACGAGAGCTTCAATCTGAT 1747
1624 GTCCCAACAAATGAATAATCTTCACTGCTTGTCTCCAGCCAGCTTTGTGGAATTCATAT 1683
1748 CTTTGGGTAGTTGGCTTAACTCAACGCTGATCATGATTTCTGTGAACTGTACAGTGTCA 1807
1684 CTTTGTGGAACAGTGGGTGATCTAATTTGTGTGCTTACCGAAATCTCGA-----GTA 1737
1808 ATCTCTAGACAGCTATCTTGGAAATGATTAATTTGGGGGACTTGTGATCTTCTCATGTCT 1867
1738 TTCTCCAGAGGCTTGTGATCTGATGATCTTGTGGGTCTATCACTCTCATGATATGATTT 1797
1868 TTAATGACAGCTTGGCAGCCGCAATTAATCTCTCTCTTTGATGAGATCACTTGACAA 1927
1798 TTCTTGCAGTTTAACAATTAATGACAGCAAGAAATTTTACAAGGCTC-----CTCA 1851
1928 CCAATTAATTAATTCGACACCGAAGCTGTCATCTTCTATATGAACATGGCACTCCAGTT 1987
1852 AACAAGCTAAGAGGTTTAACAGAGTAGTATCTCCACATGACATGGCAATTCATATCA 1911
1988 TAGAGGATATCATGAGATGACAGAGATCTTAAGTGAAGATATCATTTGGGCACGGA 2047
1912 TTTGATATATCATGAGAGTGAAGATCTTAAGCAAAAGTTTATTAATGATATGTGT 1971
2048 GCATCAAGCACTGATTAACAATGTGTTTGAAGAATTTGTAACCGGTTGGGATTTAAGCG 2107
1972 GCTTCTAGCAGGATTAACAATGTGATTAAGTTTCCGACCTATGATGCAATTAAGCA 2031
2108 CTTTACTCTGACAAACCCAGCAAGTCAATGAACAGTTTGAACAGAACTCGAGATGCTAAGT 2167
2032 CTCTACATCAGATATCCGATTAACCTTGGCGGAATTTGAGACAGAACATGACATTTGG 2091
2168 AGCATCAAGCAAGAAATCTTGTGAGCTTACAAAGCTTATTCCTCTCTCACTTGGGAGT 2227
2092 AGCATTTAGGCAAGAAACATATGACGCTTGCATGATATCTCTGCTCTTACTGCGAAC 2151
2228 CTTCTGTTCTATGATATTTGGAATAATGTAGGCTCTGGGATCTTCTTCAATGGCCCTACG 2287
2152 CTTCTTTTCTATGATCTACATGAGAAATGATCACTTTGGGACCTTCTTCAATGGGTCAATTG 2211
2288 AAGAAAAAGACTCTGATTTGGGACACAGCGCTTAAGATACATATGTTGACAGCAAAAGT 2347

Db 2212 AAGAAAGTGAAGCTTGATTTGGGAGACAAAGTTGAATGATGCGCTTGGAGCTGCACAAAGGA 2271

Qy 2348 TTAGCTTACTACACCATGACTGTAGTCCAAAGATCATTTCAACAGACGTGAAGTCGCC 2407

Db 2272 CTAGCTATCTTCAACACGATTTGTACTCTCGTAATCATTTCAACCGTGACATCAAGTCATCG 2331

Qy 2408 AACATTTCTTTGGACAAAGACTTTAGAGCTCGTTTGACAGATTTTGGAAATGCCAAAAGC 2467

Db 2332 AACATACCTCTTGAAGAGAAATTTTGAAACACATTTATCTGATTTTCGGGATTTGCTAAAGGC 2391

Qy 2468 TTGTGTGTGTCAAAAGTGCACATACCTTCAACTTACGATGGAGGACGATAGTGTACATAGAC 2527

Db 2392 ATACACGATGACAAAAACCCATGCCCTGCACCTTATGTTTGGGACAACTTGGTTATATAGAC 2451

Qy 2528 CCCGAGTATGCTCCGACATTCACGGCTCACTGAGAAATCCGATGCTTACAGTTATGGAATA 2587

Db 2492 CCAGAGTATGCTCGTACTTTCACGATTCATGAGAAATCCGATATATATACAGCTTCGGTATTT 2511

Qy 2588 GTCCCTCTTGAAGTGTGTTAACCCGAAAGAAAGCCGTGATGACGAATCCATCTCCACCAT 2647

Db 2512 GTTCTTTCTTGAAGCTTCTCACTGGGAAAGAGCAGTGTTAAACGAGCTTAACTTGATGATCAA 2571

Qy 2648 CTGATATATGTCAAAGACGGGAAACATGTAAGTGATGAGAAATGGCAGATCCACACATCACA 2707

Db 2572 CTGATATATGTCAAAGGCTGATGATATATCTGATGATGAGAAAGCATTTGATCCAGAGGTTACT 2631

Qy 2708 TCGACGTCTTAAGATCTCGGTGTGTGTAAGAAAGTTTCCAACTGGCACCTCTTATGCACC 2767

Db 2632 GTGACTTGTAATGAGACTTGGGACATATCCAGGAAGACATTTTCAGCTGGCTCTTTATGCACA 2691

Qy 2768 AAAAGACAGCCGAATGATCGAACCCACATGACACCGAGTCACTCGTGTTCTCGGACGTTTT 2827

Db 2692 AAGGAAACCTTTAGAGAGACCCACATATGCTGTGAAGTCTTAAAGGTTCTGCTCTCTCTT 2751

Qy 2828 ATGCTATCGAACAACACACC 2847

Db 2752 GTCCCATCTCGCAAGTAGC 2771

RESULT 7
US-10-519-135-7

/ Sequence 7, Application US/10519135
/ Publication No. US20060137041A1
/ GENERAL INFORMATION:
/ APPLICANT: The Australian National University
/ TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY
/ FILE REFERENCE: 94948/MRO
/ CURRENT APPLICATION NUMBER: US/10/519,135
/ PRIOR APPLICATION NUMBER: AU P53339
/ PRIOR FILING DATE: 2002-07-02
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 2751
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana ERECTA homolog
US-10-519-135-7

Query Match 33.8%; Score 1074.6; DB 6; Length 2751;
Best Local Similarity 64.0%; Pred.No. 1.3e-311;
Matches 1717; Conservative 0; Mismatches 904; Indels 60; Gaps 4;

Oy 168 TGGAGATTAAGAAGCATTCCTCAAGTGAACATGCTCTTTATGACGTGCACAATTCCAC 227
 |||||
Db 2 TGGCGATAAAGCCTTCATTCAGCAACGTGGCGAATATGCTCTTGATTTGGAGCATGTC 61
Oy 228 CTTCTTCGATTATTTGTGCTGGAGAGGTGTGCTTGTGAANAATGTCACTTCAATGTTG 287
 |||||
Db 62 ATAAACCAAGACTTTGTGCTTGGAGAGCGTCTTCTGTGATTAACGTTAGCTCAATGTTG 121
 |||||

OY	288	TTGCTCTTAATTGGTCAGATTGATCTTGATGGAGAAATCTCACCTGCTATTGGAGATC	347
Db	122	TCCTCTTAACTGTGCAAACTGTAATCTTGGTGAGAGATATCATCTGCCCCCTTGGAGATT	181
OY	348	TCAGAAGCTCTGTGCAATTGATCTGGAGGATATCGCTGTGCAACAATCCCTGATG	407
Db	182	TGAATGAACTGTCAATCAATAGACTTGGCAAGGAAATTAATGGGTGTCAAATTCAGATG	241
OY	408	AGATTGTGACTGTCTTCTTTCGAAAACCTAGACTTATCCTTTCATAGATTAATGATGTG	467
Db	242	AGATTGGAAACTGTGTTTCTCTTGCTATTGTGCAATTTCTCCACCAATTTGTGTTGGAG	301
OY	468	ACATACCGTTTTCGATTTTCGAATTGAAAGCACTTGACAGCTGATTCGAAGAAATTAAC	527
Db	302	ACATACCGTTTTCATCTCTAATCTCAAAACAGCT-----	335
OY	528	AATTGATAGACCGATCCCTTCAACACTTTCACAGATTTCCAAACCTGAAATTTGCACT	587
Db	336	-----GACCTTAATCAGATTTCCAAACCTTAAGACCTTTGACC	373
OY	588	TGGCAGAGAAATTAACCTAGTGTGAGATATCCAAAGACTTATTTACTGGAATGAAGTTCTTC	647
Db	374	TCGCAAGAAACACACTTAAGTGTGAGATATCCAAAGTTACTCTACTGGAATGAAGTTTAC	433
OY	648	AGTATCTTGGTTCGAGAGAAACAATTAGTCGTAACATTTCTCCAGATTTGTGTCAAC	707
Db	434	AGTATCTCGTTTACGTGGGAATATGTTAATCTGGAGCAATGTCTCTCGATATGTGTCAAC	493
OY	708	TGACTGTCTTTGGTATTTTGAACCTTAAGAAACAAGTTTGAACGTGATAGTATTAACCTGGA	767
Db	494	TGACGGGTCTGTGACTTGTGATGTGAGAGCAACAACCTTACTGGAACATATCCAGAGA	553
OY	768	CGATAGAGAAATTTGACTGCTTCCAGGTTTTGGAAGTTGCTCTTACAAATCAGCTTAACGTG	827
Db	554	GCATTGGCAATTTGACAAAGCTTTTBAAGATCTTGGATGTATCTTAATACAGATTACCGGAG	613
OY	828	AGATCCCTTTTGACATCGGCTTCTCGAAGTTGCAACATTATCAATTGCAAGGCAATCAAC	887
Db	614	TTATACCTTAACAATATTGGTTTCTCCAAAGTAGTACTGTCTCACTTCAAGGAACAAGT	673
OY	888	TCTCTGGGAAGATTCCATCAGTATTTGGTCTCATATGCAAGCCCTTGCACTTTAATCTTA	947
Db	674	TGACTGGCAGAAATTCGGAAGTGTATGGTCTGAATGACAGGCTCTTGCTGATATTTGAATTTGA	733
OY	948	GTGCAACTTGTGAGTGAATCTAATCTCTCCGATTCCTCGAAATCTTAACCTTACCCGAGA	1007
Db	734	GTGCAAAATGAATTAACGTGGCTTAATTCACCAATTAATTTGGGAATCTGTCAATTCACGTGAA	793
OY	1008	AATTGTATTGGCAGATTAACAAGCTGACTGGTTCAATTCCACTGAGCTTGGAAACATGT	1067
Db	794	AATGTATATCTCAATGGCAACAAGCTCACTGGACAAATCCCAACCCGAGTAGGCAATATGT	853
OY	1068	CAAAATCTCAATACCTGGAACTCAATGATATATCTCAAGGGTCAATATACCAACCAAGC	1127
Db	854	CACAGCTCAGCTATTTCACAATAATATATATAGCAATGAGGGAAGATCCACCTGAGC	913
OY	1128	TTGGGAAGCTTACTGACTGTTGTTGATCTGCAATGAGGCAACAATGATCTGGAAGAACCTTA	1187
Db	914	TTGGGAAGCTGGAACAATTTGTTGCAATCTGAATCTTGGCAACACAATCTTGTATGGGCTGA	973
OY	1188	TACCTGATCATCTGAGCTCTTTCGACAACAATCTTAACAAGCTTAATATGTTCAATGGCAACAGT	1247
Db	974	TTTCATCTTAACATTAAGTTCTGTGCTGCTGCTGGAATCAATTCATTAATGTTCAATGGAACTTCT	1033
OY	1248	TTATGTGCACTATACCCCGAGCACTTTCAAAAAGCTAGAAAAGTATGACTTAACTCTGT	1307
Db	1034	TGAGTGAAGCTGTACCACTTGAATTTCCGGAATCTTGGAAAGCTTGAATCTTAATCTTT	1093
OY	1308	CCAGCAACAATATCAAAAGGTCGAATCCCGGTGAGCTATCTCGATACGGTAACCTTAGTAA	1367
Db	1094	CTTCAAAACAGTTTCAAGGGCAAAATTAACCTGTGAGCTTGGCCATATATCATATCTTTATTA	1153
OY	1368	CATTGATCTTTCCACMAACAAGATTAATGAAATCATCTCTTCTTCCCTTGGTGAATTTGG	1427

1154 CATGGATCTGTGGCAACAATTTCTCAGGCTCAATTCATTAACACTTGGATCTTG 1213
1428 AGATCTTCTCAAGATGAATCTTGATGAATAATCAATACTGGGTAGTCCAGGCACT 1487
1214 AGATCTTCTCAATCTTAACCTTGAGCAAAATCACTGAATGGCACTTCCTGCAAAAT 1273
1488 TTGGAATCTTAAGAGCATGATGAATAATAGATCTTTCAAAATTAATGATATCTTGCCCA 1547
1274 TCGGAACTTCCAGAGCATTCAGATCATCATGTGTCTTAATTTCTTGCCGGTCTTA 1333
1548 TTCCAGAGAGCTTAACCAATTACAGAACATTAATTTGCTGAGACTGAAAAATTAATACC 1607
1334 TTCCAACTGAACCTTGCCAGTGGCAAGAACATAAATCTCTGATCTGAAACAACAAGA 1393
1608 TGACTGCTATGT---TGCTTCAATTAAGCAACTGCTCAAGTCTCACTGATTAATGATAT 1664
1394 TTGATGGAAAAATCCCTGATCAAGTAACTAATGCTTCACTTGGCAATCTGAAACATCT 1453
1665 CTCATAACAACCTGCTAGTGTATCCCTAAGAACATTAATCTTCAAGATTTTCAACAG 1724
1454 CTTCAATAATCTTTCTGGAATAATCCCACTATGAAGAACTTAAACAGTTTCCCGG 1513
1725 ACAGCTTCATGGCAATCTGCTGCTTGGGTAGTGGCTAAACTCAACGCTGATGAT 1784
1514 CCAGCTTCTTGGAAATCCATTTCTGCGGGAACCTGGGTGATCAATCTGTGGCCAT 1573
1785 CTGCTGCAACTGTAAGAGTGTCAATCTCTAAGAGCACTATTTGGAAATGCTATTTGGG 1844
1574 CTTTACCTTAAGTCAAGT---ATTACACAGAGTGGCGGTATTTGATGGTCTCTGGTT 1630
1845 GACTTGTGATCTTCTCATGCTCTTAATAGACGCTTCCAGCCGATTAATCTCTCTT 1904
1631 TCATCACTCTCATATGATGATATTAATTCGCTTCAAGTCAACAGACAGAAACAG 1690
1905 TCTTGTGATGATCACTTGACAAACAGTAACTTAATGCAACCGAGCTGCTCATCTTC 1964
1691 TCTTGAAGGCTCTTCAAAACAAAC-----CTGAAGGCTCAACGAGCTGTGATCTTC 1744
1965 ATATGAACATGGGCACTCCAGCTTACAGAGATATCAAGAAATGACAGAAATTAAGTG 2024
1745 ACATGACATGGCTATTCACACGTTTATGATATCAAGAGATTAAGAAACCTCGATG 1804
2025 AGAATATATCATTTGGGACAGAGCATCAAGCACTGTATCAAAATGTCTTGAAGATT 2084
1805 AGAATATCATTTGATGATGATGATGCTTCTGACACAGTTTCAAGTGAACCTCCAAACT 1864
2085 GTAAACCGGTGGATTAAGCGGCTTATCTCTCAACCCACAGTCAATGAACAGTTTG 2144
1865 CCCGACCTATTTGCATTAAAGCAATCAATCAATATCCAGCACTTCCGCGAGTTTG 1924
2145 AAACAGAACTGGAATGTAAGTCAAGCAAGCAAGAAATCTTGAGGCTCAACGTT 2204
1925 AAACAGAGCTTGGAACATTTGGAGCATCAAGACAGAAACATATGTAAGCTTGACGAGAT 1984
2205 ATTCCCTCTCTCACTTGGGAGTCTTCTGTTCTATGATATTTGGAAATGATAGCTCT 2264
1985 ACGCTTATCTCCCTTTGGCAACTCCCTCTTCAAGCTAATGGAATAGGCTCTCTTT 2044
2265 GGGATCTTCTCATGCGCTTACAGAAAGAAAGACTTTGATTTGGACACACGGCTTAA 2324
2045 GGGATCTTCTCATGCGCTTGGGAAAGAGTGAAGTGAAGTGAAGCAAGGCTGAAGA 2104
2325 TAGATATGAGGACCAAGGTTTACTTATCTAACCATGACTGTATGATGCAAGATCA 2384
2105 TAGTGTGAGAGCTGCGCAAGAGACTTGATATCTTCAACATGACTGCAACTGAGATA 2164
2385 TTGACAGAGAGCTGAGATCTGTCAACATTTCTTGTGACAAAGACTTGAAGGCTGTTGA 2444
2165 TCATGAGAGCATGAATCAATCAAAATATCTCTTGAATGGAATTTGGAAGCGGTTTGT 2224
2445 CAGATTTTGAATGCGAAAGCTTGTGTGTCAAAAGTCACTACTTCAACTTAAGTGA 2504

2225 CAGATTTTGGATTTGCCAAGAGCATACAGCCACCAAACTTAATGCTTCAACTATGTC 2284
2505 TGGGACGATAGGTTACATAGACCCCGAGATGCTGCACTTACGCGCTCACTGAGAAAT 2564
2285 TTGGAACATTTGATATTTGACCCAGAGTATCTGAACTTTCGCTTGAACGAGAGT 2344
2565 CCGATGTCTACAGTTATGGAATATGCTTCTTGAATGTTTAAACCGAAGAAAGCGTTG 2624
2345 CTGATATCTACAGTTTCGATATGCTTCTTGAAGCTTCAACCGGAAGAAAGCTGTGG 2404
2625 ATGACGAATCTCATCTCCACATCTGATATATGCAAAAGACGGGAAACATGAAGTATG 2584
2405 ATACCGAGGCACTTGACATCAATGATCTATCAAAAGCGGATGATTAACAGATATAG 2464
2685 AAATGGAGATCCAGACATCATCGACGCTTAAGATCTCGGTGATGTAAGAAAGTTT 2744
2465 AAGCTTGTATGAGAGGCTTCAAGTATCTTCACTGATGACTAGACACATTAAGAAAT 2524
2745 TCCAACTGGCACTCTATGCAACCAAAAGACCGCAATGATGACCCCAATGACCAAG 2804
2525 TTCAGGTAGCTCTCTGTGACCAAGCAAAATCTTTGAGAGACCAACCATGACGAGG 2584
2805 TGACTGCTGTTCTCGGCACTTTATGCTATCGGAACAACA 2845
2585 TCTTGAAGGTTCTGCTTCACTTGTCCCGTCTCCACTTCA 2625

RESULT 8
US-10-519-135-5
; Sequence 5, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT
; TITLE OF INVENTION: PLANTS PRODUCED THEREFROM
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU PS3339
; PRIOR FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 2766
; TYPE: DNA
; ORGANISM: sorghum ERECTA
US-10-519-135-5

Query Match 33.1%; Score 1050.8; DB 6; Length 2766;
Best Local Similarity 63.4%; Pred. No. 1.8e-304;
Matches 1845; Conservative 0; Mismatches 882; Indels 185; Gaps 8;

112 TCTCTTCTGCTTGAAGTCTAGTACTGCTGACTTCAAGAGAGGAGCAAGTGTGGA 171
24 TCTGTGCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 83
172 GATTAGAAAGTCAATCAAGATGTAACAATGTTCTTATAGCTGGAACAATTACCTTC 231
84 GATCAAGAAATCTCTCCGCAAGCTGCGCAACGTAAGTGAATTTGGCGCGGCA----- 138
232 TTGGATTAATTTGTCTGAGAGGTGTCTTGTGAATATGCACTTCAATGTTGTTC 291
139 ----GACTACTGCTCTGCGCGCGCTCTGTGCAAGATGACATTTCCGCTGCTGC 194
292 TCTTAATTTGTCAGATTTGAATCTTGAATGGAATCTCACTGCTAATTTGAGATCTCA 351
195 GCTCAACCTCTGCGCTCAACCTTGAAGGCGAGATCTTCCAGCGCTCGGAGCTTCA 254
352 GAGCTCTTGTCAATGATCTGAGAGGATTCGCTTGTGCAAAATCCCTGATGAGAT 411
255 GAGCTCTGCTCTCATGATCTGAAGTCAATTTGGGCTATCGGGCAAGATCCCTGATGAGAT 314
412 TGGTACTGTTCTTCTTGCAAAACCTTAAGCTTATCTTCAATGAATTAAGTGTGACAT 471

Db 315 TGGTGAATGTTCACTCACTTAGAGACGCTGACCTTTCTTCAACAACCTTGATGGCGACAT 374
Qy 472 ACCGTTTGCATTTCCAGTTGAAGCAACTTGACACCTGATTCGGAAGTAATACCAAT 531
Db 375 ACCATTTTCTAATCAAGCTGGAAGCACTTGGAACCTTGAATATGGAAGCAACACGCT 434
Qy 532 GATAGGACCGATCCCTTCAACACTTTCACAGATTCCAACCTGAAATTCGTGACTGGC 591
Db 435 GATTGGCGATCCCATCAATTTGTCAAGCTCCCAATTTGAAAGTTTGGATTTGGC 494
Qy 592 ACAGAATAAACTGAGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTTCTTCAGTA 651
Db 495 ACAAAACAACTGACTGGGAGATACCAAGCTTATCTACTGGAATGAGGTTCTTCAATA 554
Qy 652 TCTTGGGTGGGAGAAACAACCTTAGTCGGTAACTTCTCCAGATTTGTGTCACTGAC 711
Db 555 TC----- 556
Qy 712 TGGTCTTGTATTTTGAAGTAAGAAACAAGTTTGACTGTGATATACCTGAGACAT 771
Db 557 -----TTGATGTGAAGAACAAATAGCTTGAACGGGGTGAATACAGACACAT 602
Qy 772 AGGAAATTCACATGCTCCAGCTTTTGAATTTGCTCTCAACATCACTGAATCTGTGAGAT 831
Db 603 TGGGAATGTGAAGTTTCAAGTCTTGATTTGTCTTACAACCGCTTACCTGAGCAAT 662
Qy 832 CCGTTTGAATGAGGCTCTCTGCAAGTTGCAACATTTATCTGCAAGGCAATCACTCTC 891
Db 663 CCGATTCAACATTTGGTTCTTACAAAGTGTCAACATCTTCCAAAGGGAACAAGTTTCA 722
Qy 892 TGGGAAGATTCACATGATGTTGCTCATGCAAGCCCTTGACAGTCTTAGATCTAAGTGG 951
Db 723 CGGTCCAAATTCCTTCAATATTTGCTTATGCAAGGCTCTGCTGTTTGAATCTGAGTTA 782
Qy 952 CAACTTGTGAAGTGAATCTATTCCTCGATTCGGAATCTTACCTTCAACGAGAAAT 1011
Db 783 CAACCAATTAATCTGTCCTATACCATCAATAGGCACTTGACATACCTGAGAAAGCT 842
Qy 1012 GTATTTGCACAGTAACAAGTGAATGCTCAATTCCTGAGCTGAGAGTGAACATGTCAAA 1071
Db 843 GTACATTCACAGGAAATTAAGTTAACTGGGTGATACCAACAGATTTAGAAATATGTCAAC 902
Qy 1072 ACTCCATTAACCTGGAATCAATGATATCACTCAGGGTCAATATACCAACAGAGCTTGG 1131
Db 903 ACTTCATTAACCTGAATCAAGTAACTTAATCACTTACCTGAGTCAATTCACCAAGAGCTTGG 962
Qy 1132 GAAGCTTAACCTGATGTTTGTATCTGAATGTGGCAACATGATCTGGAAGACCTATAC 1191
Db 963 AAGGCTTAACAGGCTTGTGTTGACCTGAACCTTGGGAATTAACCACTGGAAGACCAATTC 1022
Qy 1192 TGATCAATGAGCTCTTGCACAAATCTTAAACAGCTTAATGTTCAATGGAACAAGTTTAA 1251
Db 1023 TGAACAACCTTAAGTTCAATGTGTGAATCTCAATAGCTTCAATGCTTAATGGAACAAGTTTAA 1082
Qy 1252 TGGCACTAATACCCGAGCAATTTCAAAAGCTGAAGAGTATGACTTAATCTGTCACG 1311
Db 1083 TGGGACCAATTCCTGCTGCTGCTGGGAAACTTGAAGATGACCTATTTAATCTGTCAATC 1142
Qy 1312 CAACAATATCAAGGCTCAATCCCGTTGAGCTATCTGATCGTAACCTTAATCAAT 1371
Db 1143 AAACCTTCAATAGGCTCTATCTCTATGAGTTATCAAGATTAACAATTTGGAACACGCT 1202
Qy 1372 GGAATCTTCCAAACAAGATAATGGAATCAATCTTCTTCTCCCTGGTGAATTTGAGCA 1431
Db 1203 GGAATTAATCTGTAAACATGATGACTGTCCAAATTCATCAATTTGGCGAGCTTAGGCA 1262
Qy 1432 TCTTCTCAAGATGAATGAGTGAATCATATTAACGTGTGATTTCCAGGCGACTTGG 1491
Db 1263 TCTATTTGAGCTTAATCTTGAAGCAAGATGCTCTAGTTGGAATCATCCCGGAGAGTTGG 1322
Qy 1492 AAATCTAAGAGCATATGGAATAATCTTCAAAATGAATATCTTGGGCCAAATTC 1551
Db 1551

Db 1323 TAAATTTAGAGAGTGCATGAGATGATTAATATCTTAATACCTTGTGGCTGATTC 1382
Qy 1552 AGAAGAGCTTAACCAATTAACAGAACAPAAATTTGCTGAGACTGGAAATAATAACTGAC 1611
Db 1383 TCAAGAACTTGAATGCTGCAAAACCTGATGTTC----- 1417
Qy 1612 TGGTAAATGTTGATTAATGCAACATGCTCACTGATCTCACTGATTAATGATATCTCAATA 1671
Db 1418 -----TAAATGTGTGATCAAA 1433
Qy 1672 CAACCTGTGATGATATCTCTTAAGAACATTAATCTTCAAGATTTTCCACAGACGTT 1731
Db 1434 TAAATTTGGCTGTGTGTCTCTGCTGCAACAACCTTACACGGGTTTTCACCTCAAGCTT 1493
Qy 1732 CATTTGCAATCCGATCTTGGGGTAGTTGGGCAAACTCAACGGTGCATGATTCGTGTCG 1791
Db 1494 TTTAGGTAATCCGTGACTGTGTGATTAATCTGGCTTGTGTGTGTGTGTGTGTGTGTGTGT 1553
Qy 1792 AACTGTACGAGTGTCAATCTGTAGACAGCTATTTCTGGAATAGCTAATGGGGGACTTGT 1851
Db 1554 CCACAGAAACCGGCTATCTCAAGGCTGCAATTAATTTGTTGTGTGTGTGTGTGTGTGTGTGT 1613
Qy 1852 GATCTTCTCAGTGTCTTAATAGCACTTGGCAGCCGATTAATCTCTCTCTTTTCTTGA 1911
Db 1614 TATCTCTTGAATGATCTTAGTAGCTTTTGCAGGCCACATCTGTCACTGCTTTTAAAGA 1673
Qy 1912 TGGATCACTTGAACAAACCGATTAATTTGCAACCGAAGCTGTATCTCTGATATGA 1971
Db 1674 TGTCACTGAAGAACCGAGTGAAGAAATGTCCCCCAAGCTGTATCTCTTAATGA 1733
Qy 1972 CATGCACTTCACGTTTACAGAGATATCATGAGATGACAGAGATCAATGAGAGTA 2031
Db 1734 CATGCCCTTCATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1793
Qy 2032 TATCAATTTGGGACGAGCATCAAGCACTGTATTAATGATGATGATGATGATGATGATGAT 2091
Db 1794 CATCAATTTGATAGGGGCGCTCAAGTACAGTTTAATATGTGTCTTAAGATGCAAAAC 1853
Qy 2092 GGTGGGATTAAGCGGCTTATCTGCAAAACCAAGTCAATGAAGAAAGTTTGAACAGA 2151
Db 1854 GGTGCAATTAATAAAGCTGTATGCCCATCAACCAAGCTTAAAGAAATTTGAACATGA 1913
Qy 2152 ACTCGAATGCTTAAGATGATCAAGCAAGAAATCTTGTAGCCTTCAAGCTTAATTCCT 2211
Db 1914 GCTTGAAGACTGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1973
Qy 2212 CTCTCACTTGGGAGTCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2271
Db 1974 ATCACTGTTGGGAACCTCTCTTATGATTAATGAAATGAGGAGCTTATGGGATGT 2033
Qy 2272 TCTTCAT---GGCCCTACGAAGAAAGAAAGCTTTGATTTGGGACACAGGCTTAAAGTAGC 2328
Db 2034 TTTAATGAAAGGTTCAATCAAGAAAGAAAGAAAGCTTGAAGGAGCTGCTTACGATATGC 2093
Qy 2329 AATAGTGCAGCAAGAGTTAGCTTATCTACACATGACTGATGATGATGATGATGATGATGAT 2388
Db 2094 TCTTGTGAGCTCAAGGCTTGTCTTACCTTACCACTGATGATGATGATGATGATGATGAT 2153
Qy 2389 CAGAGAGTGAAGTCTGTCAACATCTCTTGAACAAAGCTTAAGAGCTGTGTTGAACAG 2448
Db 2154 TGGGATGTAAATTAAGAAATTAATCTCTTGAACAAAGATTAAGAGGCTTATGACAG 2213
Qy 2449 TTTTGAATAGGAAAGGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2508
Db 2214 CTTTGAATTTGCTAAGAGCTTATGTGTCTCAAAAGCTCAACATCAACCTATGATGATGAT 2273
Qy 2509 CAGGATAGGTTACATAGACCCGAGATGCTGCACTTCAAGGCTCACTGAGAAATCCGA 2568
Db 2274 AACTATTTGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2333
Qy 2569 TGTCTACA-GTATGGAATAGTCTTCTTGAATGTTTAAACCGAGAAAGAGCGTTGATG 2627
Db 2334 TGTCTACAGGCTATGCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2393

QY 2628 ACGATCCAAATCTCCACCATCTGTAATATGTCAAAGCGGGAGCAATGAATGTATGAAA 2687
| | | | |
Db 2394 ACGAATC-----TATGAAAGACGGCAAGACAAGAGTCAATGATA 2434
| | | | |
QY 2688 TGGCAGATCCAGACATCATCGACGTGTAAGATCTCGGTGTGTGAAGAAATTTTCC 2747
| | | | |
Db 2435 CCGTGGACCCCTGACGTGGGGACACTGCAAGGACCTCGCGAGGTGAAGAACTGTTC 2494
| | | | |
QY 2748 AACTGGACTCTTATGACCAAAAGACAGCGGATGATCGACCAATGACAGAGTGA 2807
| | | | |
Db 2495 AGCTGGGCTCTCTTGTGACCAAGCGGCAACCTTGAGACGACGACGATGCAAGGTGG 2554
| | | | |
QY 2808 CTCGTCTTCGCGAGTTTATGCTATCGAAACAACACTGTGCGACTG----- 2858
| | | | |
Db 2555 TGGCGCTCTGGAATGCTGTGTGAACCGGACCGCGCCAAACCGTGGCGACCAAGC 2614
| | | | |
QY 2859 ACACGTACGAGCGCTGCTGCTGTCTGCTACGTGATGATGCAAAATCTCAAGACTC 2918
| | | | |
Db 2615 TGCGCGACCGCTCGCCACCGCTGCCAAAGTACATCAAGATGCTGACCTGCGGGCA 2674
| | | | |
QY 2919 CTATTCCTGCAATGTGCT---TTCATGAGTGTCTGATGCTCACTGTTCTTGCGT 2975
| | | | |
Db 2675 CCGCGCTCTCTCTCTGCGCAACTGACACGACCTCGAGCGCGAGCTGTCTCAAGT 2734
| | | | |
QY 2976 TTGGACAAGTTATTTCTCAGAACAGTAGTAG 3007
| | | | |
Db 2735 TCGCGAGGCGCATCTCGAAGAACATGAGTAG 2766
| | | | |

RESULT 9
US-10-519-135-3
; Sequence 3, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIEN
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU P53339
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: rice ERECTA
; US-10-519-135-3

Query Match 32.6%; Score 1035.2; DB 6; Length 3000;
Best Local Similarity 63.8%; Pred. No. 9.1e-300;
Matches 1687; Conservative 0; Mismatches 888; Indels 69; Gaps 5;

QY 234 CGGATTATTGTGTGTGAGAGGTGTGTCTTGTAATAATGTACCTTCATATGTTGCTC 293
| | | | |
Db 179 CCGACCACTGCGGGTGGCGGGGTCACTGCGCAACAGGCTCTCGCGCTCGCCC 238
| | | | |
QY 294 TTAAATTTGTAGATTTGAATCTTGATGAGAAATCTCACTGCTATTTGAGATTTCAAGA 353
| | | | |
Db 239 TGAACCTGTCAAACTTAACCTAGAGGTAGATCTGCGCGCATGAGAGCTCAAGA 298
| | | | |
QY 354 GTCCTTGTCAATGTATCTGAGAGTATGCTTGTGTGCAAAATCCCTGATGATG 413
| | | | |
Db 299 ATCTACAGTTCCTTGATCTCAAGGGAAACAAGCTCACTGGCCAAATCCAGATGAGATTG 358
| | | | |
QY 414 GTGACTGTTCTTTTGGCAAACTTAGACTTATCTTCAATGAATTAAGTGTGACATAC 473
| | | | |
Db 359 GGGAGCTGACATCTCTTAAATATTGATTTGTCTGCAACTTGCTGTATGAGACATCC 418
| | | | |
QY 474 CGTTTGCATTTTGAAGTTGAAGAACTTGAAGCGCTGATTTGAAGAAATACCAATTGA 533
| | | | |

Db 419 CTTTCTCATCTCCCAAGCTCAAGCAGCTTGAGAGTGAATTTTGAAGAACACACAGCTCA 478
| | | | |
QY 534 TAGGACCGATCCCTTCAACACTTTACAGATTCACAACTCGAAATCTTGAGCTGGCAC 593
| | | | |
Db 479 CGGACCATCTCCCTTCCAACTTGCTCCAAATCTCCAAATCTCAAGACATTGACCTGGCAC 538
| | | | |
QY 594 AGAATAACTCAGTGTGAGATACCAAGACTTATTTACTGAAATGAATTTCTTCAATATC 653
| | | | |
Db 539 AGAACGACTTACAGCGGATATCCAAAGGCTCATATCTGGAATGAAGTTCTGCAATACC 598
| | | | |
QY 654 TTGGGTTCGAGGAACAACTTACTCGTAAATTTTCCAGATTTGTGCACTGACTG 713
| | | | |
Db 599 TAGGTTTGAAGGGTAACTCACTGAGAACTTGTACCTGACATGTGCAACTGACTG 658
| | | | |
QY 714 GTCTTTGTATTTTGAAGTAAGAAACAAGTTTGACTGAGTATATCTGAGACGATAG 773
| | | | |
Db 659 GCTGTGTACTTTGATGTAAGGGAACAATCTCAAGGAGACCATTCAGAGAGCATAG 718
| | | | |
QY 774 GAAATTCAGCTGCTCCAGATTTTGGACTTGTCTTCAATCAAGCTAACTGTGAGATCC 833
| | | | |
Db 719 GGAATGCAACAGCTTTGAGATTTCTGACATTTGTATTAACAATCTGTGAGAAATAC 778
| | | | |
QY 834 CTTTTCACATCGGCTTCTGCAAGTTGCAACATTTATTTGCAAGGCAATCACTCTG 893
| | | | |
Db 779 CTTACACATAGGCTTTCTTCAAGTACCACTGCTCACTTCAAGGAATAGACTGACTG 838
| | | | |
QY 894 GGAAGATTCATCAGTATGATGTCTCAATGCAAGCGCTTGCAAGCTTATGATCTAAGTGGCA 953
| | | | |
Db 839 GGAATTTCCAGATGTATTTGCTGCTGATGCAAGCTCTTGTCTTGTAGACTGAGTAGA 898
| | | | |
QY 954 ACTTGTGAGTGAATCTATTTCTCCGATTTCTGGAATCTTACTTTCACCGAGAAATGT 1013
| | | | |
Db 899 ACGAGCTGTAGAGGCCATTTCTTATATCTGAGCAATCTATCTTATCTGAAATCTAT 958
| | | | |
QY 1014 ATTTCACATTAACAAGCTACCTGCTTCACTGAGCTTGGAAATATGTCAAAAC 1073
| | | | |
Db 959 ATTTCATGGAACCAACTTACCTGAGTCTATACCGCGAGCTTGGAAATAGTAATAC 1018
| | | | |
QY 1074 TCACTTACCTGGAACCTCAATGATATCATCTCAAGGGTCAATATACCAACGAGCTTGGGA 1133
| | | | |
Db 1019 TTAGCTACTCAACTCAATGATATGATATGATTTGGTGGCACAATTTCCAGAGAGCTTGGCA 1078
| | | | |
QY 1134 AGCTTACTGACTTGTGTGATCTGAATGTGCGCAACAATGATCTGGAAGGACTATACCTG 1193
| | | | |
Db 1079 AACTGAAAGACTTTTGAACATACTTGTCCAAACAATCTTCAAGGCTCTATTCCTG 1138
| | | | |
QY 1194 ATCATCTGAGCTTTGCAACAATCTAAACGCTTAAATGTTTCAATGGAACAAGTTTATG 1253
| | | | |
Db 1139 CAACATCAAGTTCTTGACCTGCTTAAACAATTCATATGTTATGCAATTAAGCTTAATG 1198
| | | | |
QY 1254 GCACTATACCCGAGCATTTCAAAAGCTAGAAAGTATGATCTTATCTGATCCAGCA 1313
| | | | |
Db 1199 GTTCTATTTCTGCTGCTTTCAGAAAGTTGAGAGTCTGACTTATCTTGAACTTATTTCA 1258
| | | | |
QY 1314 ACAATATCAAAAGTCCAAATCCGTTGAGCTATCTGTATCGTAACTTATGATATATGG 1373
| | | | |
Db 1259 ACAATTTCAAAAGCAATATCTTCTGAGGTTGTGCATCATCAACTTGAACACATTTG 1318
| | | | |
QY 1374 ATCTTTCAACAACAAGATTAATGGAATCTTCTTCTTCCCTTGGTGTGATTTGAGCATC 1433
| | | | |
Db 1319 ATCTTTCTTAACAATGAAATCTCTGACCAAGTTCTGTCAATTTGGATCTTAGACACC 1378
| | | | |
QY 1434 TTCTCAAGATGACTGAGTGAATAATCATATTAATCTGATGATTTCCAGGGCACTTTGAA 1493
| | | | |
Db 1379 TTCTTGAACGAAATTTGAGTGAACAACATTTTATGAGGCGCAAGTTCTCTGAGATTTGGA 1438
| | | | |
QY 1494 ATCTAAGACATCATGAAATAGATCTTTCAATAATATATCTTGCCCAATTCAG 1553
| | | | |
Db 1439 ACTTGAAGAGCGTCCAAAGTATGATATGCAACAACAACTTATCTGGTGAAGTCCGCCG 1498
| | | | |
QY 1554 AAGAGCTTAACCAATTAACGAACATATTTTGTGAGAGCTGGAATAATTAATACCTGACTG 1613
| | | | |
Db 1499 AGGAACCTGGAACAATTCAAACCTTGTATGACTGATTTCTTAACAACAATTTGGTTG 1558
| | | | |

QY 1614 GTAATGT---TGGTTCAATTAAGCCAACTGTCTCACTCTCA-----CTGATTTGAAT 1660
Db 1559 GGGAGATCCCTGCTCAATTTGGCCAACTGCTTCACTTAAATACCTTGCAATTCAGGAAT 1618
QY 1661 GTAATCTTAACAACCTCTGAGTGTATCTTGAAGAACTAATCTTCAAGATTTTCA 1720
Db 1619 TTGTCAACAACAATTTATCTGGACATGTCCGATGGCAAGAACTTCTGGAATTTCCA 1678
QY 1721 CCAAGA-----CAGCTTCA 1733
Db 1679 ATGGAAGACATCTTCTAATTTCTGATTCGAACAGTACATTAATCATTAATGACAGCTTCT 1738
QY 1734 TTGGCAATCCGTGCTTGGGGTAGTGGTAACTACCGTGCATGATTCGTGGA 1793
Db 1739 TGGGTATTCATTAATCTGCAATGTTTACTGCAAGATTCAGCTGTGGACACTCTCATGGA- 1797
QY 1794 CTGTACAGAGTGTCAATCTCTAGAGCAGCTATTTCTTGAATAGCTATTTGGGGGAACTTGTGA 1853
Db 1798 --CAAGAGTTAATATTTCAAAAGCAAGCAATGCTTGCATTAATCTTGAAGCTTATCATAT 1855
QY 1854 TCTCTTCAATGCTTATATAGCACTGTCGACCGCATATCTCTCTTCTTCTTGATG 1913
Db 1856 TGTCTGCTGCTTCTGCTGTGGCTATATATAAACAATCAACCAAGCTGCTCAAG 1915
QY 1914 GATCACTTGAACAACAGTAACTTATTCGACCGAAGCTGCTCATCTTCAATAGACA 1973
Db 1916 GATCCCATTAAGCCAGTCCAAAGAC-----CTCAAAAGCTAGTGTCTCTCAAGTGGACA 1969
QY 1974 TGGCACTTCAAGCTTCAAGAGATATCATGAGAAATGACAGAAATCTAAGTGAAGATATA 2033
Db 1970 TGGGTATTCATTAATCTGAGAGCACTATGAGGCTGACAGAAATTTAGGAGAAATACA 2029
QY 2034 TCAATTTGGGCAAGGACATCAAGCACTGTATCAAAATGTTTGAAGAAATTTGAACCGG 2093
Db 2030 TCAATTTGGGCTTGGGGCTTCAAGCACTGTCTCAAAATGTAATCAACAGGCGGCAAGGCCA 2089
QY 2094 TTGGGATTAAGCGGCTTACTCTTCAACAACCAAGTCAATGAAACATTTGAAACAGAAC 2153
Db 2090 TTGCTGTCAAGCGGCTTAAAGTATGATTAACATGAGAAATGTTCTTGGGATCTTC 2149
QY 2154 TCGAGATGCTAAGTACATCAAGCAAGAAATCTTGTGAGCTTCAAGCTTATTCCTCT 2213
Db 2150 TAGAGCAATTTGGGAGAGATACGAGCAAGAAATCTTGTTAACCTCCAGGCTTCTCGTAT 2209
QY 2214 CTCACTTTGGGAGCTTCTGTTCTATGATTAATTTGAAAATGTTAGCTTGGGATCTTC 2273
Db 2210 CTCAACATGGAATCTGCTCTTCTATGATTAATGAAAATGTTCTTGGGATCTTC 2269
QY 2274 TTGATGGCCCTTAAGAAAGAAAGAACTTGAATTTGGGACAGCGCTTAAGATGATATG 2333
Db 2270 TCCAGGCTCATCAAGAAAGTGAAGCTCAACTGGGACAGAACTAGAGATGCGGCTG 2329
QY 2334 GTGCAGACAAAGTTAGTTAGTTATCTACACCATGACTGTAGTCCAGAGATTTACACAGAG 2393
Db 2330 GAGCTGCAAGAGGCTGGCTATCTCCACATGACTGCAACCTCGATATACACAGAG 2389
QY 2394 AGCTGAAGTGTCCACATTTCTTGGACAAAGACTTGAAGGCTCGTTTGAAGATTTTG 2453
Db 2390 ATGTCAAGTCTTCCACATCTGCTCAACGAAAGCTTGAAGGCGCACTTCAGATTTTCG 2449
QY 2454 GAATTAAGGAAAGCTTGTGTGTCAAGTCACTAATTCACTTGAATGAGGCGCA 2513
Db 2450 GCAATTAAGCAATGTGCTCCCTCTGCAAGTCCAGTCTCACTTATGTGCTGGAAGCA 2509
QY 2514 TAGATTACATAGACCCGAGATAGCTGCACTTCAAGGCTCACTGAGAAATCCGATGCT 2573
Db 2510 TCGGCTATCAATTAATCGGAGATAGCAGAACTTCAAGGCTCAATGAGAAATTCGATGTGT 2569
QY 2574 ACAGTTATGGAATAGTCTTCTTGAAGTTTAAACCCGAGAAAGCGTTGATGAGCAAT 2633
Db 2570 ACAGCTTTCGAGCATGCTCTTCTGGAATTTGCTCAACGAGAAAGGCGTGCAGAACGAAAT 2629

QY 2634 CCAATCTCCACATCTGATATATGTCAAGCGGGGAAATGATGATGAAATGGCAG 2693
Db 2630 CGAATCTGATCAATGATATGATCTCCAAAGCTGATGACAAACAGTCAAGAGCGAGTGG 2689
QY 2694 ATCCAGACATCAATCAAGCTGTAAAGATCTCGTGTGTGAAGAAAGTTTCCAACTGG 2753
Db 2690 ACTCGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2749
QY 2754 CACTCTTATGACCAAGCAAGAGCGCAATGATGATGATGATGATGATGATGATGATGAT 2813
Db 2750 CCGCTTCTGTGACCAAGAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 2809
QY 2814 TTCT 2817
Db 2810 TGCT 2813

RESULT 10
US-11-218-305-13435
; Sequence 13435, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McIaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53660) B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13435
; LENGTH: 2614
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-13435

Query Match 32.2%; Score 1022.2; DB 9; Length 2614;
Best Local Similarity 68.6%; Pred. No. 6.7e-296;
Matches 1424; Conservative 0; Mismatches 648; Indels 3; Gaps 1;

QY 776 AATTGACATGCTTCCAGGTTTGGACTGTCTTCAATCACTGATGATGATCCT 835
Db 32 AACTGTAACAAGTTTCAAGGCTTGGATTGTCTTCAACCGCTTACTGACCAATCCCA 91
QY 836 TTGACATGGGCTTCTCGAAGTTGCAACATTAATCTTGAAGGCAATCAACTCTGGG 895
Db 92 TTCAACATTTGTTTCTTACAGGCTTACACTATCTTGAAGGCAATCAACTCTGGG 151
QY 896 AAGATTTCATCAAGTATGTTGCTCATGCAAGCCCTTGAAGTCTTGAATGATGCAAC 955
Db 152 CCAATTCCTTCAAGTATTTGGCTTATGAGGCTCTGCTGCTTATGATGATGATGATGAT 211
QY 956 TTGTTAGTGAATCTATTTCTCCGATTTCTGGAATCTTCACTTCAACGAAATTTGT 1015
Db 212 CAATTAATCTGCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 271
QY 1016 TTGACAGTAACAAGCTGCTGCTTCAATTTCAACCTGAGCTTGAAGAAATGCAAACTC 1075
Db 272 ATCCAAAGGCAATGATTTAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 331
QY 1076 CATTACCTGGAATCAATGATATATCACTACAGGCTCATATACCAAGAGCTTGGGAAG 1135
Db 332 CATTACCTGGAATCAATGATATATCACTACAGGCTCATATACCAAGAGCTTGGGAAG 391
QY 1136 CTTACTGACTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1195
Db 392 CTAAACAGGCTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 451

QY 1196 CATCTGAGCTCTTGCACAAATCTTAAGACCTTAATGTTTCATGGGAAACAATTAGTGGC 1255
Db 452 AACCTAAGTTTCATGTGGAATCTCAATAGCTTCAATGCTTAATGGCAACAATTAAATGGA 511
QY 1256 ACTATACCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGTCCAGCAAC 1315
Db 512 ACCATTCCTCGTGGCTGGCCGGAACCTTGAAAGCATGACCTTAATTTAACTCTCCCTCAAT 571
QY 1316 AATATCAAGGTCCAAATCCGCTGAGCTATCTGTATCGGTAACTTAAGATACATTTGGAT 1375
Db 572 TTCTAATAGGTGCTATTTCTTATGAGCTATCGAGATCAACAATTTGGACACGTTGGAC 631
QY 1376 CTTCACAAACAAGATTAATGGAATCAATTCCTTCCTGCTGATTTGGACATCTT 1435
Db 632 TTATCTGTAACATGATGACGGGTCCAATTCATCATCTTGGCAACCTTGAACATCTA 691
QY 1436 CTCAAGATGAATCTGATGAAATCATTAATCTGTGATGTTCCAGGCGACTTTGGAAAT 1495
Db 692 TTGAGGCTTAACTTGACCAAGAAATGATCTAGTTGGATTCACTCCGCGAGATTGGTAAAT 751
QY 1496 CTAAAGACATCATGAAATAGATCTTTCAATATATGATCTCTGCGCCAAATCCAGAA 1555
Db 752 TTGGAAGATGTCATGAGATGATTTATCTTAATATCATTTGGTGGTCTGATTTCTCA 811
QY 1556 GAGCTTAAACCAATTACAGAAATTAATTTGCTGAGACTGGAATAATTAACCTGACTGT 1615
Db 812 GAACCTTGAATGCTGCAAAACCTGATGTTGCTAAACCTGGAAAAACAATATTAATCTGGC 871
QY 1616 AATTTGGTTTATTAAGCAACTGTCTGCTGCTGATTTGAATGATTCATCAATCAAC 1675
Db 872 GATGTCTCTTCTGATGAATCTGCTCAATCTCAATCTTAATTTGCTCAATCAATTAAT 931
QY 1676 CTGCTAGGTGATATCCCTAAGAACATTAATCTTCAAGATTTTCCAGCAGACTGAT 1735
Db 932 TTGGCTGTGTGCTGCTCACTGACAACTTCCAGGTTTTCATGACGACTTTTGA 991
QY 1736 GGCATATCTGTGCTTGGAGTGTGCTAAACTCACCGTGTCAATCTCTGCTGAAT 1795
Db 992 GGTATCTCTGGAATCTGTGATATTTGGCTTGTGTTCTTCAATGCTTCACTGCGCACCGA 1051
QY 1796 GTACGATGTCAATCTCTAAGCAGCTAATCTTGGAAATAGTATTTGGGGGACTTGTATC 1855
Db 1052 GACAAACCGCCAAATCTCAAAAGCTGCCAATTAATGTGTGTGGGTGGACTTGTATC 1111
QY 1856 CTTCATGCTGCTTAATAGCAGCTTGGCGACCGCATATCTCTCTTTCTTGTAGGA 1915
Db 1112 CTCTGTATGATCTTATAGTATGCTATGACGGCCACATCCACTGCTTTAAAGATGCC 1171
QY 1916 TCACTTGAACAACGATTAATTCGACACCGAAGCTGTCAATCTTCAATGAAATG 1975
Db 1172 ACTGTAGCAAGCCAGTGAAGCAATGTGTCCACCAAGCTGTGATCTTCAATGAAATG 1231
QY 1976 GCACTCAACGTTTACGAGATATATGAGATGACAGAAATCTAATGGAATATATC 2035
Db 1232 GCTCTTATATGCTTTGATATATATAGATGAGATGAGAACTTGAGTGAATATATC 1291
QY 2036 ATTGGGACGAGAGATCAAGCATGTAATCAATAGTGTTTTGAAGATTTGAACCGGT 2095
Db 1292 ATTGGATACGGGGGATCAAGTACGTTTAAATGTGTTCTTAAGAAATTCGAACCACTG 1351
QY 2096 GCGATTAAGCGGCTTTACTCTACACCAACCAAGTCAATGAACAGTTTGAACGAATC 2155
Db 1352 GCATATAAAAAAGCTATGCTTACCTCCTAGAGCTTAAAGAAATTTGAACCTGACTC 1411
QY 2156 GAGATGCTATGATCAATCAAGACAGAAATTTGTGAGCTTCAAGCTTATCTCTCTCT 2215
Db 1412 GAAGCTGTGTGATCAATCAACACCGAATCTTACGCTTCAAGGATCTCTCTTCA 1471
QY 2216 CACTTGGAGGATCTTCTGTCTATGACTTATTTGGAAATGGTAGCCTCTGGGATCTTCTT 2275
Db 1472 CCGTGTGGAAACCTCTCTTTTATGATATATGAGAGTGGCAGCTTATGGGATGTTTGA 1531
QY 2276 CAT--GGCCCTAAGAAAAAAGACTCTTGTATTTGGACACACGCGCTTAAGATGATAT 2332

Db 1532 CATGAAGCTCATCAAGAAAGAAACAACTTGACTGGGTGACTGGCTACGGATGCTCTT 1591
QY 2333 GGTGCACACAAAGTTTATGCTTATCTACACATGACTGTAGTCCAAAGATCATCTCAGA 2392
Db 1592 GGTGCACCTCAAGGCTCGCTTACCTTACATGACTGACGCCCAATTAATTTACCGG 1651
QY 2393 GAGGTGAAGTCTGTCACAACTTCTTGGACAAAGACTTGAAGCTCGTTTGACAGATTTT 2452
Db 1652 GAGGTAAATCAAGAAATATACCTCTGACAAAGATTAATAGGCCATCTTACAGCTTC 1711
QY 2453 GGAATAGCAAAAAGCTTGTGTGTCTCAAGTCAATATCTTCACTTACGATGGCAGC 2512
Db 1712 GGCATCGCTTAAGGCTTATGTCTCGAAGACTCACACGCTCAACTTACGTCATGGGACT 1771
QY 2513 ATAGGTACATPAGACCCCGAGTATGCTCGGACTTCAACGCTCATGGAATCCGATGTC 2572
Db 1772 ATGGTTACATGATCCCGAGTACGCCGCACTCCGCTCAACGAAAGCTTGATGTC 1831
QY 2573 TACAGTATGAATATGCTTCTTGAAGTTGTAACCCGAAGAAAGCCGTTGATGACGA 2632
Db 1832 TACAGCTACGGATCGTTCTGCTGAGCTGCTGACCGGCAAGACGATGACAAACGAG 1891
QY 2633 TCCATCTCCACATCTGATTAATGTCAAAGACGGGGAACAATGAATGATGAAATGCA 2692
Db 1892 TGCAATCTCCATCATGATCTATCGAAGACGGCGAGCAACAGATCATGAGACGCTG 1951
QY 2693 GATCCGACATCAATGACATGAGTGAATGATCTGGTGTGTTGAAGAAAGTTTCCAATG 2752
Db 1952 GACCCGACGCTGGAGACACTTCAAGACCTGAGGAGTGAAGAGCTGTTCCAGCTG 2011
QY 2753 GCACTCTATGACCAAAAGACACCGCAATGATGACCCCAATGACACGAGTACTGCT 2812
Db 2012 GCGCTCTCTGACCAAGCGGACGCTCGGACCGGCGACGATGACAGGATGGTGGC 2071
QY 2813 GTTCTCGGAGTTTATGCTATGGAACAACACC 2847
Db 2072 GTCTTGACTGCTGCTGTGAACCCGAGCCGCC 2106

RESULT 11
US-10-953-349-22716
; Sequence 22716, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22716
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22716

Query Match 29.4%; Score 935.2; DB 6; Length 1712;
Best Local Similarity 73.5%; Pred. No. 7.1e-270;
Matches 1214; Conservative 0; Mismatches 423; Indels 15; Gaps 1;

QY 1369 ATTGATCTTCCAAACAAGATTAATGGAATCATTCCTTCCCTTGGTATTTGA 1428
Db 1 ATTGATATTTCAACAATTAATTAATGTTGCTTCAATCCCTTCTTCTGTGATTTGA 60
QY 1429 GCATCTTCTCAAGATGAATCTGATGAATCATATTAATCTGATGTTCCAGCGACTT 1488
Db 61 ACATCTTCTGAAGTTGAACCTGAGCAAGAAACAATTTTAACGAGATTAATTCACAGAAAT 120
QY 1489 TGGAAATCTAAGAAAGCATCATGGAATATGATCTTTCAATATGATATCTTGGCCAAAT 1548

Db	244	CCATTCCCTCGTGGCTGGGAAACTGAAACATGACCTATTAAATCTTTCATCAAAATT	303
Qy	1317	ATATCAAAAGTCCAAATCCCGGTAGACTATCTGATCGTAACCTAGATCATTTGATC	1376
Db	304	TCATTAAGGCGCTCATTCCTATTAGAGCTATCAAGATCAACAAATTGGACACGTTGACT	363
Qy	1377	TTTCCACAACAATATAATGGAATCAATCTCTCTCCCTGGGATTTGGAGACTCTTC	1436
Db	364	TATCCCTGTACATATGACGGGTCCAAATTCATATCCATATGGCAACCTGAGGATCTAT	423
Qy	1437	TCAAGATGAACTTGAATGAAATCAATAATACGTGTAGTTCCAGGGGACCTTGGAAATC	1496
Db	424	TGAGGCTTAATTGAGCAAGATATCTAGTTGGAATTCATCCCTCGGAGTTGGTATT	483
Qy	1497	TAAAGACATCATGGAATATAGATCTTTTCAATTAATATATCTCGGCCCAATTCAGAG	1556
Db	484	TGAGAGGTGTCATGAGATGATTTATCTTATATCATCTTGGTGTCTGATTTCTCAAG	543
Qy	1557	AGCTTAACCAATTACAGAACATAATTTTGTGGAAGCTGGAAATATAATTAACCTGACTA	1616
Db	544	AACTTGGAATGCTGCAAAACCTGATGTGTCTAAACCTGGAACCAACAAATTAACCTGGC	603
Qy	1617	ATGTGGTCTATTAGCCCAACTGTCTCACTCACTCATGTATTAATGATATCTCATTAACAC	1676
Db	604	ATGTCTCTTCTCTGATGAATGCTTTCAGCCTCATATCTTAAATGTGTCATACATTAAT	663
Qy	1677	TCGTAGTGATATCCCTTAAGAACATACTTCTCAAGATTTTCCACAGACGCTTCATTG	1736
Db	664	TGGCTGGTGTCTGCTCCACTACGACCAACATTCACACGGTTTTCATATGACAGCTTTTAG	723
Qy	1737	GCAATCTCTGTGCTTTGGCGGTAGTTGGCTAAACTCACCGTGTCAATCTCTGTGGAATCG	1796
Db	724	GTAATCTCTGAGCTGTGTGATATATGGCTTGTGTTCTTCAATGTCTGTCCATGTGCCACCGAG	783
Qy	1797	TACAGGTTCATCTCTAGACAGACTATTTCTTGGATATGCTATTTGGGGACCTTGTGATCC	1856
Db	784	ACAAACGCCCAATCTCAAAAGGCTGCCAATATTTGGTGTCTGTGGGTGGACTTTTATCC	843
Qy	1857	TTCTCATGTCTTAATATAGACGCTTCCGACCGCATTAATCCTCTCTTTCTTGATGAT	1916
Db	844	TCCTGATGATCTTATGTAGCTGTATAGACGGCCACACCAATCCACCTGTTTTAAAGATGCA	903
Qy	1917	CACTTGACAAACCAAGTAATTAATTCGACACCGAAGCTGTATCTTTCATATGAACATGG	1976
Db	904	CTGTAAAGCAACCAAGTGAAGCATGTGTCCACCCCAAGCTGTGATCTTTCATATGAACATGG	963
Qy	1977	CACGCCACGTTTAAAGAGATATCATATGAGAAATGACAGAGAACTCTAAGTGAAGATATATCA	2036
Db	964	CTTTCATGCTCTTGTATGATATATAATAGAGATGATCGAAACTTATGATGAGAAATATATCA	1023
Qy	2037	TTGGGCAACGAGATCAAGCACTGATATCAATGTGTTTGGAAATTTGTAAACCGGTG	2096
Db	1024	TTGGATTAAGGGGACATCAAGTACTGTTTATATATGTGTTCTTAAGAAATTTGCAACAGTGG	1083
Qy	2097	CGAATTAAGCGGCTTACTCTCACAACCCACAGTCAATGAACAGTTTGAACAGAACTCG	2156
Db	1084	CAATTAATAAACAATGTATGCCCCACTACCTGCAGAGGCTTTAAGAAATTTGAAACTGAGCTCG	1143
Qy	2157	AGATGCTAATGAGATCAAGACAGAAATCTTGTGAGCTTACAAAGCTTAATCTCCTCTCTC	2216
Db	1144	AGACTGTTTGGTACATCAACACCGGAATCTAGTCAAGCTTCAGAAAGGATCTCTGTTGTAC	1203
Qy	2217	ACTTGGGAGATCTTCTGTTCTATGACTATTTGGAAATGATAGCCTCGGATCTTCTCTC	2276
Db	1204	CTGTTGGGAACCTCCTCTTTTATGTATTATAGAGAGTGGCAGGCTTAATGGGATGTTTATC	1263
Qy	2277	AT---GGCCCTACGAGAAAGAAAGACTCTTGAATTGGGACACACGGCTTAAGTATGATATG	2333
Db	1264	ATGAAGGCTCATCCAGAGAAAGAAACAACTTGACTGGGTGACTTCGGCTTACGGAATCCCTCTTG	1323
Qy	2334	GTGACAGCAAGAGTTTACTTATCTACACATATGACTGTATGTCMAAGATCATTTCAACAG	2393
Db	1324	GTGACGCTCAAGGCTCGCTTACCTTCAACATGATGTGACGCCACAGATATATTAACCGGG	1383

OY	2394	ACGGGAAGTCTCCAAATCTCTTGGACAAAGCTTAAGGCGCTGTTGACAAATTTG	2453
Db	1384	ACGTAATAATCAAGAAATTAATCTCTCGCAAAAGTTATAGGCGCATCTTACAGCTTCG	1443
OY	2454	GAATAGCGAAAGCTTGTTGTGTGTCAAAAGTCACATTAATTCACCTTAGCGTAGGGCAGA	2513
Db	1444	GCATCGCTAAGAGTTATATGTCTCTGAAAGATCAAGTCACCTAAGTCATGAGGCACTA	1503
OY	2514	TAGGTTACATAGACCCCGAGTATGCTGGCACTTCAAGGCTCACTGAGAAAATCCGATGTCT	2573
Db	1504	TTGGTTACATTGAATCCGAGTAAACCCCGCACTCCCGCTCAACGAAGAATCTATGTCT	1563
OY	2574	ACAGTTATGGAATATGCTCCCTCTTAGTGTGTTAACCCGAAAGAAAGCGTTATGACGAAT	2633
Db	1564	ACAGCTAGCGCATGTCTTCTGCTGGAGCTGCTGACACCGCGAAGAAACCAATGACAAAGT	1623
OY	2634	CCAAATCTTCACCAATCTGATTAATGTCAAAAGACGGGAAACAATGAATGATGGAATTCGCAG	2693
Db	1624	GCAATCTTCATCACTTGATCTTATCGAAAGACGGGACGACGAAGATCATGAGACGGTGG	1683
OY	2694	ATCCAGACATCAATCCGACGTTGAAGAATCTCGGATGTTGTAAGAAAGTTTCCAACTGG	2753
Db	1684	ACCCCGAGTGGGAGACACTTGCAAAGGACTGGGCGAGGTAAAGTCTGTTCCAGCTGG	1743
OY	2754	CACCTCTATGACCAAAAGACAGCCGATGATTCGACCCACATGSCAACCCAGGTGACTCGTG	2813
Db	1744	CGCTCTCTGCAACCAAGGCGCAGCCCTTCGGACCGGACGACATGACGAGGTGTGTCGCG	1803
OY	2814	TTCTTCGCGAGTTTATGCTATCGGAACCAACCAACC	2847
Db	1804	TCCCTGACTGCTGATGAACCCCGAGCGCGCC	1837

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RESULT 13
US-11-218-305-14406
; Sequence 14406, Application US/11218305
; Publication No. US2006014495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaIRD, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14406
; LENGTH: 1714
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-14406

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	Query Match	Similarity	Score	714.2	DB	9	Length	1714
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							Gaps	4
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DB	13	CTTGGCTCAAAACAAGTTAAGTGTGGAATTCGACATCTAATATATTGGATGAGGTCTT	72					
QY	646	TCAGTATTTTGGGTTTGGAGGAAACAATTAGTGGTAACTTTCTCCAGTTTGTGTCA	705					
DB	73	TCATTACTCTGGGATGCGCAG-ATAAGTTTGAAGGAAGCCTCTCTCCGATATGTGCA	131					
QY	706	ACTGACTGGTCTTTGGTATTTTGAAGTAAGAAACAAGTTTGACTGGTACTATATACCTGA	765					
DB	132	GTTAACTGGCTCTGGTACTTTTGAATGTGAAGAACATATGCTTTGACGGGTGCATATCCAGA	191					

QY 766 GACGATGAAATGCACTGCTTCCAGGTTTGGACTGCTACATCAGTAACGTG 825
 DB 192 AACCATGGGAACCTGACAGCTTTCAGGCTTGAATTTGCAACATCATCTTACG 251
 QY 826 TGAGATCCCTTTGACATCGGCTTCTGCAAGTTGCAACATTTATCTGCAAGCAATCA 885
 DB 252 AGAAATCCCGTTCAATATGGTTTCTGCAAGTGGCTACGTTATCTTTGCAAGGAA 311
 QY 886 ACTCTCTGGGAAGATTTCATAGATTTGGTCTCATGCAAGCCTTGCAGCTTAAATCT 945
 DB 312 GTTCTCTGGCTTCTTACCATCAGATTTGGCTTATCAGAGCGCTTCAGGCTGATCT 371
 QY 946 AAGGGCACTGTTGATGATCTATTTCCCGATTCTCGGAATCTTACTTACCGA 1005
 DB 372 GAGTTTCAATGAGTATCTGGCCCAATACCTCTTATCTGGGCACTTGACATACCTGA 431
 QY 1006 GAAATTTATTTGACAGATTAACAAGCTGATGTTCAATTCACCTGAGCTTGGAAAT 1065
 DB 432 GAAATTTATCTGCAAGCAATAGATTAACTGATGATACCGCCAGAGCTTGTATAT 491
 QY 1066 GTCAAACTCCTTACTGTAACCTGAACTCAATGATATCATCTACGGGTATATACCA 1125
 DB 492 GTGCACTGCTATTAAGCTGAACTGAAAGCAATCTGTTGATGCTGCTTCTCTGA 551
 QY 1126 GCTTGGGAGCTTACTGATCTTGTGATCTGAATGTGGCCAAAGATCTGGAAGACC 1185
 DB 552 TCTTGGAAATCTTACAGATTTGTTGAATGAACTTGGCAACAACTTATAGAAC 611
 QY 1186 TATACCTGATCATCTGAGCTCTTGGCAAACTTAAAGCTTAAATGTTACGGAACAA 1245
 DB 612 TATCCCGAAGATTTAAGTTATGCGCAATCTCATAGTTTCAATGCTTATGCAATTA 671
 QY 1246 GTTTAGTGGCACTTATCCCGAGCATTTCAAAGCTTGAAGATATGATTAATCT 1305
 DB 672 CTGGAATGGAACCTTACAGCTTATTTCAACAGCTGAGAGTCTGATTAATGAAATCT 731
 QY 1306 GTCCAGCAACAATTAAGAGTCCCAATCCGGTGGAGCTATCTGATTCGTAACCTAGA 1365
 DB 732 GTATCAAAATCATCTCAGTGAGCACTTCCAAATGAGTTGCAAGATGAGAAATTTAGA 791
 QY 1366 TACATTGATCTTTCACAACAAGATTAATGAAATATCTTCCCTTGGTGGATT 1425
 DB 792 CACTCTGATCTTATCCCTGTAACATGATCATCTGTTCAATTCCTCAGCTATGGGAACT 851
 QY 1426 GAGCATCTTCTCAAGATGAATCTGATGAATCATATACTGTTAGTTCAGGCGA 1485
 DB 852 AGAGCATCTTTTGGAGCTCAACTTAACAAATAATATGCTGAGCAATCTCTGCTGA 911
 QY 1486 CTTTGGAAATCTAAGAGCATCATGAAATATGATCTTCCAAATATATATCTCTGCCC 1545
 DB 912 ATTTGGAACTTAAAGAGCATCATGAGATGATTTGCTTAAACAACCTCAGTGCTCT 971
 QY 1546 AATTTCCAGAGAGCTTAACCAATTAACAGAAATATTTTCTGAGCTGGAATAATAA 1605
 DB 972 GATTTCCAGAGAGTGGAGTGCATCAAAATTTGATATCTGTAAATTTAGAAAGCAATA 1031
 QY 1606 CTTGATCTGTAATGTTGGTTCAATTAAGCAACTGCTCAGTCTCACTGTATTAATGAT 1665
 DB 1032 TATTAAGAGAGATGCTCTTCACTTATTTACTGCTGATCTCAATATCTTAAATGATC 1091
 QY 1666 TCATTAACAACCTGTAAGTATATCCCTAAGAACAAATATCTTCAAGATTTTACCGA 1725
 DB 1092 ATTAACAACATCTTATGTAAGTATCTTCAAGAACAAATCTTCAAGATTTTACCGA 1151
 QY 1726 CAGCTTCAATGGCAATCTGCTGCTTGGTGGTATGTTGCTAACT-----CACC 1773
 DB 1152 CAGCTTCTTGGGTAACCTGAGCTTGTGGCTATATGCTTCACTCTGCTTCAAGCAACA 1211
 QY 1774 GTGTCAATGATTTCTGTCGAACGTGACAGATGTCATCTTACAGACAGCTAT----- 1824
 DB 1212 ATTAACAACATGCGAGCAAAATGAAGATCTCTTACCGCAAGGCTCAATGTTTGCAGC 1271

QY 1825 TCTTGAATAGCTATTTGGGGAGCTTGATCTTCTCATGATCTTATATAGACCTTCCG 1884
 DB 1272 TATTTGGTTGGTGGCCGTATTTGTTATATGATCTGCTATCTAGTATTTTGTCTG 1331
 QY 1885 ACCGATATCTCTCTCTCTTTCTTATGATGATCACTTGAACAACAGTAATTTGAC 1944
 DB 1332 GCCATATATCTTCCAGTCTCAAGATGCTCTGTAACAAACAGATTAACCTTCTTC 1391
 QY 1945 A-----CCGAGCTCCGATCTTCTTCAATATGAACATGACCTCCAGCT 1986
 DB 1392 AGCATCAACAACATTCATCTCCAGCTTGTGATCTTCAATATGAACATGAGCCCTTAT 1451
 QY 1987 TTACGAGATATCATGATGATGATGACAGAGATCTAAGTGAAGATATATCAATTTGGGCG 2046
 DB 1452 ATATGATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1511
 QY 2047 AGCATCAAGCATGATATCAATATGTTTGAAGATTTGAACCGGTTCCGATTAAGC 2106
 DB 1512 AGCCTCAAGTACAGTCTTACAGATGCGACCTGAAGAACTGCAAGCAATTCGATTA 1571
 QY 2107 GCTTACTCTCACACCCACATGATGATGAACAGTTTGAACAGACTGAGATGCTAAG 2166
 DB 1572 GCTGTATGCTTACCTTACCTGAGCTTGAAGATTTGAGATGATGATGATGATGATG 1631
 QY 2167 TACATCAAGCAGAAATCTTGTGAGCTTACAGCTTATTCCTCTCTCATCTTGGGAG 2226
 DB 1632 AAGCATCAACACCGAATTTTGAAGCTTCAAGGGTACTCCTGTGACATCTGGGA 1691
 QY 2227 TCTTGTGTTCTATGATTTTGG 2249
 DB 1692 TCTCTCTCTATGATTAATG 1714

RESULT 14
 US-10-449-902-2426
 ; Sequence 2426, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agricultural Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-40205X1-US
 ; CURRENT APPLICATION NUMBER: US/10/449, 902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2426
 ; LENGTH: 1688
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: AK060260
 ; DATABASE ENTRY DATE: 2001-12-06
 US-10-449-902-2426

Query Match 17.4%; Score 552.4; DB 6; Length 1688;
 Best Local Similarity 65.4%; Freq. No. 6; se-155;
 Matches 887; Conservative 0; Mismatches 436; Indels 33; Gaps 4;

QY 1698 ACATATATCTTCAAGATTTTCAACGAGCTTCAATGGCAATCTGATCTTGGCGTA 1757
 DB 3 ACATATATTTTCAAGATTTTCAACGAGCTTCTTGGTATCTGATCTGATGCT 62
 QY 1758 GTTGGCTAAATCAGCGGTGATGATTTCTGTCGAACGTGACAGTGTCAATCTTACAG 1817
 DB 63 ATTGCGTTGGTGTCTGCTGCTACTCACACAGTATGACAGAGATCTCTGTCTCAAGGT 122

1818 CAGCTATCTTGGAAATGCTATTTGGGGAACTTGTGATCTTCTCATGCTTTAATACAG 1877
123 CTGGAATCTTTGGGATTTGCTGTACTGCTGGCTTTGTTATCTGCTATGATCTTACTGCTG 182
1878 CTTGCGGACCGCATTAATCTCTCTCTTTCTTGATGATCACTGACAAACGAG----- 1931
183 CTTGCTGGCCACACTGGGACAGAGTGTCCCAAGATGCTTTTGTGTAACCAATATATCC 242
1932 -----TAACTTATTCGACACCGAAGCTCGTATCTCTCATATGAAATGGGAC 1979
243 ATGCATCAACATCAAGTAATGTTCTCCAAAGCTTGTATCTTTCATGTAACATGGCAT 302
1980 TCCAGCTTTACGAGATATCATGAAATGACAGAGAACTTAAGTAGAATATCATTTG 2039
303 TCCCTTGTTAGAGATATATATGAGATGACTGAAAATTTGAGGAGAGATACATTTACG 362
2040 GGCACGAGATCAAGACTGTATACAAATGTGTTTGAAGATTTGTAACCGGTTGCGA 2099
363 GGTATGGGGCATCAAGACAGGTGTACAAATGTGTACTGAAACCTGCAGACCGGTTGCAA 422
2100 TTAAAGCGCTTTACTCTCAACAAACCAAGTCAATGAAACAGTTGAAACAGAACTCGAGA 2159
423 TAAAAAATTTGATATGCTCATACCAACAGAGCTGAAGAAATGAGACTGAGCTTGAGA 482
2160 TGCTAATAGCATCAAGACAGAAATCTTGTAGCCTTACAACTTATTTCTCTCTGACT 2219
483 CTGTTGAAGATATCAAGACCGGAAATCTGTCAACCTTCAAGGGATTTCCCTATCACCTG 542
2220 TGGGAGCTCTTCTGTTTATGACTATTTGGAAAATGTTAGCTTGGGATTTCTTCAAT- 2278
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2279 --GGCCCTAGAAAGAAAAGCTGTGATTTGGGACACACGGCTTAAGATGATATGTTG 2336
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2337 CAGCACAAGGTTTATGCTTATCATCAACATGACTGTAGTCCAAAGATCATTCACAGAGAG 2396
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723 TGAAGTGAAGAAATCTCTTCTAGACAAAGACTTAGAGCAATCTTGCCCACTTTGGTA 782
2457 TAGGAAAAGCTTGTGTGTCAAAGTCACTACTTCAACTTAGTGTGGGACGATAG 2516
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2517 GTTACATAGACCCGAGATAGCTGCACTTCAAGGCTCACTAGAAAATCCGATGTCTACA 2576
843 GCTACATTTGACCTGAGTACGATGACATCCGCTCAAGAGAAATCGGATGTCTACA 902
2577 GTTATGGAATAGTCTCTTGTAGATTTTAACTCCGAAAGAAAGCCGTTGATACGAATCCA 2636
903 GCTATGACATTTGCTCTCTGAGGCTACTTACAGGCAAAAACCAAGTGTATATAGTACA 962
2637 ATTCACCAATCTGATATATGTCAAAGACGGGAAACAATGAAGTATGGAATGGCAGATC 2696
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US-10-519-135-21
; Sequence 21, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU PS3339
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: partial maize ERECTA
US-10-519-135-21

Query Match 16.7%; Score 530.8; DB 6; Length 1273;
Best Local Similarity 69.2%; Pred. No. 1,7e-148;
Matches 769; Conservative 0; Mismatches 337; Indels 6; Gaps 3;

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1 CTTGGAATCTGTGGATTTGGCTTGGTTCTTCAATGCTGTCCACTGGCCACCGAGCAAA 60
1802 GTGTCAATCTCTAGAGCAGCTATTTTGGAAATGCTATTTGGGGAAGCTTGTGATCTTCTC 1861
61 CCGCAATCTCAAGGCTGCATATATGATGTGCTGTGGTGGAGACTTGTATCTCTCTG 120
1862 ATGCTTATPAGAGCTTCCGACCGCATATCTCTCTTCTTGTATGATGATCACTT 1921
121 ATGATCTTAGTAGTGTATGACAGCCACACATCTCACTCTTTTAAAGTCCACTGTA 180
1922 GACAAACAGATTAATTTGACACCGAAGCTGTCATCTTCAATATGAAATGCACTC 1981
181 AGCAAGCAGATGAGCAATGATTCACCCAGAGCTGTATCTTCAATATGAACTGGCTCTT 240
1982 CAGCTTTACAGAGTATCATGAGATGACAGAGATTAAGTGAAGATATATCATTTGGG 2041
241 CATGCTTTGATATATATGAGAGTATGAGAACTTGTAGAAATCATCATTTGGA 300
2042 CAGGAGCATCAAGCACTGTATACAAATGTTTGAAGATTTGTAACCGGTTGCGATT 2101
301 TAGGGGCAATCAAGTAAAGTTTATTAATGTGTTCTAAGAAATGCAACAGTGGCAATA 360
2102 AAGCGCTTTACTCTCAACACC-ACAGTCAATGAACAGTTTGAACAGAACTCGAGAT 2160
361 AAAAGCTGTATGCTCCACTACCTGCAAGACCTTAAAGATTTGAAACTAGGCTCGAGAC 420
2161 GCTAATGATCAAGACAGAAATCTTGTAGCCT--ACAAGCTTATTCCTCTCTCTCAC 2218
421 TGTGTGATGATCAAAACACCGGAATCTAGTCAAGCTTGCACAAAGGTACTGCTGTGCACT 480
2219 TTGGGAGTCTTCTGTTCTATGACTATTTGAAATGATGATGATGATGATGATGATGATGAT 2278
481 GTTGGGAACCTCTCTTTTATGATATATGAGAGTGGCAGCTTATGAGGATGTTTTCAT 540

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Title: US-10-519-135-1

Perfect score: 3176

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3136.2	98.7	3176	US-11-027-304-1	Sequence 1, Appl1
2	1486.6	46.8	2750	US-10-425-114-13156	Sequence 13156, A
3	1441.4	45.4	4060	US-10-424-599-28166	Sequence 28166, A
4	1161.8	36.6	3089	US-11-027-304-7	Sequence 7, Appl1
5	1112.8	35.0	3100	US-11-027-304-5	Sequence 5, Appl1
6	1032.2	32.5	3162	US-10-425-115-182550	Sequence 182550, A
7	1015.4	32.0	2533	US-10-425-114-30583	Sequence 30583, A
8	1015.4	32.0	2644	US-10-425-115-77614	Sequence 77614, A
9	995.8	31.4	1872	US-10-425-114-10637	Sequence 10637, A
10	986.6	31.1	3115	US-10-437-963-21341	Sequence 21341, A
11	940.4	29.7	1859	US-10-425-114-7634	Sequence 7634, Ap
12	785.2	24.6	2985	US-10-437-963-67070	Sequence 67070, A
13	758.6	23.9	2523	US-10-425-114-31616	Sequence 31616, A
14	694.8	21.9	3233	US-10-437-963-18958	Sequence 18958, A
15	680	21.4	1798	US-10-425-114-31442	Sequence 31442, A
16	625	19.7	650	US-09-770-149-528	Sequence 528, App
17	560.2	17.6	1496	US-10-424-599-125524	Sequence 125524, A

18	543.4	17.1	1456	US-10-425-114-17976	Sequence 17976, A
19	533.8	16.8	4356	US-10-101-464A-888	Sequence 888, App
20	533.8	16.8	4356	US-10-864-252-888	Sequence 888, App
21	515.6	16.2	542	US-09-770-152-994	Sequence 994, App
22	504.4	15.9	1297	US-10-425-115-57919	Sequence 57919, A
23	493	15.5	1848	US-10-425-115-45210	Sequence 45210, A
24	489	15.4	501	US-09-770-961-418	Sequence 418, App
25	480.6	15.1	1384	US-11-096-568A-27210	Sequence 27210, A
26	457.2	14.7	1266	US-10-424-599-14049	Sequence 14049, A
27	429.8	13.5	1582	US-10-424-599-33950	Sequence 33950, A
28	410.4	12.9	1416	US-10-425-114-11712	Sequence 11712, A
29	398.6	12.6	1258	US-10-767-701-12314	Sequence 12314, A
30	371.2	11.7	1079	US-10-425-114-19885	Sequence 19885, A
31	356.2	11.2	1119	US-10-425-115-63542	Sequence 63542, A
32	340.4	10.7	1121	US-10-425-114-32472	Sequence 32472, A
33	339.6	10.7	584	US-10-021-923-9775	Sequence 9775, App
34	276.4	8.7	935	US-10-767-701-106	Sequence 106, Appl
35	275	8.7	6240	US-10-221-596B-22	Sequence 22, Appl
36	271.6	8.6	748	US-10-424-599-142176	Sequence 142176, A
37	258	8.1	499	US-10-767-701-21429	Sequence 21429, A
38	248.4	7.8	3375	US-09-938-842A-667	Sequence 667, App
39	248.4	7.8	3375	US-09-938-842A-667	Sequence 667, App
40	241.8	7.6	3468	US-10-437-963-64229	Sequence 64229, A
41	239.2	7.5	2381	US-10-425-115-123127	Sequence 123127, A
42	234.8	7.4	911	US-10-424-599-33951	Sequence 33951, A
43	227.2	7.2	722	US-10-424-599-28164	Sequence 28164, A
44	226.2	7.1	579	US-10-424-599-80004	Sequence 80004, A
45	225.4	7.1	3222	US-10-101-464A-839	Sequence 839, App

ALIGNMENTS

RESULT 1
US-11-027-304-1
; Sequence 1, Application US/11027304
; Publication No. US20050223428A1
; GENERAL INFORMATION:
; APPLICANT: Torii, Keiko U.
; APPLICANT: Snpak, Elena D.
; FILE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
; TITLE REFERENCE: UMOT122663
; CURRENT APPLICATION NUMBER: US/11/027,304
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/558,529
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 3176
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)..(2981)
US-11-027-304-1

Query Match 98.7%; Score 3136.2; DB 13; Length 3176;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	27	CTTTAAAGATATCTTAAAGACGCTGTTTAAAGCTGTGTGAGAAATGGCTCTGT	86
DB	1	CTTTAAAGATATCTTAAAGACGCTGTTTAAAGCTGTGTGAGAAATGGCTCTGT	60
QY	87	TTAGAGATATGTTCTTCTTGGCTTCTTCTGCTTGAAGCTTACTGTGACTT	146
DB	61	TTAGAGATATGTTCTTCTTGGCTTCTTCTGCTTGAAGCTTACTGTGACTT	120
QY	147	CAGAGAGGAGGAGCAAGCTTCTGAGATTTAAGATTTCAAGATTTGAACATGTTT	206
DB	121	CAGAGAGGAGGAGCAAGCTTCTGAGATTTAAGATTTCAAGATTTGAACATGTTT	180

207 TTTATGACGTGACAACTTCACTTCTCGATATATGTGTCGAGAGTGTCCTGTG 266
181 TTTATGACTGGACAACTTCACTTCTCGATATATGTGTCGAGAGTGTCCTGTG 240
267 AAAATGCACTTCAATGTTGTTGCTCTTAAATTTGTCAAGATTGAATCTTGATGAGAAA 326
241 AAAATGCACTTCAATGTTGTTGCTCTTAAATTTGTCAAGATTGAATCTTGATGAGAAA 300
327 TCTGACCTGGATATGAGATCTCAAGAGTCTTGTCAATTGATCTGCGAGGTAAATGCT 386
301 TCTGACCTGGATATGAGATCTCAAGAGTCTTGTCAATTGATCTGCGAGGTAAATGCT 360
387 TGTCTGAGCAAAATCCCTGATGAGATGTTGTGA CTGTTCTTTTCCAAAATCTTAGACTTAT 446
361 TGTCTGAGCAAAATCCCTGATGAGATGTTGTGA CTGTTCTTTTCCAAAATCTTAGACTTAT 420
447 CCTTCAATGAAATTAAGTGTGACATACCGTTTGTGATTTGGAAGTTGAACACTTAGAC 506
421 CCTTCAATGAAATTAAGTGTGACATACCGTTTGTGATTTGGAAGTTGAACACTTAGAC 480
507 AGCTGATTTGGAAGATTAACCAATTTGATAGGACCGATCCCTTCAACCTTTACAGATTC 566
481 AGCTGATTTGGAAGATTAACCAATTTGATAGGACCGATCCCTTCAACCTTTACAGATTC 540
567 CAACCTGAAAAATTTCTGGAATTGGCAGACAAATTAACCTGATGATAGATCAAGACTTA 626
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867 TATCATGCAAGGCAATCAACTCTCTGAGAGATTTCCATCAGTATGATGATCTCATGCAAG 926
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927 CCTTGCAGTCTTGAATCTAAAGTGGCAACTTGTGTGAGTGAATCTATTCTCCGATTTCTCG 986
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987 GAAATCTTACTTTTACCCGAGAAATTTGATTTGTGCACATTAACAACCTGACGTTCATATTC 1046
961 GAAATCTTACTTTTACCCGAGAAATTTGATTTGTGCACATTAACAACCTGACGTTCATATTC 1020
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1107 CGGGTCATATACCAACGAGAGTGGGAAGCTTACTGACTGTTGATCTGAATGTGSCCA 1166
1081 CGGGTCATATACCAACGAGAGTGGGAAGCTTACTGACTGTTGATCTGAATGTGSCCA 1140
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LENGTH: 2750
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: JC-GMFL02220115B11_FLI
US-10-425-114-13156
Query Match 46.8%; Score 1486.6; DB 8; Length 2750;
Best Local Similarity 74.8%; Pred. No. 0;
Matches 1883; Conservative 0; Mismatches 619; Indels 15; Gaps 1;
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1 AGATCTGATTTTGAAGAACACCAATTTGATAGGACCGATCCCTTCAACATTTTCTCAGA 60
564 TTCCAACTGAAATTTCTGAGCTTGGCAGACAAATTAATCTCAGTGTGATACCAAGAC 623
61 TTCTGATTTGAAGATTTGACCTGCTCAAAATATCTTACGCGGAAATATCCAAAGGC 120
624 TTAATTTCTGAGATGAAAGTTCTTCAATCTTGGTGTGGAGGAAACAATTTAGTGTGTA 683
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Qy 1824 TTTCTTGAATAGCTATTTGGGGAGCTTGTGATCTTCTCATGATCTTAATAGAGCTTGGC 1883
Db 1321 TTTCTTGAATAGCTATTTGGGGAGCTTGTGATCTTCTCATGATCTTAATAGAGCTTGGC 1380
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Db 1381 GACCAATATGATCTCTCTCTTTCTTCTGATGATCAATTTGAACAAACAGTAACTTTCTCC 1440
Qy 1944 CACGAGAGCTGTATCTTATATATGAACATGAGCACTTCAAGTTTGAAGAGATATCAATGA 2003
Db 1441 CCCCCAAGAGTATGATCTTATATGAATATGAGCACTAAGTATGAATGAATATCAATGA 1500
Qy 2004 GAATGAGAGAGATCTAAGTGAAGATATCATTTGGGAGAGAGATCAAGAGCTATAT 2063
Db 1501 GAGTGAAGTGAAGAGCTGATGAGAGATATTAATTTGATGAGAGATCAAGTATAT 1560
Qy 2064 ACAATGATTTTGAAGATTTGAACCGGTGCGATTAAGCGGCTTTACTCTCAACAC 2123
Db 1561 ATAATGATGTTCTTAAGATTTGCAAGCGGTGCTATCAAGAGATCTATCTCATATC 1620
Qy 2124 CACAGTGAATGAACAGTTTGAACAGAGCTGAGAGCTTAAGTGAATGAACAGAGAG 2183
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Db 1681 ATCTGTCAGCTCTCAAGGATTAATCTTGTCTCCATATGGGCACTCTCTGTATATGATCT 1740
Qy 2244 ATTTGGAAGATGATAGCTCTGGAGATCTTCTTCAATGGCCCTTAAGAGAGAGAGCTTTG 2303
Db 1741 ACATGAGAGAGAGAGCTTATGAGAGATCTTCTTCAATGAGCTTCAAGAGAGAGAGCTTTG 1800
Qy 2304 ATTTGAGAGAGAGCTTATGATATGATATGATGAGAGAGAGAGTTTGATGATATGATACCC 2363
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Qy 2364 ATGATCTGATGAGAGAGATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2423
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Qy 2424 AAGCTTGAAGAGCTCTTGAAGATTTTGAATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2483
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Qy 2484 CACATCTTGAAG 2543
Db 1981 CCAATCTTCTTCAATTAATGAG 2040

Qy 2544 CTTACAGAGCTCACTGAGAGAAATCCGATGCTAAGTATGAGAAATAGCTCTTGAAGTGT 2603
Db 2041 CTTACAGCTCTCACTGAG 2100
Qy 2604 TAAACCGAG 2663
Db 2101 TAACTGAG 2160
Qy 2664 CCGGAG 2723
Db 2161 CAG 2220
Qy 2724 TCGGTGTGAG 2783
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Qy 2784 ATGAG 2843
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Qy 2889 ACCTGATGAG 2948
Db 2401 ACCTGATGAG 2460
Qy 2949 CTTGTATGCTCAAGCTTTTCTTCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 3005
Db 2461 CTTGATGCTCAAGCTTTTCTTCTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 2517

RESULT 3
US-10-424-599-28166
; Sequence 28166, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21 (53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 28166
; LENGTH: 4060
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(4060)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_125435C.1
US-10-424-599-28166

Query Match 45.4%; Score 1441.4; DB 8; Length 4060;
Best Local Similarity 69.0%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 886; Indels 36; Gaps 4;

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Qy 128 TTAGTATGCTATGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187
Db 564 --TGTCAATCTGTGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 621

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Dd		622	AGGATGTGATAATGTTCTCTATATATGGACTGATACACATCATCAGATTAATGTGCC	681
OY		248	TGAGAGGTGTGTCTTGTGAANAATGTACACTTCATATGTTGTGCTTAATTGTCCAGAT	307
Dd		682	TGGAGAGGGATATGCAATGTATATATCTCACCTTCATATGTTGTGTGACTCAATCTTCAAGG	741
OY		308	TTGAATCTTGATGAGAAAATCTCACCTGTCTATGAGATCTTCAAGAT-----	355
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OY		356	----CTCTTGCAATGATCTGCCAGATATGCTGTCTGCACAAATCCCTGATGAAAT	411
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OY		472	ACCGTTTTGCATTTGGAATGMAACAATTGACAGCTGATTTGGAAMATMACAAT	531
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OY		532	GATAGGACCGGATCCCTTCAACACTTTCACAGATTTCCAAACCTGAAAATTTTGGACTTGGC	591
Dd		982	GATTGGCCMAATGACCAACCGTTTGTCTCCAAATTCCTGATTTGGAAGATTTGACACTGGC	1041
OY		592	ACAGAAATMAACTCAGTGTGTGAGATACCAAGAATTATTTATCTGAAATGAGAAGTCTTCAGTA	651
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OY		710	ACTGCTCTTGTGATTTTGAAGCTTAAGAAAACAACAGTTGACTGTGATATPACTTCAAGC	769
Dd		1162	CTGGCACTCTTCCCTCTGTTTGGGAAGCAATCTCTCAAAAACAGTGAAGTGAAGAG	1221
OY		770	ATAGAAATPGACATCGCCTCCAGSTTTTGGACTGTGCTCAATCAGCTPAACGTGTAG	829
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OY		950	GGCAACTTGTGAGTGAATCTATTTCTCTCCGATTTCCGAAAACTTACTTTACCGAGAA	1001
Dd		1402	TGTAAATGTTAAGGATTCGATTCCTCTTACTTGGGCAATTTGACTTACACAAAAA	1461
OY		1010	TTGTATTTGCAACATPAACAGCTGACTGGTTCAATTTCCACCTGCACTTGGAAAACTGTCA	1061
Dd		1462	TTGTACTTGCATGAAAAACAAGCTGACTGGCTTCAATCCCCCAGAGCTTGGAAATATGTCA	1521
OY		1070	AAACTCCATTAACCTGGAATCTCAATGATATCATCTCAGGGCTCATATACACAGAGCTT	1121
Dd		1522	AAAGCTTCACTTTTGGAACTGAATGATPAACATTTAAGTGGACATATCTCCACTGAGCTT	1581
OY		1130	GGGAAGCTTACTGACTTGTTTGATCTGAATGTGGCCAAACATGATCTGGMAGAACCTATA	1181
Dd		1582	GGAAAGCTTACTGATCTGTTTGACTTAAATGTGTGAAAACAACAACTCTCAAGGGGCCAAT	1641
OY		1190	CCTGATCATCTGAGCTCTTGGCACAATCTPAACACCTTAAATGTTCATGGGAAACAAGTTT	1241
Dd		1642	CTGTATATCTTGAAGCTCATGTAAAAATCTCAACAGCTCTCAATGTGTGATGCAATGCAACAAGTTG	1701
OY		1250	AGTGGCACTATACCCCGAGCATTTTCAAAAGCTGAGAAGTATGACTTACCTTATCTGTCC	1301

Db	1702	AATGGATCAATTTCCCCCTTCTTTGCAGAGTTTGGAGGCAATGACCTCTTGAATCTTTCT	1761
Qy	1310	AGCAACAATATCAAAAGGTCCAAATCCGGTTGAGCTATCTGTAATCGGTAACTTAGATACA	1369
Db	1762	TCCAAACAATCTTCAGGGCGCAATTCCAATAGAACTGTCGGGAAATTGGCAATTTGGATACA	1821
Qy	1370	TTGGATCTTTCCAAACAACAAGATTAATAGAAATCACTTCCTCTTCCCTTGGGATTTTGGAG	1429
Db	1822	TTGGATATTTCCAAACAATACTTAAGTTGGTTCATCCCTCTTCTCCCTTGGGACTTGGAA	1881
Qy	1430	CATCTTCTCAAGATGAATCTTGAGTAAGAAATCATCTTAATCTGGTGAATTCACAGCGACTTT	1489
Db	1882	CATTTTCTGAAGTTGAATCTTAGACAGAAACAATTTAACAGGAATATTTCCACGCAAAATT	1941
Qy	1490	GGAATCTTAAGAGCATCATAGAAATAGATCTTTCMAATAATGATATCTCTGGCCCAATT	1549
Db	1942	GGAATCTTGAAGATGTTAAGAAATTTGATCTTTCAATATATCAACTCTGCGCTTGATT	2001
Qy	1550	CCAGAGAAGCTTAAACAATTAACAGACATAATTTTCTGAGACTGGAATAATATAACCTG	1609
Db	2002	CTGTATCAACTTAAGTACGCTTCCAAACATGATATCTTTGAGACTTGAATAATACAAATTG	2061
Qy	1610	ACTGGTAATGTGGTTGATTAAGCCCAATGTCAGTCACCTGATTAATGAATGAATATCAT	1669
Db	2062	ACTGGCAATGGGATCACTTCAAAATTTGCAATTAATGCTCTCTACTTAATATGTCTCAT	2121
Qy	1670	ACAACCTCGTAGGTGATATCCCTTAAGAACATTAATCTTCCAAATTTTCAACAGACAGC	1729
Db	2122	AACAACATATTTGGTGTATTCACAGAGTAACAATTTACAGAGTTTCCCGTCAGACGT	2181
Qy	1730	TTCAATGGCAATCTCGGTCTTTGGCGGTAAAGTTGGCTAACTCACCGTGCATGATCTTCGT	1789
Db	2182	TTCAATGGAAACCTCGGTCTTTGGGTAAATTTGGCTGAATTTGGCCGTGCATGTGGCTCGC	2241
Qy	1790	CGAATCTGAAGGTCAATCTCTAGAGCAGCTATCTTGGAAATAGCTATTTGGGGGACTT	1849
Db	2242	CTTCAAGAGGAGTTACATTAATCTTAAGGCTGCAATCTTGAATTAATCTTGGTGGCCCTT	2301
Qy	1850	GTCATCTCTTCATAGTCTTAAATAGCAGCTTGCAGCCGATATCTCTCTCTTTCTT	1909
Db	2302	GTGATTTCTTCTTAATGATTAATGCTGCCGAGAGACGACAGAAAGGGTCCCTCTCTTTCT	2361
Qy	1910	GATGATCAATTTGACAAACCAAGTTAATTTCTCCCCCCTCAAGCTAGATTTCTTCATATG	2421
Db	2362	GATGATCAATTTGACAAACCAAGTTAATTTCTCCCCCCTCAAGCTAGATTTCTTCATATG	2421
Qy	1970	AACATGGCACTCCACCGTTTACGAGATTAATCATAGAAATGACAGGAATCTTAATGAGAG	2029
Db	2422	AATATGGCACTCACTGTGTATGAAGATTAATGAGATGACTGAAACCTGAGAGAGAG	2481
Qy	2030	TATATCTTTGGGCGCGAGAGATCAAGCACTGTATACAAATGTGTTTGAAGAAATTGAAA	2089
Db	2482	TATATTAATTTGAGATTAAGAGCAATCAAGTACAGTTTATTAATGTGTTCTTAAGAAATTGCA	2541
Qy	2090	CCGGTTCGATTAAGCCGCTTAACTCTCAACAACCCACAGCTCAATGAACAAGTTTGAACA	2149
Db	2542	CCGGTTCGATTAAGAGAGATCTATCTCACTATCCCAATGATTAAGAATTGGAACCT	2601
Qy	2150	GAACTCGAATGCTTAAGTAGATTAAGACACAAGAAATCTTGTGAGCTTACAAAGCTTAATCC	2209
Db	2602	GAACTTGAAGCGGTGGCAGATATACACACCGGATCTGTCACATCTCCAAAGTTATATCC	2661
Qy	2210	CTCTCTCACTTGGGGAATCTTCTGTTATATGACATTAATTTGAAATGTGTAGCCTCTGGGAT	2269
Db	2662	TTGTCTCCCAATATGGGCACTCTCTGTATTTATGACTACATGAAAAATGGCAAGTCTATGGGAT	2721
Qy	2270	CTTCTTCATGGCCCTTACGAAGAAAAGAACTCTTGATTTGGACACACGCGCTTAAAGATACA	2329
Db	2722	CTTCTTCATGGCACTTACGAAGAAAAGCTTGACCTGGGAGCTGCTTAAAAAATAGCA	2781
Qy	2330	TATGTGACAGACAAAGTTTACGTTATCTACCATGACTGTATGTCCAAAGATTAATTCAC	2389

Db 2782 CTTGGAGACGACAGAGGGCTTCTTATCTACACATGATTCCTCTAGATCATCCAC 2841
Qy 2390 AGAGACGTGAGTGTCTCCACATTCCTTTGAGCAAAAGATAGAGGCTCGTTGACAGAT 2449
Db 2842 AGAATGTGAATATCATCTACATTCCTTATGAGATGACAGCTTGAAGCTCATCTCAT 2901
Qy 2450 TTTGGAAATAGGAAAAGCTTGTGTGTGTCAAAGTCACATTAATCTTACATGATGAGC 2509
Db 2802 TTTGGCATTTGGCAAAAGTCTGTGCCCCCTCAAAAGTCCCATCTTACTTACATATGAGC 2961
Qy 2510 ACAGTAGTTACATAGACCCCGAGATAGCTGACATTCACAGGCTCAGTGAAGAAATCCAT 2569
Db 2862 ACAATTTGCTATATAGACCCGAGATGCTAGAACTTCACTCTACAGAAAGTCTGAT 3021
Qy 2570 GTCTACAGTTATGAAATAGTCTTCTTGAATGTTTAAACCCAGAAAGAGCGTGTATGAC 2629
Db 3022 GTGTACAGTTACGATATTTGTTTACTTGAATGTTGCTTAACTGAGAAAGCTGTGACAT 3081
Qy 2630 GAATCCAAATCTCCACCATCTGATATATGTCAAAGACGAGGAACAATGAATGATGAAATG 2689
Db 3082 GAATCCAAATCTCCACCATCTGATATTTTGTCCAAAGGACAGCAATGACGATGAGAAAC 3141
Qy 2690 GCAGATCCAGATCATCATGACGCTGTAAGATCTCGGTGTGTGAGAAAGTTTCCAA 2749
Db 3142 GTTGAATCCAGATTAATCTGACCATGCAAGAGACCTGTAAGAAAGGTTATCAG 3201
Qy 2750 CTGACATCTCTATGACCAAAAGACAGCCGATGATGACCCACATGACCAAGATGACT 2809
Db 3202 CTGTCTATTTATGACCAAAAGAGGACGACGATGATGAGCCGACATGACGAAAGTACA 3261
Qy 2810 CGTGTCTCGGACGTTTATGCTATC-----GGAACCAACACCTGCTGCG 2854
Db 3262 CGTGTACTCGGAAACCTTGTCTGTCAAAACACCCACCAAGCAATGACGACTACCA 3321
Qy 2855 ACTGACACGTAGGAGACCGCTGCTGTTGCTGATGCTGATGATGATGCAAACTCAAG 2914
Db 3322 CTGTCTTCAATTCATCTGCAAAAGTGCATGCTACGATGATGATGCAAACTCAAG 3381
Qy 2915 ACTGCTCATCTGCTCAATGCTCTTCCATGAGTCTTGTGATGCTCAACTGTTCTTCGG 2974
Db 3382 ACTGACACCTTGTGAGACTGCCCCCTCAATGACACCTCAATGCTCAACTTCTCTCAG 3441
Qy 2975 TTTGGAACAAGTATTTCTCAGAACAGTGAAT 3005
Db 3442 TTTGGAGAAGTATCTCTCAAAACAGTGAAT 3472

RESULT 4
US-11-027-304-7
; Sequence 7, Application US/11027304
; Publication No. US20050223428A1
; GENERAL INFORMATION:
; APPLICANT: Torii, Keiko U.
; APPLICANT: Shpak, Elena D.
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
; FILE REFERENCE: UW0122663
; CURRENT APPLICATION NUMBER: US/11/027,304
; PRIORITY FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/558,529
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3089
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (186)..(3089)
US-11-027-304-7

Query Match 36.64; Score 1161.8; DB 13; Length 3089;
Best Local Similarity 65.24; Pred. No. 0;

Matches 1760; Conservative 0; Mismatches 927; Indels 12; Gaps 3;
Qy 150 AGAGAGGACGACGCTGCTGAGATTAAGAAATCATTCATTAAGATGACAAATGTTCTTT 209
Db 274 ACAGAGAAAAGCTTATGAGCTTAAGAGCTTATTCACAGAAAGTGGCAATATGCTTC 333
Qy 210 ATGACGAGAACCTTCACTTTCGGATTATGTGTCTGAGAGAGTGTCTTTGAAA 269
Db 334 TTGATGGAGAGATGTTCAATACCAAGACTTTTGTCTTGAAGAGGTGTCTGTGATA 393
Qy 270 ATGTACCTTCAATGTTGTGCTTAAATTTGTCAGTTTGAATCTTGAAGAGAAATCT 329
Db 394 ACGTTACCTCAATGTTGTCTTAAATCTGTAACCTGAATCTTGTGAGAGATAT 453
Qy 330 CACCTGCTATTTGAGATCTCAAGAGTCTCTGCAATGATCTGCGAGTAAATCGCTGT 389
Db 454 CATTTGCCCTTGGAGATTTGATGATGATGCAATCAATAGACTTGCAGAAATTAATTTG 513
Qy 390 CTGACAAATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449
Db 514 GTGTCAAATTTCCAGATGATGATGAAACGTGTCTCTTGTCTTATGATGATGATGATGAT 573
Qy 450 TCAATGAATTAAGTGTGACATACCGTTTTCGATTTGGAAGTGAAGCACTTGAGAGC 509
Db 574 CCAATTTGTTGTGAGACATACCGTTTTCATCTCTTAACTCAACACAGCTGAGATTC 633
Qy 510 TGATTTGAAGAAATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
Db 634 TGAACCTTAAGAAATTAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 693
Qy 570 ACCTGAATTTCTGAGCTTGGACAGAAATTAACCTGATGATGATGATGATGATGATGATGAT 629
Db 694 ACCTTAAGACCTTGAACCTGCAAAAGACAGCTTACCTGATGATGATGATGATGATGATGAT 753
Qy 630 ACTGGAATGAGATTTCTCAATCTTGGGTTGGAGAGAAACAATAGTGTGATTAATTT 689
Db 754 ACTGGAATGAGATTTCAATCTTGGGTTGGAGAGAAACAATAGTGTGATTAATTT 813
Qy 690 CTCAGATTTGCTCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749
Db 814 CTCCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 873
Qy 750 CTGCTATTAATCTGAGACGATGAGAAATTTGCACTGCTTCCAGGTTTGAAGCTTGTCT 809
Db 874 CTGGAATTAATCTGAGACGATGAGAAATTTGCACTGCTTCCAGGTTTGAAGCTTGTCT 933
Qy 810 ACAATCACTTAATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 869
Db 934 ATAAATCAATTAATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 993
Qy 870 CATTGCAAGCAATCAACTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 929
Db 994 CACTTCAAGCAATCAACTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053
Qy 930 TTGCACTTGAATCTTAAGTGAAGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 989
Db 1054 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1113
Qy 990 ATCTTAATTTCAACGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1049
Db 1114 ATCTGATTAATTTCAACGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1173
Qy 1050 CTGAGCTTGAAGCAATGCAAACTCCATTAATCTGAGAACTGATGATGATGATGATGATGATGAT 1109
Db 1174 CCGAGCTAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1233
Qy 1110 GTCAATATCAACAGAGCTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1169
Db 1234 GAAAGATCCCACTGAGCTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1293
Qy 1170 ATGATCTGGAAGAGCAATTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1229
Db 1294 ACAATCTTGAAGAGCAATTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1353

QY 1230 ATGTTCAATGGGAACAAGTTAGTGCACATPACCAGGAGATTTCMAAGCTGAAGA 1289
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 QY 1290 TGAATTAATCTGTCGAGCAACAATATCAAAAGGTCGATCCCGGTGAGCTATCTC 1349
 DB 1414 TGAATTAATCTGTCGAGCAACAATATCAAAAGGTCGATCCCGGTGAGCTATCTC 1473
 QY 1350 GTATCGGTACTAGATACATTTGATCTTTTCAACAACAAGATTAATGATCTTCTT 1409
 DB 1474 ATATCATCAATCTTGAATACATGATGATCTGTCGACCAATTTCTCAGGCTCAATTCAT 1533
 QY 1410 CTTCCTGCTGATTTGGAGCATCTTCTCAAGATGATGATGAGTAATCAATTAAGT 1469
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 QY 1470 GTGTAGTTCAGGAGCATTTGGAATCTGAAGACATCATGAAATAGATCTTTCAAATA 1529
 DB 1594 GCAATTTGCTGAGATTCGGGAACTCCGAGCATTCAGATCATGATGTCATTTA 1653
 QY 1530 ATGATATCTGTGCGCCATTTCCAGAAAGCTTAAACATTAAGAAATATTTTGTCTGA 1589
 DB 1654 ATTTCTTGGCGGTATTTCAACTGACCTTGGCCAGTTGCAAGAACATTAACCTCTCTGA 1713
 QY 1590 GACTGGAAATTAATPAACTGACTGATGATGATGATGATGATGATGATGATGATGATG 1646
 DB 1714 TACTGAACAACAACAAATTCATGAGAAATCCCTGATCAGCTTAACTGATCTTCACTG 1773
 QY 1647 TCACTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1706
 DB 1774 TTTGCAATCTGAAATCTGCTTCAATTAATTTTGTGAATATCCCATATGAAGAACT 1833
 QY 1707 TCTCAAGATTTTCAACAAGAGCTTCAATGAGCAATCTGCTTGTGCTGATGCTGAA 1766
 DB 1834 TTTACAGTTTTCCTCCGCGAGCTTCTTGAATATCAATTTCTGCGGAGAACTGCGGTTG 1893
 QY 1767 ACTGACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1826
 DB 1894 GATCAATCTGTGCGCCATCTTAACTTAAGTCAAGT---ATTCAACAAGATGCGCTGA 1950
 QY 1827 TTTGGAATAGCTATTTGGGAGGAGCTTGTGATCTTCTCATGATGATGATGATGATGATG 1886
 DB 1951 TTTGATAGGTTCTCGGTTTCACTCTCATATGATGATGATGATGATGATGATGATGATG 2010
 QY 1887 CGATTAATCTCTCTCTTCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATG 1946
 DB 2011 CAAAGCAGCAAGAAACAGTCTTGAAGGCTTTCAAAACAAC-----CTGAAGGGTCAA 2064
 QY 1947 CGAAGCTCGTCACTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2006
 DB 2065 CGAAGCTCGGATTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2124
 QY 2007 TGAAGAGATCTTAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2066
 DB 2125 TTTACAGAAACCTCGATGAGAAATACATGATGATGATGATGATGATGATGATGATGATG 2184
 QY 2067 AATGTGTTTGAAGATGTAACCGGTTGCGATTAAGCGGCTTTACTCTCAACACCAC 2126
 DB 2185 AGTGCACCTTCAGAAACCTTCCGACCTTATGCAATTAAGCAATCAATCAATCAATCCCA 2244
 QY 2127 AGTCAATGAAACAGTTTGAAGCAAGATGATGATGATGATGATGATGATGATGATGATG 2186
 DB 2245 GCAATCTTCGCGGATTTGAAGCAAGATGATGATGATGATGATGATGATGATGATGATG 2304
 QY 2187 TTTGAGCTTCAAGATTTATCT 2246
 DB 2305 TATTAAGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2364
 QY 2247 TGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2306
 DB 2365 TGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2424

QY 2307 GGGACACAGCGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2366
 DB 2425 GGGAAACAGCGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2484
 QY 2367 ACTGATGTCAGGATCAATTCACAGAGAGCGTGAAGTGTGTCACATTTCTTGGACAAAG 2426
 DB 2485 ACTGACACCTTGAATATTCATGAGACATCAAGTATCAATCAATCAATCAATCAATCAAT 2544
 QY 2427 ACTTAAGGCTCGTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGAT 2486
 DB 2545 ATTTGAAGCGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2604
 QY 2487 ATACTCAACTTCTGATGAGGACGATGATGATGATGATGATGATGATGATGATGATGATG 2546
 DB 2605 ATGCTTCAACTTATGTTCTTGAAGATTTGATGATGATGATGATGATGATGATGATGATG 2664
 QY 2547 CACGGCTCACTGAGAAATCCGATGTCATGATGATGATGATGATGATGATGATGATGATG 2606
 DB 2665 CGGCTGCAAGCGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2724
 QY 2607 CCGGAAGAAAGCGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2666
 DB 2725 CCGGCAAGAAAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2784
 QY 2667 GGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2726
 DB 2785 ATGATTAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2844
 QY 2727 GTGTGATGAGAAAGTTTTCACATGCGACCTCTATGACCAAAAGACGCGAATGATC 2786
 DB 2845 GACACATCAAGAAACATTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 2904
 QY 2787 GACCCACATGACCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2845
 DB 2905 GACCCACATGACCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2963
 RESULT 5
 US-11-027-304-5
 ; Sequence 5, Application US/11027304
 ; Publication No. US20050223428A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Torii, Keiko U.
 ; APPLICANT: Shpak, Elena D.
 ; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
 ; FILE REFERENCE: UMOT12263
 ; CURRENT APPLICATION NUMBER: US/11/027,304
 ; CURRENT FILING DATE: 2004-12-30
 ; PRIOR APPLICATION NUMBER: US 60/558,529
 ; PRIOR FILING DATE: 2004-04-01
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 3100
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis Thaliana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (200)..(3100)
 US-11-027-304-5
 Query Match 35.0%; Score 1112.8; DB 13; Length 3100;
 Best Local Similarity 63.9%; Freq. No. 2,7e-309;
 Matches 1738; Conservative 0; Mismatches 967; Indels 15; Gaps 3;
 QY 131 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 190
 DB 263 GTTGTCTTGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 322
 QY 191 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 250
 DB 323 AACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 382

QY	251	AGAGGTGTCCTTGTGAAATGTCACCTTCAATGTTGTGCTTTAATTGTGCAGATTGG	310
Db	383	CGAGGTGTTTTCTCGACACAGCGTAGGCTACCTCGTGTCTCTCGAAATTGTGCCAGCTCG	442
QY	311	AATCTGATGAGAAATCTCACTCCGTATTTGGAGATCTCAAGAGCTCTCTTGCAATTGAT	370
Db	443	AATCTTGGAGGGAGATATCTCCAGCTATTTGGAGCTTACGGAATTTGGCAATCAATAGAC	502
QY	371	CTGCGAGGTAATCGCTGTCTGGAACAAATCCCTGATGGAGATTGGTGACTGTCTCTCTTGG	430
Db	503	TTTGCAGGTTAATTAACTAGCAGGTCAATTTCCAGATGAGATTGGAAACTGTGCTCTCTT	562
QY	431	CAAAACTTAGACTTATCTCTTAATGAATTAAGTGTGACATACCGTTTGGATTGGCAAG	490
Db	563	GTTTATCTGGAAATTTGTCCGAGAAATCTGTTAATAGGAGACATACCTTTCTCAATCTTAA	622
QY	491	TTGAAGCAACTTGGACAGCTGATTTCTGAGAAATTAACAAATTGATANGAACCGATCCCTTCA	550
Db	623	CTCAAGCAGCTTGAACCTCTGAATCTGAAGAACATACGCTCACAGGCTCTGTATCCAGCA	682
QY	551	ACACTTTACAGATTCCTCAAACTCGAAATTTCTGACCTTGGACACAGAAATTAACCTGATGT	610
Db	683	ACCTTAACCCAGATTTCCAACTTAAGAGACTTGATCTTGTGGCAATCAATCAACGGGT	742
QY	611	GAGATACCAAGACTTATTACTCGAATGAGTCTTCTAGTATCTTGGGTGGCAGGAAC	670
Db	743	GAGATATGAAATGTCTTACTCGAATGAAATTTTGGCAGTATCTTGGATTACGAGGGAAT	802
QY	671	AACCTTAGTCGGTAACATTTCTCCAGATTGTGTCAACCTGATCTTTGGTATTTTGAC	730
Db	803	ATGTTGACTGGAAGCTTATCTTCTGATATGTGTACGCTTAACCGGTTGTGTACTTTGAT	862
QY	731	GTAAGAAACAACAGTTTACTGTAGTATTAACCTGAGACGATAGGAAATTTGACATGCCCTTC	790
Db	863	GTCGAGGAAATTAATCTAACCTGGAACCATCCCGGAGAGCATCGGAATTTGACAAAGCTTT	922
QY	791	CAGGTTTGGACTGTCTCTAACATACGTTAATCTGTGATACCTTTTGACATCGCTTC	850
Db	923	CAAAATCCCTGGACATATCTTAATACAGATTAACAGAGAGATTCCTTCAATATGCGCTTC	982
QY	851	CTGCAAGTGAACATTTATCAATTCGACAGGCATCACTCTCGGGAAGATTCCTACATGCTG	910
Db	983	CTCCAGTTGCTACTCTGTCACTTCACAGGAACAGATTGACGGGTAGAAATTCAGAAATT	1042
QY	911	ATTGGTCTCATGCAAGCCCTTGACAGTCTTAAATCTAAGTGGCAACTTGTGATGATGATCT	970
Db	1043	ATTGGTCTAAATGCAAGGCTCTTGCTGTTTGGATTTGAGTGCATATGAGCTTGTGTGCTCT	1102
QY	971	ATTCTCCGATTTCTGGAAATCTTAATCTTCAACCGAAGAAATTTGATTTGGACAGTAACAAG	1030
Db	1103	ATCCACACCGAATACTTGGCAATCTCTCATTTTACCGGAAGTTGATCTTCATATGCGAATATG	1162
QY	1031	CTGATCGGTTCAATTTCCACTGAGCTGGGAACATGTCCAAACCTCAATACCTGGAACTC	1090
Db	1163	CTCACTGTGTCCAAATCCCTCTGAGCTTGGGAATATGTACCTCTCAGCTAATTTGCACCTA	1222
QY	1091	AATGATTAATCAATCTCACGGGTCAATTAACACAGAGCTTGGGAAGCTTACTGACTTGT	1150
Db	1223	AACGACATTAATCTAATGTGGAACTATTCACCTGAGCTTGGAAAGCTGGAGCAATTTGTTT	1282
QY	1151	GATCTGAATGTGGCCACAAATGATCTGGAAGACCTATACCTGATCAATCTGAGCTTTGC	1210
Db	1283	GAACTGAATCTTGGCCACAGCCGTTTATGTAAGGCCCATACATCAATTAAGTCTCATGT	1342
QY	1211	ACAAATCTAAACAGTTTAAATGTTCAATGGGAACAAGTTTATGGCACATATACCCCGAGCA	1270
Db	1343	GCAGCTTGAATCAATTAATGTTCATGGGAACCTTGAATGATCTAATTCACCTGGCG	1402
QY	1271	TTTCAAAAGCTAGAAAGATGACTTAATCTTATCTGTCCACAACAATATCAAAAGTCTCA	1330
Db	1403	TTTCCGCAATCTCGGAGCTGATCTTATCTGATCTTTCTGTGMAACAATTTCCAGGAAAA	1462
QY	1331	ATCCCGTTGAGCTATCTCGATCGGTATCTTGAATACATTGATCTTTCCACAACAAG	1390

Db	1463	ATACAGTGGAGCTTGGACATATATCAATCTTGACAAACTAGATCTGTCTGGCAATAC	1522
Qy	1391	ATAATGGAATCATCTCTTCCCTTGATTTGGAGCATCTTCAAGATGACCTG	1450
Db	1523	TTCTCAGGTCCTATACCATTAACGCTTGGGATCTTGAACACTTCTCATTTAACTT	1582
Qy	1451	AGTAAATCATATTAACGTGTGATGTTCCAGGCACTTTGGAAATCTAAGAGCATATG	1510
Db	1583	AGCAAAACCATCTTAAGTGACATTAACCTGCAGAGTTTGGAACTTTCGAGCATTCAG	1642
Qy	1511	GAATTAATCTTTCAATTAATGATATCTGCGCCCATTCGAGAGGCTTAACATTA	1570
Db	1643	ATGATATGATATCATTTCAATCTGCTCTCCGAGTTATTCCACTGAACCTTGGCAATTG	1702
Qy	1571	CAGAAACATATTTTGTGAGACTGGAATATTAATCACTGACTGGTAATGTT---GGTTCA	1627
Db	1703	CAGATTTTAAACTCTTTAATATTTGAACACACAGCTTCATGGGAAATTCAGATCAG	1762
Qy	1628	TTAGCCAACTGTCTCAGTCTTCACTGATTAATGATATCTCATTAACAACCTTGATGAT	1687
Db	1763	CTTACGAACCTGCTTCACTCTGTCAATCTGAATGTCTCTTCAACAATCTCTCCGGATA	1822
Qy	1668	ATCCCTAAGAACATTAATCTTCTCAAGATTTTACACAGACGCTTCATTTGGCAATCCGTG	1747
Db	1823	GTCCACCAAGAAAACCTTCTCAGTTTGTCTCACGCCAGCTTTGTTGAAATCCATAT	1882
Qy	1748	CTTTGCGGTAGTTGGCTAAACTCACCGTGTATGATTTCTCGTCAGACGTGTACAGTGTCA	1807
Db	1883	CTTTGTGGAAACTGGTGTGATCTAATTTGTGTGTCCTTACCGAAATCTCGA-----GTA	1936
Qy	1808	ATCTTACAGCAGCTATTTCTTGAAATAGCTATTTGGGGAATTTGATTCCTTTCATGGTC	1867
Db	1937	TTCTCCAGAGGTGCTTGTATCTGATGTTCGTGCTTCAGCTCATCACTCTCTATATGATATT	1996
Qy	1868	TTAATAGAGCTTCCGACCGCAATATCTCTCTCTTTCTGTATGATCACTTGACAA	1927
Db	1997	TTCTCTGAGTTTCAATCAATCAATGACACAGAAAGATTTCAAGGCTC-----CTCA	2050
Qy	1928	CCAGTAACTTATTTGACACACGAGACCTGTCATCTTATATGAACATGGCACTCCAGTT	1987
Db	2051	AAACAGCTGAAGGTTTAAACCAACTGTATCTTCCACATGACATGGCAATTCATATCA	2110
Qy	1988	TACGAGATATCATGAGATGACAGAGATCTAAGTAGAAGTATATTCATTTGGCACCGA	2047
Db	2111	TTTATGATATCATGAGAGTACGTGAGATCTTAACGAAAATTTAATATGATATGTGT	2170
Qy	2048	GCATTCAGACCTGTATCAAAATGTGTTTGAAAGATTGTAAACCGGTTCGATTAACCGG	2107
Db	2171	GCTTCTAGCAAGGTATCAAAATGTGCATTTAAAGTTCCGACCTATTTGCCATTTAACGA	2230
Qy	2108	CTTTAACTCTCAACACCAACAGTCAATGAAACAGTTTGAACAGAACTCGAGATCTAAT	2167
Db	2231	CTTCTCAATCATGTATCCGCAATTAACCTTCCGGGAATTTTGAACAGAACTTGAAGCAATTGGG	2230
Qy	2168	AGCATCAAGCACAGAAATCTTGTAGGCTTACAGACTTATTCCTCTCACTTGGGAGT	2227
Db	2291	AGCATATAGGCACAGAAACATATAGTCAAGCTTGATGATATGCTCTGTCTTACTAGGCAAC	2350
Qy	2228	CTTCTGTATTATGACTATTTGGAAATGTGATGCTCTGGGATCTTTCTCATAGGCCCTACG	2287
Db	2351	CTTCTTTTCTATGACTCATATGGAATAATGATCACTTTGGGACCTTCTTCAATGGGCTCATGG	2410
Qy	2288	AAGAAAAAGACTCTTGATTTGGGACACACGGCTTAAATAGATATTTGTGACGACCAAGT	2347
Db	2411	AAGAAAGTGAAGCTTGTGTTGGGAGACAGAGTTGAAGATAGCGGTTGGAGCTGCACAAAGA	2470
Qy	2348	TTAGCTTATCTACACCATGACTGTATGTTCAAGATCTTCAAGAGACGTGAAGTGTCTC	2407
Db	2471	CTAGGCTATCTTCCACACAGATTGTATCTGTGATCAATTCACCGTGACATCAATCTCATCG	2530
Qy	2408	AACATCTCTTGGACAAAGACTTGAAGCTGTGTGACAGATTTTGGAAATAGCGAAAGC	2467

Db 2531 AACATCTCTTGTGATGAAATTCGAAGCACACTTATCTGATTTGGGATTTGCTAAGAGC 2590
Qy 2468 TTGTTGTGTGCAAGAGTCACTTCACTTACCTGATGAGGACAGATAGGTTACATAGAC 2527
Db 2591 ATACCACTGACCAAAACCACTGCTGCACTGATGATTTTGGAAACAATTTGTTATATAGAC 2650
Qy 2528 CCCGAGATGCTGCGACATTCGACGCTGACGAGAAATCCGATGCTTCAAGTTATGAAATA 2587
Db 2651 CCAGAGTATCTGCTGATCTTACGATCAATGAGAAATCCGATATATACAGCTTCGATTT 2710
Qy 2588 GTCTCTTGTGATTTTAAACCCGAAGAAACCGTGTATGACGAAATCCACCAT 2647
Db 2711 GTTCTTCTTGTGATCTTCACTGAGGAAAGACAGTGTATTAACGATTAACCTTGATCAA 2770
Qy 2648 CTGATATGTCAAAGAGCGGGAACAATGATGTAATGGAATGCGATTCAGATCACA 2707
Db 2771 CTGATATGTCAAAGCGTGTATGATTAATGATGTAAGCAAGTTGATCCAGAGTTACT 2830
Qy 2708 TCGACGTGTAAGATCTCGGTGTGTGTAAGAAAGTTTCCAACTGCGACTCTATGACAC 2767
Db 2831 GTGACTGTATGACTTGGACATATCAGAAAGCAATTCAGCTGCTCTCTTATGACA 2890
Qy 2768 AAAAGACGCGGATGATGACCCCAATSCACCAAGGTGACTGCTGTCTGCGCAGTTT 2827
Db 2891 AAGCGAAACCTTTAGAGAGACCAATGCTTGAAGTCTTAGGGTTCTGCTCTCTT 2950
Qy 2828 ATGCTATCGGAACACACACC 2847
Db 2951 GTCCCATCTCTGCAAGTAGC 2970

RESULT 6

US-10-425-115-182550
; Sequence 182550, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 369326
; SEQ ID NO 182550
; LENGTH: 3162
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MFT4577_98067C.1
US-10-425-115-182550

Query Match 32.5%; Score 1032.2; DB 9; Length 3162;

Best Local Similarity 63.5%; Pred. No. 5.3e-286; Matches 1644; Conservative 0; Mismatches 933; Indels 12; Gaps 4;

Qy 305 GATTGAATCTTGTATGAGAAATCTCACTGCTATGAGATCTCAAGAGTCTTGTCA 364
Db 14 GATCTAAACCTCGGAGGAGATCTCGCGCTATAGGACGCTCAAGAGCTCAAGTTG 73
Qy 365 ATTGAATCTGGAGTATGCTCTGTCTGACCAATCCCTATGAGATGAGTGTCTTCT 424
Db 74 GTGATCTCAAGCTGAACAGCTCAAGGCCAAATCCAGATGAGATGGGGAATGGGTC 133
Qy 425 TCTTTCGAAAACCTTAGACTTATCTTCAATGAATTAAGTGTGATACCGTTTTCGATT 484
Db 134 TCTTAAATATTTGATTTGTGGGCAACTTGTCTGATGAGACATCCCTTCTCCATC 123
Qy 485 TCGAAGTTGAAGCACTTGAAGCAGCTGATTTCTGAAGATTAACAATGATGAGACCGATC 544
Db 194 TCTAAGCTCAAGCACTTGAAGCAGCTGATTTTGAAGAACCAACCACTCACCGGACCATC 253

Qy 545 CTTTCAACACTTTTACAGATTTCCAAACCTGAAATTTCTGGACTTGGCAGAAATTAATC 604
Db 254 CCTTCACACTGTGACAGATTTCCAAATCTCAGACCTTGATCTGGCGGCAACAACTT 313
Qy 605 AGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTTTCTGAGTACTTGGGTGCGA 664
Db 314 ACCGGGAGATTCGCCAGGCTCATCTGATGAAAGTACTACAAATACCTAGGCTTGAGG 373
Qy 665 GGAACAACCTTAAGTCGTAACATTTCTCCAGATTTGTGTCACTGACTGCTTTGGTAT 724
Db 374 GGTAACTCACTGACTGAACTTTGTCACTGACATGTGCAACTGACTGCGCTGTGTAC 433
Qy 725 TTTGAGTGAAGAAACAAGCTTGTGATGATGATATGATCTGAGACGATGAGAAATTCGAT 784
Db 434 TTGACATTAAGGGGGAACAATCTCAGAGAACATTTCCAGAGGCAATGAGAACTGCACT 493
Qy 785 GCCTTCAGGTTTGTGACCTTGTCTCAATCAGCTAACTGATGAGATCCCTTTGACATC 844
Db 494 AGCTTGAAGATTTCTGATATTTTATACCAACCAATCTGAGAAATACCATCAACATA 553
Qy 845 GGCCTTCTGCAAGTTGCAATTAATCATTTGCAAGCAATCACTCTCTGGGAAATTTCCA 904
Db 554 GGTAACTTCAAGTACGACACTGCTCACTCAGGAAATGACTGATTTGGCAAAATTTCTT 613
Qy 905 TCAGTATGTGTCTCAATGCAAGCCCTTGCAGCTTATGATTAAGTGGCAACTGTTGAGT 964
Db 614 GAAATGATGTGCTCATGACAGGCTCTTGTCTGATCTTGAAGTGAATGAACTGGTG 673
Qy 965 GATCTATTTCTCCGATTTCTCGAAATCTTACCTTTCACCGAGAAATTTGATTTGCAAGT 1024
Db 674 GGGCTTATTTCTCTTATCTTATCTTGGCAACTGTCTTACACAGGCAACTATTTTACATGGC 723
Qy 1025 AACAGTGACTGTGTTCAATTTCCACTGAGCTTGGAAACATGTCAAATCTCCATTACCTG 1084
Db 734 AACAACTCACTGACATATATACACACAGAACTGGGGAACATGTAACCTTACCTGCTG 793
Qy 1085 GAACCAATGATATATCATCTCAAGGGTCAATATATACCAACAGAGCTTGGGAACTTACTGAC 1144
Db 794 CAGCTGATGACATGATATTTAGTGGCAATCCAGCTGAGCTTGGCAAACTCAGAG 853
Qy 1145 TTGTTGATCTGATGATGCGCAAAATGATCTGGAAGACCTTATCTGATCATCTGAGC 1204
Db 854 TTATTTGAATGATCTTGGCAACAAATCTTGAAGGCAATATCTCTGCAAACTGAGC 913
Qy 1205 TCTTGCACAAATTAACAGCTTAAATGTTCACTGGAACAAGTTTGTGCACTATATACC 1264
Db 914 TCTTGAAGTCACTGAACAAATTCATGTGATGCGCAATGATGATGCTTATCCCT 973
Qy 1265 CGAGCAATTTCAAAAGCTAAGAAATGATGACTTACCTTAATCTGCCAGCAACATATCAAA 1324
Db 974 GTGTGTTTCCAGAGCTGAGAGATTTGACATTAACCTTCTTCAAACTGATCAAA 1033
Qy 1325 GGTCAATCCCGGTAGACTATCTGATCGTAATGTAATGATGATGATGATGATGATGATGAT 1384
Db 1034 GGGCAATTCCTCTGAGCTGTGCTACATAGTCAATTTGACACACTAGATCTTCTTCA 1093
Qy 1385 AACAGATTAATGAAATCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1444
Db 1094 AATGAATTTCCCGGCGCAGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1153
Qy 1445 AACTGATGAAATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1504
Db 1154 AATTTGATGAAATCAATCTCACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1213
Qy 1505 ATCATGAAATATGATCTTCAATATATGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1564
Db 1214 GTCCAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1273
Qy 1565 CAATTAACAAGCAATATTTTGTGAGACTGGAATATATATATATATATATATATATATATAT 1621
Db 1274 CAGCTCAAAACCTTGTATGCTGATCTTAAACAAAGATTTGCTGGGAGATCCCT 1333

QY 1622 GGTTCATTAGCACTGCTCAGTCTCATCTGATTTGATGATCTCATTAACACCTGTA 1681
Db 1334 GCTCAGCTGGGTAACTGTTAGTGTACCTTAACCTGATCAACAACTTCTCT 1393
QY 1682 GGTGATATTCCTTAAGAAACAATTAATCTTCAAGATTTTTCACAGACGTTTATGGCAAT 1741
Db 1394 GGGGACATCTCCGTCATCGAAAACCTTCTCAAAAGTTCCCAATGAGAGCTTCATGGGTAAT 1453
QY 1742 CTTGCTGTTGGGTAAGTGGCTAACTCAACGTCATGATTCGTCGACGTAAGCA 1801
Db 1454 CTGATGCTTCATGCTGTAAGTGTACGCAAGACTCCAGCTGTGACATTTCTATGAAACCA--A 1510
QY 1802 GTGTCAATCTCTAGAGAGCTATTCTTGAAATAGCTATTGGGGGACTTGTGATCTTCTC 1861
Db 1511 GTTAGCATCTCTCGGAGCGGCTTGCTGATGATTTAGGCTTCGTCATTTCTCTGCG 1570
QY 1862 ATGCTTTAATAGAGCTTGGCCGACCGCATATCTCTCTCTTTTCTGATGATCACTT 1921
Db 1571 ATCGTGTGCTGGGATATATACAGACCAACGACGACAGC--TACCTGAGAAAAGCATCC 1627
QY 1922 GACAAAACAGTAATCTTATTCGACACGAGCTCGTCACTCTTCAATATGAACATGGCACTC 1981
Db 1628 GACAGGCACT--GCAAGGCGCCCAAGGCTGGTGTCTTCTGATGATGATGGCCGTG 1684
QY 1982 CAGCTTACGAGATATCATGAGATGACAGAGAATCTAAGTGAAGATATATCATTTGGG 2041
Db 1685 CACACGTACGAGGATCATATGAGGCTGACGAGAACTGAGCGAAGATCATCATCGGA 1744
QY 2042 CACGAGCATTCAGCATCTGTATCAAAATGTGTTTGAAGATTTGAACCGGTTGCAAT 2101
Db 1745 TACGCGCGCTGACACCGTGTATCAGGTGTACCTCAAGACGCGGACGATGCGCGTC 1804
QY 2102 AAGCGGCTTACTCTCAACACCCAGTCAATGAAACGTTTGAACGAACTCGAGATG 2161
Db 1805 AAGGCGCTCTACAGCCAGTACACCAAGCTCCGGAGTTTCAGAGGAGCTGGAACAG 1864
QY 2162 CTAAATGATCAACGACAGAAATCTTGTAGCTTCAAGCTTATCTCTCTCACTTG 2221
Db 1865 ATCGGCGAGCATCCGCGACAGGAACTCGTCAAGCTTCCAGCGCTCTCCCTCCAC 1924
QY 2222 GGGAGTCTTCTGTATGATTAATTTGGAAAATGTAGCTCTTGGATCTTCTTCATAGGC 2281
Db 1925 GGGAACTGTCTGTATGATTAATTTGGAAAATGTAGCTCTTGGATCTTCTTCATAGGC 1984
QY 2282 CCTACGAAAGAAAAGACTCTTGTATGGACACAGGCTTAAATAGATATGTCAGCA 2341
Db 1985 CCGTCGAAGAAAGTGAAGCTGACTGGGACACAGAGCTGAGATGCGAGTGGCGCGC 2044
QY 2342 CAAGGTTAGCTTATCTACACGATGATGATGATGATGATGATGATGATGATGATGATG 2401
Db 2045 CAGGCGCTGCGTACCTCCACGACGATGCAACCGCGCATCTGTGACCGGGAAGTCAAG 2104
QY 2402 TCGTCCAACTTCTCTTGAAGAAAGTGAAGCTGTTGAGATGATGATGATGATGATGATG 2461
Db 2105 TCTCCAACTTCTCTTGAAGAAAGTGAAGCTGTTGAGATGATGATGATGATGATGATG 2164
QY 2462 AAAAGCTTGTGTGTCAAAAGTCAATATCTTCACTTACGATGAGGACGATGATGATGATG 2521
Db 2165 AAGTGTGCTGCGCGCGCGCAAGTCCACGCTCCACCTACGCTGCGGACCATGGGTAAC 2224
QY 2522 ATAGACCCGAGATATGCTCGCATTCACGCTCACTGAGAAATCGATGCTTCAAGTTAT 2581
Db 2225 ATGACCCGAGATATGCTCGCATTCACGCTCACTGAGAAATCGATGCTTCAAGTTAT 2284
QY 2582 GGAATATCTCTTCTTGAAGTTAATCCGAAAGAAACCGTGTGATGAGAAATCGAATCTC 2641
Db 2285 GGGTGTCTCTCTGAGCTGTCTACGAGGAGAAAGCGTGTGACACGATTCACACTG 2344
QY 2642 CACCATCTGATATATGTCAAAGACGAGGAAACATGATGATGATGATGATGATGATGATG 2701
Db 2345 CACCATCTGATATCTCTGAGAGCGGACGACGAGATGATGATGATGATGATGATGATG 2404
QY 2702 ATCATCATGACGTGTAAAGATCTCGTGTGTGTAAGAAAGTTTTCACATGCGCATCTCTA 2761

Db 2405 GTGTGCTGACGTGACAGGACATGAACTGTGTGGGAAAGGCTTCCAGCTGCGCTGCTG 2464
QY 2762 TGACACCAAGAGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2821
Db 2465 TGACACCAAGAGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2524
QY 2822 AGTTTATGCTATGCAAAACCACTGTCGACACTGACAGTTCAGGAGCGTGTGT 2881
Db 2525 TCCCTCTGCTGCGCGCGCGGCAAGCTTCCGCGTCCAGAGCGGCGGCGGCTTGGCGCGG 2584
QY 2882 TCGTCTAC 2890
Db 2585 GCGGCGAC 2593

RESULT 7
US-10-425-114-30583
Sequence 30583, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 30583
LENGTH: 2533
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73041B04_FLI
US-10-425-114-30583

Query Match 32.08; Score 1015.4; DB 8; Length 2533;
Best Local Similarity 68.7%; Pred. No. 3.2e-281;
Matches 1413; Conservative 0; Mismatches 641; Indels 3; Gaps 1;
QY 794 GTTTTGGACTTGTCTTCAATCAAGTACGATGATGATGATGATGATGATGATGATGATGATG 853
Db 48 GTTGGGATTTGTCTTCAACCGCTTACTGACCAATCCCATTCACATGATGATGATGATGATG 107
QY 854 CAAGTTGCAACATTTATCATTTGCAAGGCAATCACTCTGCGAAGATTCATCATGATGAT 913
Db 108 CAAGTTGCAACATTTATCATTTGCAAGGCAATCACTCTGCGAAGATTCATCATGATGATG 167
QY 914 GGTCTCATGCAAGCCCTTGAAGTCTTGAATGATGATGATGATGATGATGATGATGATGATG 973
Db 168 GGTCTTATGCAAGCTCTGCGTGTCTTGAATGATGATGATGATGATGATGATGATGATGATG 227
QY 974 CTTCCGATTCGGAATCTTACTTCAACGAGAAATGATGATGATGATGATGATGATGATGATGATG 1033
Db 228 CATCTTATCTAGCACTTGAATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 287
QY 1034 ACTGTTCAATTCACCTGAGCTTGAAGCAATGATGATGATGATGATGATGATGATGATGATG 1093
Db 288 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 347
QY 1094 GATATATATCTACAGGCTCATATACACGAGCTTGGAGGATGATGATGATGATGATGATG 1153
Db 348 GATATATCACTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 407
QY 1154 CTGAATGTCGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1213
Db 408 CTGAATGTCGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 467

Db 108 CAAAGTGGCTACACTATCTTGCAAGGAGCAAGTTCAGTGGCCCAATTCCTTCAGTAAT 167
Qy 914 GGCTCATGGAAGCCCTTGCAAGTCTTGAATCTAGTGGCAACTGTGGAGTGAATCTAT 973
Db 168 GGGCTTAATGAGGCTCGCTGCTGATCTGAGTACCAACCAATTAATCTGGGCTATA 227
Qy 974 CCTCCGATTCGGAATCTTACTTTACCGGAAATTTGATTTTGCACAGTAACAAGCTG 1033
Db 228 CCAATCTACTAGGCACTTGACATACAGTGAAGCTGACATGCAAGGCAACAGTTA 287
Qy 1034 ACTGGTCAATTCACCTGAGCTTGGAAACATGTCAAAATCTCAATCTTGAATCTCAAT 1093
Db 288 ACTGGAATGATACCAAGCTGAGTAATATGTCACACTTCACTTACCTGAACTGAAT 347
Qy 1094 GATTAATATCTCAAGGCTCAATATACCAAGCTTGGAAAGCTTACTGACTGTGAT 1153
Db 348 GATTAATATCTCAAGGCTCAATATACCAAGCTTGGAAAGCTTACTGACTGTGAT 407
Qy 1154 CTGAATGTCGCAACAATGATCTGGAAGGACCTTATACCTGATCTGAGCTTTGACA 1213
Db 408 CTGAAGCTTGGCAATACCACTTGAAGGACCAATCTGACAACTTAAGTCAATGATG 467
Qy 1214 AATCTAAACAGCTTAAATGTTATGGAACAAGTTTATGAGCACTATACCCGAGCATTT 1273
Db 468 AATCTCAATAGCTTCAATGCTTATGGAACAAGTTTATGAGCACTATACCCGAGCATTT 527
Qy 1274 CAAAGCTAAGAAATGATGACTTATCTGTCGCAACAATATCAAGGCTCAATC 1333
Db 528 CGGAACTTGAAGCAATGACTTATTTAAATCTTCAAAATTTCAATAGGCTCAAT 587
Qy 1334 CCGGTTGAGCTATCTCGATCGATCTGATGATCAATGATCTTCTTCAACAACAGATA 1393
Db 588 CCAATGAGCTATCAAGATCAACAATTTGGAACAGTTGAGCTTATCTGTAATCATGATG 647
Qy 1394 AATGGAATCAATCTCTTCTTCTGATTTGAGCACTTCTTCAAGATGAATGAT 1453
Db 648 ACCGGTCAATTCATCATCTGATGGAACCTGAGCATCTATGAGGCTTAACTTATGAG 707
Qy 1454 AGAAATCAATTAATCTGATGATTCAGAGGCACTTGGAAATCTAAGAGATCATGGA 1513
Db 708 AAGATATATCTAGTGAATTCATCTCTGCGAGTTGATTTGAAGATGTCATGAG 767
Qy 1514 ATAGATCTTCAATAATGATATCTCTGCGCAATCTCAGAGAGCTTAAACCAATTAAG 1573
Db 768 ATGATATTAATCTAATATCAATCTGATGATCTGATCTCTCAAGAACTTGGAACTGCA 827
Qy 1574 AACAATAATTTTCTGAGACAGTGGAAATTAATTAATTAATGATGATGTTGATCTTAC 1633
Db 828 AACCTGATGTTGCTAATACTGGAACAACAATAATTAATGCTGCAATGCTCTCTGATG 887
Qy 1634 AACCTGCTCAGCTCAGCTGATTAATGATTAATTAATTAATTAATTAATTAATTAATTA 1693
Db 888 AACCTGCTCAGCTCAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 947
Qy 1694 AAGAAACAATAATTTCTCAAGATTTTCAACAGACAGCTTCAATTTGCAATCTCTGAT 1753
Db 948 ACTGACAACAACCTTCAACAGGTTTCAACAGACAGCTTCAATTTGCAATCTCTGAT 1007
Qy 1754 GGTAGTGGCTAATACTCAGCTGATGATTTCTGTCGAAGTGAAGTGAAGTGAAGTGA 1813
Db 1008 GGTATATGCTGCTGATTTATGCTGCTCACTGCAACGAGCAACGAGCCCAATTTCA 1067
Qy 1814 AGAGCAGCTATTTCTGGAATAGCTATTTGGGGGACTTGGATCTTCTCATGAGTCTTAATA 1873
Db 1068 AAGGCTGCTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
Qy 1874 GCAAGCTTGGCAAGCAGCAATTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1933
Db 1128 GCTGATGAGGAGGAGCAACATTCACCTGCTTTTAAAGTGCACATGTAAGAACAGCTG 1187
Qy 1934 ACTTATTCGACAGGAGCTGCTATCTTATATGAACATGAGCACTTCAGCTTATGAG 1993
Db 1188 AGCAATGCTCAACCAAGCTGCTGATCTTCTATATGAACATGAGCTTCTTCTTCTGAT 1247

Qy 1994 GATATCATGGAATGACAGAGAAATTAAGTGAAGATATCATTTGGGACGAGCATCA 2053
Db 1248 GATATTAATGAGATGACTGAGAACTTGAATGAGAAATATCACTTGGATACGGGACATCA 1307
Qy 2054 AGCACTGATATCAAAATGCTGTTTGAAGAAATTTGAACCGGTTGCAATTAAGCGCTTTAC 2113
Db 1308 AGTACAGTTTATTAATATGTTTCTTAAAGAAATTCGAACCAAGTGGCAATTAAGAAAGCTGAT 1367
Qy 2114 TCTCAACAACCCACAGTCAATGAAACAGTTTGAACCAAGAACTGAGATGCTAATGATCATC 2173
Db 1368 GCCACATCAACCTTGAAGGCTTAAAGAAATGAAACAGAGCTGCAAGCTGTTGATGATC 1427
Qy 2174 AAGCAGAAATCTGAGGCTTACAGCTTATTTCCCTCTGATCTGAGGAGTCTTCTG 2233
Db 1428 AAGCAGGAAATTAATGATGAGCTTCAAGGATCTGCTGATGATGATGATGATGATGAT 1487
Qy 2234 TCTATGACTATTTGGAATGAGGCTTCTGAGATCTTCTGAT--GGCCCTACGAG 2290
Db 1488 TTTATGATTAATATGAGAGTGGAGCTTATGGAGTGTATGATGATGATGATGATGATGAT 1547
Qy 2291 AAAAAAGCTTGAATTTGGGACACAGGCTTAAATAGATATGATGATGATGATGATGATGAT 2350
Db 1548 AAGAAACAATTAATGATGAGCTGAGCTGCTGATGAGATGCTGCTGATGATGATGATGAT 1607
Qy 2351 GCTTATCTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2410
Db 1608 GCTTACCTTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1667
Qy 2411 ATTCTCTGGAACAAGCTTGAAGGCTGTTGATGATGATGATGATGATGATGATGATGAT 2470
Db 1668 ATACTCTGCAACAAGCTTATGAGGCTTATGAGGCTTATGAGGCTTATGAGGCTTATGAG 1727
Qy 2471 TGTGTGCAAGTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2530
Db 1728 TGTGTGCAAGTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1787
Qy 2531 GAGTATGCTGCACTTCAAGGCTCACTGAGAAATCCGATGATGATGATGATGATGATGATGAT 2590
Db 1788 GAGTATGCTGCACTTCAAGGCTCACTGAGAAATCCGATGATGATGATGATGATGATGATGAT 1847
Qy 2591 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2650
Db 1848 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1907
Qy 2651 ATATGTCGAAGAGGAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2710
Db 1908 ATCTATGCAAGAGGAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1967
Qy 2711 ACCTGTAAGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2770
Db 1968 ACCTGTAAGATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2027
Qy 2771 AGACAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2830
Db 2028 CCGGAGGCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2087
Qy 2831 CTATCGGAACAACACC 2847
Db 2088 AACCCGAGCCGCC 2104

RESULT 9

US-10-425-114-10637
; Sequence 10637, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei

1 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
2 OF INVENTION: Plants and Uses Thereof for Plant Improvement
3 FILE REFERENCE: 38-21(5313)B
4 CURRENT APPLICATION NUMBER: US/10/425,114
5 CURRENT FILING DATE: 2003-04-28
6 NUMBER OF SEQ ID NOS: 73128
7 SEQ ID NO 10637
8 LENGTH: 1872
9 TYPE: DNA
10 ORGANISM: Glycine max
11 FEATURE:
12 OTHER INFORMATION: Clone ID: 700954473_FLI
13 US-10-425-114-10637

Query Match 31.4%; Score 995.8; DB 8; Length 1872;
Best Local Similarity 73.98; Pred. No. 1.2e-275;
Matches 1283; Conservative 0; Mismatches 437; Indels 15; Gaps 1;

1286 AGTATGACTTACCTTAATCTGTCAGACACATATCAAGTCCATCCCGTTGAGCTA 1345
2 AGCATGACCTCTTGAACTCTTCTCCACAACTTCAGGCGCAATTCATTAAGACTG 61
1346 TCTGTATCGGTAAGTATGATGATCTTCCAAACAAGATMAATGATATCAT 1405
62 TCGCGGATGGCAATTTGGATGATGATGATTTCAAAACATTAAGTTGGTTCATC 121
1406 CCTTCTTCCCTTGGTATTTGGAGCATCTTCTCAAGATGAATTTGAGTAAATCATATA 1465
122 CCTTCTTCCCTTGGTATTTGGAGCAATCTTCTGAAGTTGAATCTAAGCAGAAACAATTTA 181
1466 ACTGTGTAGTTCAGGCGCACTTTGGAAATCTAAGAAAGCATCATGGAATATAGATCTTTCA 1525
182 ACGAGATTAATTCACAGCAAGATTTGGAAATCTTGAAGTGTATGAAATTTGATCTTTTCA 241
1526 AATTAATGATATCTGTGCGCCCAATTCAGAAAGCTTAACCAATTAACGAATATTTTG 1585
242 AATTAATCACTCTGTGGCTGATTCCTGATGAACTTAAGTACAGCTTCAAACATGATATCC 301
1586 CTGAGACTGGAAATTAATTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1645
302 TTGAGACTTGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 361
1646 CTGACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1705
362 CTCTCTCTACTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
1706 TTCTCAAGATTTTACACAGACAGCTTCATTTGCAATCTGATCTTTGCGGTAGTGGCTA 1765
422 TTACCAAGGTTTCCCTGACATTTGATGAAACCTGTGCTTTGTGTGATTTGGCTG 481
1766 AACTCACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1825
482 AATTTCCCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
1826 CTGGAATAGCTAATTTGGGGGACTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1885
542 CTGGAATTAATCTTTGGTCCCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
1886 CCGCATTAATCTCTCTCTTTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1945
602 CCGCATATGCTCTCTCTCTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
1946 CCGAAGCTGCTATCTCTTCAATGAAATGCACTGCACTGTTAAGAGATATATGAGA 2005
662 CCAAACTGTGATTTCTTCAATGAAATGCACTGCACTGTTAAGAGATATATGAGA 721
2006 ATGACAGAGATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2065
722 ATGACAGAGATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 781
2066 AATGTGTGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2125
782 AATGTGTGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841

QY 2126 CAGTCATGAAACAGTTTGAACAGAACTGAGATGCTAAGTAGATCAAGCAGAGAAAT 2185
DB 842 CAATGATTAAGAAATTTGAACAGTGAATCTGAGACGTTGGCAGCATCAAGCAGAGAAAT 901
QY 2186 CTGTGAGCCTTACAGATTAATTTCCCTCTCTCACTTGGGAGTCTTGTCTTAATGATAT 2245
DB 902 CTGTGAGTCTCAAGATTAATTTCTTGTCCCATATGGGATCTCTGTTTATGATAC 961
QY 2246 TTGGAATATGATGCTCTGGGATCTTCTTCAATGAGCCCTTACGAAGAAAGAACTTTGAT 2305
DB 962 ATGGAATATGAGCAGTCTATGGGATCTTCTTCAATGAGCCTTACGAAGAAAGAAAGCTTTGAC 1021
QY 2306 TGGGACACACCGGTTAAGATAGATATGGGAGCAGCAAGGTTTACTTATCTACACCAT 2365
DB 1022 TGGGACCTGCTTAAATATAGCACTTGAAGCAGCAAGGCTTCTTATCTACACCAT 1081
QY 2366 GACTGTATGTCAGATGATCAATTCACAGAGACGTGAAGTCTTCAACATTTCTTGGACAA 2425
DB 1082 GATTGCTGCTTGAATCAATTCACAGAGATGTAATCAATCTAATCTTATTTGATGCA 1141
QY 2426 GACTTGAAGCTGCTTGAAGATTTTGAATGCAAGAAAGCTTGTGTGTCAAAGTCA 2485
DB 1142 GACTTGAAGCTGCTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGAAGATTTTGA 1201
QY 2486 CATACCTCAATCAATGATGATGAGGACAGATAGATTAATGATGATGATGATGATGATGATGAT 2545
DB 1202 CATACCTCAATCAATGATGATGAGGACAGATAGATTAATGATGATGATGATGATGATGATGAT 1261
QY 2546 TCAGGCTCACTGAGAAATCCGATGCTTCAAGTATGATGATGATGATGATGATGATGATGATGAT 2605
DB 1262 TCAGGCTCACTGAGAAATCCGATGCTTCAAGTATGATGATGATGATGATGATGATGATGATGAT 1321
QY 2606 ACCGGAAGAAAGCCTTGAATGCAATTCATTCACATCTGATTAATGTCAAAGAGC 2665
DB 1322 ACTGGAAGAAAGCCTTGAATGCAATTCATTCACATCTGATTAATGTCAAAGAGC 1381
QY 2666 GGGAAATGAGTGTATGGAATATGCAATTCATTCACATCTGATTAATGTCAAAGAGC 2725
DB 1382 GCAACCAATGAGTGTATGGAATATGCAATTCATTCACATCTGATTAATGTCAAAGAGC 1441
QY 2726 GGTGTGTGAAGAAATTTTCCAACTGAGCATCTTCAATGCAAGAAAGAGCAGCAATGAT 2785
DB 1442 GAGGCTGTAAAGAAATTTTCCAACTGAGCATCTTCAATGCAAGAAAGAGCAGCAATGAT 1501
QY 2786 GAGGCTGTAAAGAAATTTTCCAACTGAGCATCTTCAATGCAAGAAAGAGCAGCAATGAT 2835
DB 1502 AGGCGAATGAGCAGAGTGAACAGTGTACTGGAAGCCTTGTGTCAAACACCCCA 1561
QY 2836 -----GGAACCAACCTGCTGAGATGACAGTCAAGCAGCAGTGTGCTGTAC 2890
DB 1562 CCAAAAGCAATGAGTGTGACATCACTGCTTCAATGCAAGAAAGAGCAGCAATGAT 1621
QY 2891 GTGAT 2950
DB 1622 GTGAT 1681
QY 2951 TGTGAT 3005
DB 1682 TGTGAT 1736

RESULT 10
US-10-437-963-21341/c
; Sequence 21341, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 21341
LENGTH: 3115
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_26620C.1
US-10-437-963-21341

Query Match 31.1%; Score 986.6; DB 8; Length 3115;
Best Local Similarity 64.9%; Pred. No. 7,76-273;
Matches 1630; Conservative 0; Mismatches 724; Indels 159; Gaps 5;

510 TGAATCTGAAGAATTAACCAATGTATAGACCGATCCCTCAACACTTTCCACAGATTCCAA 569
2760 TGATATTGAAGAAACACCAACTGATCGAGTATCCATCAACCTCTCACAGCTCCCAA 2701
570 ACCTGAAAATTTCTGACTTGGCAGAGATAAATCACTGAGTGAATACCAAGATTATTT 629
2700 ATTGAAGATTGTTGACTTGGCAGAGATAAATCACTGAGTGAATACCAAGATTATTT 2641
630 ACTGGAATGAAGTTCTTCAATCTTGGGTTGCGAGAAACACTTGTGCTGAATTT 689
2640 ATTGGAACGAGGTTCTTCAATCTTGGGTTGCGAGAAATTAATTTGAAGGCGAGACTT 2581
690 CTCGAGATTGTCGACTGACTGATCTTGGTATTTTGAAGTGAAGAAACAGATTGA 749
2580 CCCGAGTATATGCGACTGATGCTGCTTGGT----- 2547
750 CTGCTAGTATACCTGAGACGATAGAAAATTGCACTGCTTCCAGTTTGGACTTGTCT 809
2546 -----CTTGGATTGCTT 2533
810 ACAATCAGCTTACCTGTGAGATCCCTTTTGAATCGGCTTCTGCAAGTTCGCAATAT 869
2532 ACAATAAATCTTCTGATCAATTCCTTTCAACATTTGTTCTTCAAGGTCATACACTAT 2473
870 CATTGCAAGCAATCACTCTCTGGAAGATTCCATCAGTATGTTGCTCATCAAGCC 929
2472 CTTTGCAGGAGACATGTTTACTGCTCTATTCATCAATGTTATGACTTATGAGGCTC 2413
930 TTGCACTCTTATAGATCTAAGTGGCAACTGTTGAGTGAATCTATTCCTCCGATTCGAAA 989
2412 TCCTGTATGAGATCTGAGTTACCAACCAATTTGCTGCTCATTCATCGATCTAGGCA 2353
990 ATCTTACTTTACCGAATAATTGTAATTTGCAAGTAACAAGCTGACTGTTCATTTCCAC 1049
2352 ATTAAATATCACTGAGAAAGCTGTATATGCAAGGCAATTAAGTTAAAGGTCATTAAC 2293
1050 CTGAGCTTGGAAAATCATCTCAAAAATCTCATTTACTGAACTCAATGATATCATCTCAGG 1109
2292 CTGAGCTTGGAAAATCATCTCAACCTTCATTTACTGAACTTAAAGATTAATCAATTAGCG 2233
1110 GTCATATACCAACGAGACTTGGAAAGCTTACTGACTGTTGATCTGAATGTGCCACA 1169
2232 GGTTCATTTCTCCCGAGATTCGGAAGCTTAACAGGGTATTTGACTTAAACCTTCAACA 2173
1170 ATGATCTGGAAGGCTTATCTGATCATCTGAGACTCTTGCACAAATCTAAAGCTTAA 1229
2172 ACAACTTTGAAGGCTCAATCCCTGATTAACATTAAGCTATGTGAATCTCAATAGCTTCA 2113
1230 ATGTTCAATGGAACAAGTTTATGAGCACTATACCCGAGCAATTTCAAAAGCTAAGAAAGTA 1289
2112 ATGTTTATGCGCAACAGTTAAATGAGCAATCTCTCTCATTTGCAATTAATCTTGAAGCA 2053
1290 TGACTTACTTAAATCTGTCCAGCAACATATCAAAAGTCCAAATCCCGGTTGAGCTATCTC 1349

2052 TGACTTATTTGAATTTGTCTATCAAAATTTTCTAAGTGGTTCATCTATGAGCTATCGA 1993
1350 GTATCGCTACTAGATATGATGATGATCTTCCAAACAAGATAAATGAAATATTCCTT 1409
1992 GAATCAACAATTTGGACACCTTT----- 1970
1410 CTTCCTTGGTGAATTTGAGACATCTTCTCAAGATGAATGAACTGATAGAAATCATATACTG 1469
1969 -----AACTTGACCAACAATGCTAGTAG 1945
1470 GTGTAGTTCCAGCGACTTTGGAATCTAAGAATCATGAAATGATCTTCAATA 1529
1944 GATTCATTTCTCGAGAAATTTGGCAACTGAGGAGTATCAAGGAGATGAATATGTCACA 1885
1530 ATGATATCTCGGCCCAATTTCCAGAAAGGCTTAACCAATATACGAAATTAATTTTGCTGA 1589
1884 ATCATCTTGGCGGTTGATTTCTTCAAGAACTCGGAATCTGCAAAATCTGATGTTTAA 1825
1590 GACTGAAAATTAATACTGACTGTATATGTTGTTTATTAGCCAACTGTCTCAGTCTCA 1649
1824 ATCTCAAAAACAACATTAATCTGGGATGTCCTTCACTGATGAATGCTTCAGGCTCA 1765
1650 CTGTATTGAATGATCTCATTAACAACCTGCTAGGTATCTCTTAAGAACATTAATCTTCT 1709
1764 ATATCTTAAATGTATCTATTAATAATTTGGCTGTGTTGACTTACTGATTAACAATCTTCT 1705
1710 CAAGATTTTACACAGACAGCTTATTTGCAATCTGCTGTTGCGGATGTTGCTAACT 1769
1704 CAGGTTTTCCTGACAGCTTTTGGGATATCAGAGACTTTGATATTTGCTGTTGTT 1645
1770 CACGCTGCTCATGATCTCTGTCGAACCTGTACAGTGTCAATCTTACAGCAGTAATCTT 1829
1644 CTTCGTCGCTTATGCTGCGCATCAACAGAAACCACTAATCTAAAGGCTGCAATCTT 1585
1830 GAATAGCTATTTGGGAGACTGTGATCTCTCATGCTTAAATAGCAGCTTGGCCAGCCG 1889
1584 GAAATGCGGAGGAGGCTGTATCTCTGATGATCTTGAAGGAGCTGGAAGGCTC 1525
1890 ATATCTCTCTCTCTTCTTCTGATGATCACTTACAAACAGTAATCTTATTCACACCA 1949
1524 ATATGCTCACTGTTTTCAAAGATGTCCTGTAGCAAAACAGTAGAGCAATGTTCCCCCA 1465
1950 AGCTGCTCATCTTCAATGATGAACATGCACTCCACGTTTACGAGATATCATGAGATGA 2009
1464 AGCTGTTATCTTCAATGATGAACCTTCCCTTCTTGTATGCGAGATATATATGACATGA 1405
2010 CAGAGATCTTAAGTGAAGATATATCATTTGGGACGAGATCAAGCATCTGTATACAAAT 2069
1404 CTGAAAACCTGAGTGAAGATATCATTTGGGATAGCGAGCATCCAGACGCTTATTAAT 1345
2070 GTGTTTGAAGATTTGAACCGGTTGCCATTTAAGCGGCTTATCTCTCACACCCAGT 2129
1344 GTGTTTGAAGAACCGCAACAGTGGCAGTAAAAAAGCTATATGCCCCACTATCCACAGA 1285
2130 CAATGAAAACGTTTGAACAGAACTCGAGATGCTAATGATCATGACACAGAAATCTTG 2189
1284 GCTTCAAGGAATTTGAACCTGAGCTTGAAGCTTGGTATGATCAACACCGGAATCTAG 1225
2190 TGAGCTTACAAAGCTTATCTCTCTCTCACTTGGGAGCTCTTCTGTTCTATGACTATTTGG 2249
1224 TCAGTCTTCAAGATATTTCCCTATCTCTGTTGGAATCTTCTCTTATGATTAACATGG 1165
2250 AAATGCTAGCTCTGAGGATCTTCTTCAAT---GGCCCTACGAGAAAAGACTCTTGAT 2306
1164 AAATGAGACCTCTGAGGATGTTTGTGATGAAGTCCAACTAAGAAAGAAAACCTTGAT 1105
2307 GGAACACAGGCTTAAAGATATGATATGCTGACACACAGGTTTATGCTTATCTACACATG 2366
1104 GGGAACTGCTTACGAATGTCTAGTGGGCGCCCAAGGCTTGTATCTTATCATCATG 1045
2367 ACTGTACTCCAAAGATCATTTACAGAGAGCTGAAGTGTCTCAACATTTCTTGGACAAAG 2426

Db 1044 ACTGTACCCACGAGTAAATACAGAGGATGTGAATCAAAAATATATCTCTTGATAAG 985
 Qy 2427 ACTTAGAGGCTCGTTTGAACAGATTTTGAATAGGAAAAGCTGTGTGTAAGTAC 2486
 Db 984 ATTATGAGGACATCTTACAGACTTTGGCAATGTGCAAGAGTTGTGTTCAAAAATC 925
 Qy 2487 ATTCTTCACTTACGTATGGGCAAGTAGGTTTATATAGACCCCGAGTATGCTGGACT 2546
 Db 924 ACAGTCCACCTATGTATGGAACTATGTGCTATATGACCTGAGATGTGCTGCACT 865
 Qy 2547 CACGCTCACTGAGAAATCCGATGTCTACATTAAGAAATAGTCTTCTTGAATGTTAA 2606
 Db 864 CCGTCTCATGAAATGATGTCTATGATCTATGAGCTATGCTATGCTGTGAGCTGCA 805
 Qy 2607 CCGAAGAAAGCCGTGTGATGACGATTCATCTCCACCATCTGATATATGTAAGACGG 2666
 Db 804 CCGGAAAAAGCCGTGTGACAAACGAGTGCATCTCCATCTTGTCTTCAAAAGACGG 745
 Qy 2667 GGAACAATGAAGTATGGAATGGCAGATCCAGATCCAGATCGACGCTGTAAGATCTCG 2726
 Db 744 CTATCAATGCTGTCTATGAGACAGTCCAGCCGACATTTGACAGACTTGGCAAGATCTTG 685
 Qy 2727 GTGTGTGAAGAAAGTTTTCACCTGACATCTCTATGACCAAAAGACAGCCGATGATC 2786
 Db 684 GTGAGTCAAGAAAGTGTTCAGCTGGCGCTCTTTGACCAAGACAAACATCGGATC 625
 Qy 2787 GACCCACATGACACAGGTGATCTGTGTCTGCGCAGTTTATGCTATCGGAACACAC 2846
 Db 624 GGCAGCAATGACAGAGTGTGTGCGCTGCTGAGCTCCATGATTCGCCGACCCGAC 565
 Qy 2847 CTGTGC-----GACTGACAGCTGACGAGAGCTGGCTGTGCTGCTAGCTGATG 2897
 Db 564 CGAAGTCCGACAGACACTGGCCATGCGCAGCGCCGCTGCTGCCAGCTACATCAACG 505
 Qy 2898 AGTATGCAATCTCAAGACTCTCTCATTTCTGCAATGCTC---TTCCATGAGTCTTCTG 2954
 Db 504 AGTATGCACTTATAGAGGACACGAGCGTGTCTCTGCGCAACTGCTGTGATCTTCCG 445
 Qy 2955 ATGCTCACTGTTTCTTCTGCTTGGACAGTATTTCTCAGACAGTGAAGTAG 3007
 Db 444 ATCTGTAGCTGTTCTCAAGTTTGGCAGAGCTATTTCTCAGAACACAGAGTAG 392
 RESULT 11
 US-10-425-114-7634
 ; Sequence 7634, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 7634
 ; LENGTH: 1859
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700676958_FLI
 US-10-425-114-7634
 Query Match 29.6%; Score 940.4; DB 8; Length 1859;
 Best Local Similarity 74.4%; Pred. No. 1.2e-259;
 Matches 1206; Conservative 0; Mismatches 401; Indels 15; Gaps 1;
 Qy 1399 AATCATCTCTTCTCCCTGTGTGATTTGGAGCATCTTCTCAAGATGAACCTTGAAGTAA 1458

Db 4 AAGATCCCTTCTTCCCTTGTGATCTTGAACATCTTCTGAATGATCTATAGCGAAA 63
 Qy 1459 TCATATTAAGTGTGTAGTTCAGCGCACTTGGAAATCTTAAGACATCATGAAATAGA 1518
 Db 64 CAATTTACAGAAATTAATCCACAGAAATTTGAAATCTTGAAGATGTGTGAATAGA 123
 Qy 1519 TCTTTCAATTAATATCTCTGCGCCCAATTCGAAAGAGCTTAACCAATTAAGACAT 1578
 Db 124 TCTTTCAATTAATCACTCTGCTGCTTGAATCTCTGATGAACCTTATGAGCTTCAAAAT 183
 Qy 1579 AATTTGCTGAGCTGGAATATATACTGATGTATGTGTTTCAATTAAGCACTG 1638
 Db 184 GATATCTTGAAGCTTGAATTAACAAATTTGATGCGGAGTGTGCAATCACTTCAATG 243
 Qy 1639 TCTGAGTCTGATTTGAATGTATCTTAACCACTGTGTAGTATATCTTCAAGAA 1698
 Db 244 CATTAAGCTCTCTCTTAAATGTCTTAATCAAACTATTTGTGTATCTCCAAAGAG 303
 Qy 1699 CAATTAATCTCAAGATTTTCAACAGACCTTATTTGCAATCTGTGCTTGGGTAG 1758
 Db 304 TAACTTAATCAAGGTTTCCCTGACAGTTTCAATTTGAACCTGTGCTTGTGTGTA 363
 Qy 1759 TTGGCTAACTCAACCGTGTATGATTTCTGCGAATGTATGAGATGCAATCTTGAAGC 1818
 Db 364 TTGGCTGAATTTGCGGTGATGTGTGCTGCTTCAAGACGAGTTAATATCTTAAGC 423
 Qy 1819 AGCTATTTCTGAATAGCTATTTGGGAGCTTGTGATCTTCTCATGTCTTAATAGACG 1878
 Db 424 TGCCATCTTGAATTAATCTTGTGTGCTTGTGATTTCTTATGTATTTGTGCGAGC 483
 Qy 1879 TTGCCAGCCGATATCTCTCTTCTTGAATGATCTTGAACAACTGAATCACTTA 1938
 Db 484 TTGCCAGCAATATGCTCTCTCTTCTTGAATGATCTTGAACAACTGAATTT 543
 Qy 1939 TTGCAACCGAGCTGTATCTCTTCAATGAACATGCACTGCTTACAGAGATAT 1998
 Db 544 CTCCTCCCAAGCTATGATTTCTTCAATGAATATGCACTGATATGTATGAAGTAT 603
 Qy 1999 CATGAGATGACAGAAATTAAGTGAAGATATATCTTGGCAGCAGACATCAAGAC 2058
 Db 604 CATGAGATGACAGAAATCTGAGTGAAGATATATTTGATGATGAGACATCAAGTAC 663
 Qy 2059 TGTATCAATGTGTTTGAAGATTTGAACCGGTGCGATTAAGCGCTTACTCTCA 2118
 Db 664 AGTTTAAATGTGTTTGAAGATTTGAACCGGTGCGATTAAGCGCTTACTCTCA 723
 Qy 2119 CAACCCAGCTCATGAGAAACAGTTTGAACAGAACTGAGATCTAATGACATCAAGCA 2178
 Db 724 CTATCCCAATGTATTAAGAAATTTGAACCTGAACCTTGAACCGTTGGCAGATCAAGCA 783
 Qy 2179 CAGAAATCTTGTAGACCTACAGACTTATCTCTCTCACTTGGGAGTCTTCTGTTCTA 2238
 Db 784 CCGAAATCTGTGACGCTCCAGAGTTATCTTCTGCTCCCATGAGGATCTCTGTTTGA 843
 Qy 2239 TGACTATTTGAAATGTAGCTCTGAGATCTTCTTCAATGAGCGCTTACGAAAGAAAGAC 2298
 Db 844 TGACTATGAGAAATGTAGCTCTGAGATCTTCTTCAATGAGCTTACGAAAGAAAGAA 903
 Qy 2299 TCTTATTTGGACACAGCGCTTAAGATAGATATGTGACGACCAAGGTTTACTTATCT 2358
 Db 904 GCTTGAGTGGAGCTGTGTCTTAATAATAGCACTTGGAGCAGCAAGGCGCTTGTATCT 963
 Qy 2359 AACACATGATGTATGCTCAAGATCATTTACAGAGACGTGAAGTGTCTCAACATCTCTT 2418
 Db 964 AACACATGATGTGCTCTGAATCATCCAGAGATGTGAATCATCTTAACATTTCTAT 1023
 Qy 2419 GACCAAGACTTATGAGCTGCTTGAAGATTTTGAATGAGAAAGCTGTGTGTC 2478
 Db 1024 GAGTGCAGCTTGAAGCTATCTCACTGATTTTGGCATTTGCCAAAGTCTTGGCCCTC 1083
 Qy 2479 AAGTCACTACTTCAACTTACGTATGGGACAGATAGTTATGATAGACCCGAGATATGC 2538

Db 1084 AAGTCCACTACTTCTTACATATATGGGCAATTTGGCTATATAGACCTGAGTATGC 1143
Qy 2539 TCGACTTTCACGGCTCACTGGAATATCGATATGTCTACAGTTATGGAATAGTCTTCTGA 2598
Db 1144 TAGAATCTTACAGTCTCACTGGAAGTCTGATGTGTACAGTTACGGTATTTGTTTACTTGA 1203
Qy 2599 GTTGTTAACCGGAAGAAAGCCGTTGATGACGAATCCAAATCTCCACATCTGATATATGTC 2658
Db 1204 GTTGTCTAATCGGAAGAAAGCTGTTGACAAATGATCCAACTCCACATCTGATTTTGTGTC 1263
Qy 2659 AAAGACGGGGGAACAATGATGATGGAATGCGAGATCCAGACATCTCATGAGCTGTAA 2718
Db 1264 CAAGGACGCAACCAATCAAGTATGGAACAGTTGATCCAGACATCTTCTGCAATCCAA 1323
Qy 2719 AGATCTGGTGTGTGTAAGAAAGTTTTCACACTGCTATGACCAAAAGACAGCC 2778
Db 1324 GGACTTGGAGACTTAAAGAAAGTTTATCAGCTTGTCTATATGCAAAAGGCGAGCC 1383
Qy 2779 GAATGATGACCAACCAATGCAACGAGTACCTGTTCTCGGCAAGTTTATGCTATGC --- 2835
Db 1384 AGCTGATAGGCGCAATATGCAAGATGACAGTGTACTCGGAAGCCCTGTGCTGTCAAA 1443
Qy 2836 -----GGAACAACCACTGCTGCGACTGACAGCTGACGAGCGCTGCTGTTG 2883
Db 1444 CACCCCAACCAAGCACTAGTGCATCAACCACTGCTTCAATCTGCAAAAGTGC 1503
Qy 2884 GTGCTACGTCGATGATGATGCAATCTCAAGACTCTCATCTGCTCAATTTGCTTTCAT 2943
Db 1504 ATGCTTACGTGATGATGATGCAAACTTCAGACTCCACACTTGTGTAATGCCCTCAAT 1563
Qy 2944 GAGTCTTCTGATGCTCAACTGTTCTTCCGTTTGAACAAGTTATTTCTCGAAGACGTGA 3003
Db 1564 GAGCACTCAGATGCTCAACTCTTCTCAAGTTGAGAAAGTATCTCTCAAAACAGTGA 1623
Qy 3004 GT 3005
Db 1624 GT 1625

RESULT 12

US-10-437-963-67070/C
; Sequence 67070, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; NUMBER OF SEQ. ID NOS: 204966
; SEQ. ID NO 67070
; LENGTH: 2985
; TYPE: DNA
; ORGANISM: *Oryza sativa*
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67963C.1
US-10-437-963-67070

Query Match 24.7%; Score 785.2; DB 8; Length 2985;
Best Local Similarity 60.0%; Pred. No. 1,1e-214;
Matches 1571; Conservative 0; Mismatches 853; Indels 194; Gaps 8;

Qy 438 TAGACTTATCTTCAATGATTAAGTGTGACATACCGTTTTCATTTGCAAGTTGAGC 497
Db 2771 TCGACTTGAAGTGAATGAATCTTCTGGGCAATCCCTGATGAGATTGGCGATTGCACT 2712

Qy 498 AACTGAGCAGCTGATTTCTGMAAATTAACCAATTTGATAGACCGATCCCTTCAACATT 557
Db 2711 CGCTTAAACTCTGATCTTGAAGAACACACAGCTGTGGGAGATGATCCGTCACACTCT 2652
Qy 558 CACAGATTCACAACTGAAAAATTTCTGACTTGGCACAGAAATTAACATCTGATGTGATAC 617
Db 2651 CTCAGCTAACCAAAATTTGMAATTTTGGACTTGGCTCAAAACAGCTTAAATGGTGAATTC 2592
Qy 618 CAGACTTATTTACTGGAATGAAAGTTCTTCAATCTGAGTGTGGGTTGCGAGAAACAATCTAG 677
Db 2591 CGAGTTAATCTATGGAATGAAAGTTCTTCAATCTGAGTGTGGGTTGCGAGAAACAATCTAG - 2533
Qy 678 TCGGTAACTTTCTCCAGATTTGTGTCACTGACTGTCTTTGTGATTTTGAAGTAAAG 737
Db 2532 -----GGGCAAAATAGTTCCGGGATTCAGGA 2508
Qy 738 ACAACGTTGACTGCTGATGATACCTGACAGCATAGAAATTCGACTGCTTCCAGTTT 797
Db 2507 GCAATATTTTGAAGGAAGCCCTCTCTCTGAGATGTGCCAGTTGACTGCGCTGTGTAAT 2448
Qy 798 TGGACTTGTCTCAATCACTAAGTGTGATGATCCCTTTGATGATGCGCTTCTGCAAG 857
Db 2447 TGGATCTGTCTTACACCGGCTCAAGGAGAAATCCCATTCACATTTGCTTCTTCAAG 2388
Qy 858 TTGCAACATTATGATTCGAAGGCAATCACTCTTGGGAAGATTCATCAGTATTTGTC 917
Db 2387 TGGCTATATTGTCTTTCGAAGGAAACAATTTCTGCGCCATATTCATCAGTATTTGGCC 2328
Qy 918 TCATGCAAGCCCTTGCAGTCTTATGATCTAAGTGGCAATTTGATGATCTATTTCTC 977
Db 2327 TTATGCAAGGCGCTCGAGTGTGATCTGATGTTCACCAATTTGTCTGGGCAATTCAT 2268
Qy 978 CGATTCGGAATCTTACTTTTACCGAGAAATTTGATTTGACAGATTAACAAGCTGACTG 1037
Db 2267 CAATCTTGGCAATTAATCACTGAGAACTGTACCTCTCAAGCAATAGCTTAAGT 2208
Qy 1038 GTTCAATTCACCTGAGCTTGGAAACATGTCAAACTCCATTAACCTGGAACCTAATGATA 1097
Db 2207 GATCAATACCAACCGAGCTTGTATATGTGCACTTCAATTC --- 2164
Qy 1098 ATCATCTACGGGTCAATATACCAACAGAGCTTGGAAAGCTTACTGACTTGTGATCTGA 1157
Db 2163 -----TTGA 2160
Qy 1158 ATGAGCCACAATGATCTGGAAGACCTATACCTGATCTGAGCTTTCACAATATC 1217
Db 2159 ACCTGCAACCAACACTTGAAGACCAATCCCTGATATATAGCTCATGATGAATC 2100
Qy 1218 TAAACAGCTTAAATGTTCAATGGAACAAGTTAGTGGCACTATACCCGACATTTCAA 1277
Db 2099 TCATTAAGCTTGAATCTATCAATCAAACTATCTAGTGGAGCAATTCATGAACTAGCAA 2040
Qy 1278 AGCTAAGAAATGATGACTTCAATCTGTCGACCAACATATCAAAAGTCCCAATCCGG 1337
Db 2039 AAATGAAAACTTGGACACATGTGACTTATCTGTAACATGATGTGCTGTGCAATTCCT 1980
Qy 1338 TTGAGCTATCTGATCTGATCGTAACTTATGATCTGATCTTTCACAACAACAGATTAAT 1397
Db 1979 CGGCAATTTGGAGCTTATGAGCATCTTTGAGACTAAATTTTACCAATATATATTTGGT 1920
Qy 1398 GAATCATTTCTTCTTCCCTTGTGATTTGGAGCATCTTCAAGATGAACCTGAGTAGAA 1457
Db 1919 GATACATCTCTGCTGATTTGGAACCTTGAAGAGTATCATGAGATATTCCTCT --- 1865
Qy 1458 ATCATATTAATCTGTATGTTTCCAGCGGACTTTGGAATCTTAAGACATATGAAAAATAG 1517
Db 1864 -----CCTCTGTTTATAGT 1851
Qy 1518 ATCTTCAATTAATGATCTGTGCCAATTCAGAGAGCTTAAACAATTAACAGACA 1577
Db 1850 ATTGTCTAATATCACTTGTGTGTTGATTTCCACAGAGTTGGCAGTCTCAAAAC 1791

QY	1578	TAATTTTGTGAGACTGGAAAAATATAACGACAGCTGTAATGTTGGTCTATTAGCAACT	1637
Db	1790	TGATATGTCTAAACGTGGAAGATAATATAACGGGGAAGTTCCTTCACTTAATTAAC	1731
QY	1638	GTCACGTCTCACTGATATTTGAATGTATCTCATTAACAACCTCGTAGGTATATCCCTAGA	1697
Db	1730	GCTTAGGTCTCAATGTCTTTAAACGATATCATACAAACACTGGCTGGCAATTGTACCAACG	1671
QY	1698	ACAATAACTTCTCAAGATTTTCCACGACAGCTTCATTGGCAATCTGTGTCTTTGCGGTA	1757
Db	1670	ACAAATAATTTTTCACGATTTTCCACGGCAGGCTCTTGGGTATATCTGGACTGTGGCT	1611
QY	1758	GTGGCTTAACCTACCCGTGTATGATTTCTGTGCAACGTGTACAGTGTCAATCTCTAAG	1817
Db	1610	ATTGGCTGTGTTCTTCGTGCTACTCCACAGTCATGTGCAAGATCCCTGTCTCAAGGT	1551
QY	1818	CAGCAATTTCTTGGAAATAGCTATATGGGGGACTTGTATCTTCTCATGGCTTAATAGAG	1877
Db	1550	CTGCATTTCTGGGATTTGTGTAGCTGGGCTGTGTATCTCTGTGATGATCTTACGTCTG	1491
QY	1878	CTTGGCCGACCGCATATCTCTCCCTCTTTCCTTGATGATATCACTTGACAACAGTAATTT	1937
Db	1490	CTTGTGGGCACACCTGGGCAACAAGTTCACCAAGATGTCTTTAAGCAACACAGATACC	1431
QY	1938	ATTGCACACCG-----AACTGTCATCTTCAATATGAACATGCA	1978
Db	1430	ATGCACCTACCAATCAAGTATGTTGCTCTCCAAAGCTTGTATATCTTCAATGAACATGCA	1371
QY	1979	CTCCACGTTTACGAGGATATATGAGGATGTGACAGGAATCTTAATGATGAATATATCATTT	2038
Db	1370	TTCTCTGTGACGAATATATATGAGATGACTGAAATTTGAGGGAACAACTACATTAATC	1311
QY	2039	GGGACGAGAGATCAAGACCTGTATACAAATGTGTTTGAAGAAATTTGAAACCGGTGCG	2098
Db	1310	GGGATATGGGCATCAAGACAGTGTACAAATGTGTACTGAAGAACTGCAACCGGTGTCA	1251
QY	2099	ATTAAAGCGGCTTTACTCTCACACCCACAGTCATGAAGAAACAGTTGAAACGAATCTGAG	2158
Db	1250	ATAAAAAATTTGTATGTCTCACTACCCACAGAGCTGAAGGAATTCGAGACTGACGTTGAG	1191
QY	2159	ATGCTAATAGATCAACACACGAAGATTTGTGAGCCCTACAAAGCTTATTCCTCTCTCAC	2218
Db	1190	ACTGTGGAAGATATCAACACCGGATCTTGTACGCTTCAAGGTAATTCCTATCACT	1131
QY	2219	TTGGGAGTCTTCTGTTCTATGACATATTTGGAATGTGTAGCTCTTGGGATCTTCTTAT	2278
Db	1130	GCTGGGAATCTTCTCTTCTTACGACTACTTGGAAAATGCAAGTCTCTGGGATGTTTACAT	1071
QY	2279	---GGCCCTACGAAAGAAAAAGACTTGTATTGGGACACACGGCTTAAAGTACATATGT	2335
Db	1070	GCAGGCTCATCCAAAGAACAAATAAGATTGGGAGGTGAAGCTCCGGATTTGCTTGTGT	1011
QY	2336	GCAGCACAAAGTTTAGCTTATCTACACATGACTGTAGTCCAGAGTATTC-ACAGAGA	2394
Db	1010	GCGGACAAAGCTGTGGCTTATCTTCATCATGACTGCAACCCACGGATTAATCAATAGGGA	951
QY	2395	CGTGAAGTCGTCAACATTCCTTGGACAAGAAAGCTTAAGGCTGTGGAACAATTTGG	2454
Db	950	TGTGAAGTCGAAGATATTCCTTCTAGACAAGGACTATTAAGCAACATCTTGGCAGCTTGG	891
QY	2455	AATAGCGAAAAGCTTGTGTGTGTCAAAGTCAATCTTCAACTTACAGTATGGGACGAT	2514
Db	890	TATTCGCAAGAGCTTGTGCACCTCAAAACACACACATCAACCTATGTGATGGGATCAT	831
QY	2515	AGGTTACATAGACCCCGAGTATGCTGCACCTTACCGGCTCACTGAGAAATCCGATGTCTA	2574
Db	830	AGGCTACATTTGACCTGTAGTACGATGCAATCCCGCTCAACGGAATGCGATGTCTA	771
QY	2575	CAGTTATGAATATGCTTCTTGAATGTATTAACCCGAAAGAAAGCCGTATATGACGATC	2634
Db	770	CAGCTATGACATTTGCTCTCTGGAAGTCTTACAGGCAAAAAGCCAGTGCATATGAGTG	711
QY	2635	CAATCTCCACATCTGATATGTCAAGACGGGGAACATGATGATGAAATGGCAGA	2694

Db	710	CAATCTCCATCTATTGATTCCTATCCAAAGCCGACAGACAACGGGTCAATGGAGATGGTCGA	651
Oy	2695	TCCAGACATCATCGACGATGTAAAGATCTCGGTGTGGTGAAGAAATTTTCCAACTGGC	2754
Db	650	CCCGAGATCTGCCGATACGTGTCAAAAGATCTTTGGCGAGGTCAAGAAAGGTGTTCCAGTTGGC	591
Oy	2755	ACTGCTTATGCAACCAAAAGACAGCCGAATGTATCGAACCAATGCAACGAGTACGTGT	2814
Db	590	GCTGCTTTTGACGACGAAGGAGCGCTTGTGATTCGACCGACGATGACGAGGTGCGGTGT	531
Oy	2815	TCCTGGCAGTTTATGCTATCGA-----ACAACCACTGTCTGCGACTGACACGTC	2865
Db	530	CTGTGAGCTGCTGTGTATACCCCGACCCGCCCTCAAAAGCCGGCACTGCGACCGGATTTGCC	471
Oy	2866	AGCGACCGCTGGCTGTTGTGTGCTACGTCGATGAGTATGCAAAATTCAAAGACTCTCATTC	2925
Db	470	ACAGTGTGTCACCGGTTCCGAGCTATGTCAACGAGTACGTGAGCTTACGAGCGCGACAC	411
Oy	2926	TGTCAAATTG---CTCTTTCATGAGTGTCTTGATGCTCAACTGTTTCTTGCGTTTGACA	2982
Db	410	GCTCTCTCGTGAATAATTGTCGACGCGGTGAGATGCGGAGGCTCTTCTGAAATTCGGCGA	351
Oy	2983	AGTATTTTTCGAACAGTGAAGTATGTTTTCGTTAGGA	3020
Db	350	GGTGAATATCACAGAAACAGAGTGAAGTGAATATCTTA	313

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RESULT 13
US-10-425-114-31616
; Sequence 31616, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31616
; LENGTH: 2523
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73195H08_F11
US-10-425-114-31616

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	Query Match	Similarity	Score	DB	Length
	Best Local Match	62.4%	758.6	8	2523
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Db	2	AATGAGCTGATGTGGCAAAATTCCTGAGTATTTGGCTCATGACGGCTTGCTGCTCTA	61		
Qy	941	GATCTAAGTGCCAACTTGTTGAGTGATCTATTCTCTCGATTCTCGGAAATCTTACTTTC	1000		
Db	62	GACCTTGTAGTAGAATGAACTGGTGGGGCCATTCCTCTTATCTTGGCAACTGCTCTAC	121		
Qy	1001	ACCGAGAAATTTGATTTGGCAGATGAACAGCTGACTGGTCAATTTCCACCTGAGCTTGA	1060		
Db	122	ACAGGCAAACTCTATTTCATGTCGCAAAACTCACTGCAATATACCAACAGAACTGGG	181		
Qy	1061	AACATGTCAAACTCCATTAACCTGGAACTGAATGATATATCATCTCACGGGTATATACCA	1120		
Db	182	AACATGTGTAACCTTACCTACTCTGACGCTGAATAGACATATAAATTAGTGGGCACATCCCA	241		

QY 1121 CAAAGCTTGGGAAGCTTACTGACTGTGTTGATGTAATGAGCAACAATGATCTGGAA 1180
DB 242 GCTGAGCTTGGCAAACTCAGAGAGTATTGTAATGTAATCTTGCAACAATCTTGAG 301
QY 1181 GGACCTTATCTGATCTGAGCTCTTGCAACAATCTAAACACTTAAATGTTCAATGG 1240
DB 302 GGGCATATCCCTGGAAACATCAGCTCTTGACAGTCAAGCAAAATTCATGTTATGGC 361
QY 1241 AACAAAGTTAGTGGCACTATACCCCGAGCATTTCAAAAGTAGAAGATGACTTACCTT 1300
DB 362 AATGAGCTGATGAGCTCTATCTCTGCTGTTTCCAGAACTGGAGAGTTGACATACCTA 421
QY 1301 AATCTGTCAGCAACAATATCAAAAGTCCATCCCGTTGAGTATCTCGTATCGGTAC 1360
DB 422 AACCTTCTTCAAAAGCTTCAAGGCCAGATCCCTGAGCTTGTCACATATGTCAC 481
QY 1361 TTGATATCATTTGATCTTTTCCAAACAAGTAAATGGAATCATCTCTTCTCCCTGGT 1420
DB 482 TTGGACACACTAGATCTTCTTACAAATGTAATCTCCGGGCCAGTTCTCTTACTATGGT 541
QY 1421 GATTGGAGCATCTTCTCAAGATGAACCTGAGTAGAATCATATTAAGCTGTTAGTTCCA 1480
DB 542 GATTCAGACATCTTCTTGAATTAATTTGATGTAATCAATCTCACTGATCTGTGCT 601
QY 1481 GCGCACTTTGGAAATCTAAGAGCATGAGAAATAGATCTTCAAAATATGATATCTCT 1540
DB 602 GCTGAATTTGGAACTTGAGAAAGTGTCCAGATGATGACATGTCAGCAACAACCTGTCT 661
QY 1541 GGGCAATTTCCAGAAAGCTTAAACCAATTAAGAAATATTTTGTGAGCTGAGAAAT 1600
DB 662 GGGTACCTCCCTGAGAAAGCTTGACAGCTGCAAAACCTGATGACCTGATCTTAAACAC 721
QY 1601 AATAACCTGACTGCTTAATGT---TGTTTATTAGCCAACTGCTCAGTCTCATGATTTG 1657
DB 722 AACGTTTGGTGGGAGATCCCTGCTCAGTGGCTAACTCTCAGTTTATGAGCTTA 781
QY 1658 AATGATCTCAATCAACCTCTGATGATATCCCTAAGAAACAATCTTCAAGATTT 1717
DB 782 AACCTGTCATCAACAACCTCTGAGGCACTCCGTCATGAAACCTTCTCAAGATTC 841
QY 1718 TCACCAACAGCTTCAATTTGGCAATCCGTGTTTGGCGTATGTTGGCTAAATCCAGCT 1777
DB 842 CCAATGAGAGCTTCAATGGGTAATCTGATGCTCATGTAATCCCAAGATCCAGCTGT 901
QY 1778 CATGATTTCTGTCGATGATCTGAGTGAATCTCTAGAGAGCTATTTCTTGAATAGCT 1837
DB 902 GGACATTTCTATGAAAC---CAAAGTTAGCATCTCTGAGAGCGGCTTGCTGCAT---G 955
QY 1838 ATTGGGGAGCTTGTGATCTTCTCATGATCTTAAATAGACGCTTCCGACCGCATATCTT 1897
DB 956 ATCTTAGGCTTCGATATGCTCTGTCATCGTCTGGGATATACAAAGCAACAG 1015
QY 1898 CTTCTCTTTCTTGAATGATCTGTAACAACCAATTAATTTGACACCGAAGCTGTC 1957
DB 1016 CCAAGCTTACCTGAAAGCACTCCGACAAAGCAAT---GCAAGGCCACCAAACTGCTG 1072
QY 1958 ATCTTATATGAACATGAGCACTCCAGCTTACAGAGTATCATGAGATGACAGAAAT 2017
DB 1073 GTTCTTCAATGATGATGAGCCGCTGACACGATGACAGATCATGAGGCTGACGAGAAC 1132
QY 2018 CTAAATGAGAAATATATGATTTGGCAGAGCATCAAGCACTGTATCAAAATGTTGTTT 2077
DB 1133 CTGAGCGAAGAAATCATCATGATGATGAGCGCGCTGAGACCGGTATCAGGTGAGCTTC 1192
QY 2078 AAGAAATGTAAACGGGTGGATTAAGCGGCTTACTCTCAACCAAGCTCATATGAAA 2137
DB 1193 AAGAGCGGCAAGGCGATGCGGTAAAGGCGCTTACAGCCGTAAACCAAGCCTCCGG 1252
QY 2138 CAGTTTGAACAGAACTGAGATCTAATAGATCAAGCAGAGAAATCTTGTAGCCTTA 2197
DB 1253 GAGTTTGAGAGCGAGCTGAGAGATGCGGACGATCCGGGCAAGAACTCTGTAGCCTTC 1312
QY 2198 CAAGCTTATCTCTCTCACTTGGGAGTCTTCTGTTTATGATATTTGGAAATAGT 2257

DB 1313 CACGCTTCTCGCTCTCTCCCTCACGGGAACCTGCTTCTACACATACATGAGAAACGGC 1372
QY 2258 AGCCTCGGAGATCTTCTTCAATGAGCCCTAAGAAAGAAAGCTTGAATTTGGACACACGG 2317
DB 1373 TCCCTGTGGATCTTCTTCAATGAGCCGCTGAGAAAGGTGAAGCTGATGGACACAGAG 1432
QY 2318 CTTAAGATAGCATATGATGAGCAGCAAGAGTTTATGATATACACATGACTGATGCA 2377
DB 1433 CTGAGATTCGACATGAGGCGCGCGGAGGGGCTGGCGTACTCCACACAGCTCAACCCG 1492
QY 2378 AGGATCATTTACAGAGACGTGAAGTGTCTCAACATTTCTTTGCAAAAGCTTATGAGGCT 2437
DB 1493 CGCATCTGACCGGAGCGTCAAGTCTCTCAACATCTGCTGAGACGGCACCTTCGAGGCG 1552
QY 2438 CGTTTGCAGATTTTGGATAGGAAAGAGTTGTTGTTGTCAAAGTCAATATCTTCACT 2497
DB 1553 CACCTGTCCGACTTCGACATGCGCAAGTGTGTCGGCGCGCAAGTCCACGCTTCACC 1612
QY 2498 TACGTGATGGGCAAGATAGTTTATATAGACCCGAGATGCTGCACTTACAGGCTCACT 2557
DB 1613 TAGGTGCTGGGCAACATCGGCTATCATGACCCGGAATGAGCCGCAAGCTCAAGCTCAAC 1672
QY 2558 GAGAAATCCGATGTCTTACATTTATGAAATGCTCTTCTTGAATTTTAACTTAACTTGAAG 2617
DB 1673 GAGAAATCCGATGTCTTACATTTATGAAATGCTCTTCTTGAATTTTAACTTAACTTGAAG 2677
QY 2618 GCGGTGATGACGATCAATCTTCAACATCTGATTAATGCAAAAGACGGGAAACAATGAA 2677
DB 1733 GCGGTGACAAACAGATCTTCAACCTTGCACACAGTACTCTGAAAGGCGCACAGACAG 1792
QY 2678 GTGATGGAATTTGCAATGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2737
DB 1793 GTGATGGAAGCCGAGGACCCGAGAGTGTGCGTACAGTCAAGATCAATCAATCAATCAAT 1852
QY 2738 AAAGTTTCCAACTGAGTCTTATGATGACCAAAAGACAGCCGATATGATCAACCAATG 2797
DB 1853 AAGGCTTCCAACTGAGTCTTATGATGACCAAAAGACAGCCGATATGATCAACCAATG 1912
QY 2798 CACGAGTGAATGATGATCTTCCGAGATTTATGATGATGATGATGATGATGATGATGAT 2857
DB 1913 CACGAGTGAATGATGATCTTCCGAGATTTATGATGATGATGATGATGATGATGATGAT 1972
QY 2858 GACACGTCAAGCAGACGCTGAGTGTGCTGCTAC 2890
DB 1973 AAGGCGGCGGCGGCTTGGCGGCGGCGGCGAC 2005

RESULT 14
US-10-437-963-18958
Sequence 18958, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bouharov, Andrey A.
APPLICANT: Barabuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 18958
LENGTH: 3233
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_24466C.1

Thu Sep 7 09:31:07 2006

us-10-519-135-1.rnpbm

Page 21

QY 2794 AATGCACGAGTACTCGTGTCTCGGCAGTTTATGTCTATCGGAACAACACC 2847
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 Db 1373 GATGCACGAGGTGTGCGCGCTCTTGACTGCTGTGTGAACCCGGAGCCGCGGCC 1426
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Job time : 3718 secs
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Qy 378 GTAATCGCTGTCTGGACAATAATCCCTGATGAGATTGATGCTGTTCTTTTGCAAAACT 437

Db 477 GAAATGCTCTCAGGCGCAAAATTCGCCGAGATTTGAGATTTCTCTGCATTGAAAATCT 536

Qy 438 TAGACTTATCTTCAATGAATTAAGTGTGACATACCCTTTTCGATTTTGAAGTTGAAGC 497

Db 537 TAGATGCTCTTTAAATTAATTTATACGGAGACATTCCTTTTCAATATGAAATTTAAAC 596

Qy 498 AACTGAGAGCGTGAATTTGGAAGATAAACCAATTTGATAGGACCGATCCCTTCAACACTT 557

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Qy 1158 ATGT 1161

Db 1257 AAGT 1260

RESULT 2

US-10-101-464A-839

/ Sequence 839, Application US/10101464A

/ Patent No. 6768041

/ GENERAL INFORMATION:

/ APPLICANT: Strubala, Timothy

/ APPLICANT: Nieuwenhuizen, Nicolaas

/ APPLICANT: Higgins, Colleen M.

/ TITLE OF INVENTION: Compositions Isolated from Plant Cells

/ TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

/ FILE REFERENCE: 11000.102062

/ CURRENT APPLICATION NUMBER: US/10/101,464A

/ CURRENT FILING DATE: 2002-03-18

	Query Match	7.1%;	Score 225.4;	DB 3;	Length 3222;
	Best Local Similarity	45.7%;	Pred. 1.2e-61;		
	Matches 1015;	Conservative	0;	Mismatches 1166;	Indels 18; Gaps 6;
QY	426 CTTTGCAAACTTGAAGCTTATCTCTCAATGATTAAGTGTGACATACCGTTTGCATTT				485
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QY	486 CGAAGTTGAACCACTTGAGAGCTGATCTCGAAGATTAACCAATTGATAGAC---CGA				542
Db	504 GGAATTTGACAAATCTTGAGCTCTTCAGCCCGGGTATTTAATATGTCTCAATCGCGAACA				563
QY	543 TCCCTTCACACTTTCACAGATTCCTCAAACTGAAATTTCTGGAAGTTGGACAGATAAAC				602
Db	564 TTCCAGAGAGCTCATGCGACTGACAGACTCAGATTTGGCTGTATCTTAACGAATTGCAACT				623
QY	603 TCAAGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTTCTTCAGTATCTTGGTTGC				662
Db	624 TTTATGGGTTCATTCAGCTTCTCTGAGCAATCTTTCGAGCTGGAAACCTGAGACTCT				683
QY	663 GAGAAACACTTATGTTGGGTACATTTCTCCAGATTTGTGTCAACTGACTGTCTTTGGT				722
Db	684 CGATGAATGATCTTACTGGAAGAAATTCCTCAAGAGCTCGGGAGCTTCAGAAAGCTGTATC				743
QY	723 ATTTTGAAGTAAAGAACACAGTTTGAAGTGTATATACCTGAGACGATAGGAATTGCA				782
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QY	783 CTGCTTTCAGAGTTTGTGACTTGTCTTCAATACGTTACTGTGTGAGATCCCTTTGACA				842
Db	804 CATCATGAGAGATTTTGATGCTCTCCAGAAATTTCTGTGTGGAGAAATTCGGCAGACT				863
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QY	1080 ACCGGAAGCTCAATGATATATCATCTCAAGGGTCTATTACCAACGAGCTTGGGAAGCTTA				1139
Db	1104 ATATTTCTTTGTTCTTGATPAACGAATTTACAGGCCAAATCCCTGAATCCTATGGAACTGTA				1163
QY	1140 CTGACTTGTATTGATCTGAATGTGGCCCAACATGATCTGGAAGGACTTAATCCTGATATC				1199
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QY      1740 ATCTGCTTTTGGCGTAGTTGCTAAACTCACCCTGTCAATGATTCCTGCGCAACTGTAC 1799
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QY      1860 TCAATGCTTAATAGACGCTTGCAGCCGATATCTCTCTCTTCTTGATGAGATCAC 1919
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Db      1995 ATGAATATCTGGAATCATGAGAGAGACATTAATTTGATGAGGCTGTGATGAG 2054
QY      2040 GGCAGGAGATTAAGACGCTGTATCAAAATGTTTGTGAAGATTTGAACCGGTTGCCA 2099
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QY      2100 TTAAAGGGCTTTACTCTCAACAACCAAGTCAATGAAACAGTTTGAAGCAAGATCGAGA 2159
Db      2115 AAAAATGCCACCAATGGCGGACAGGGCTGTATTAACGAGAAATTTGAAGGAGAAATTTGAGA 2174
QY      2160 TGTAAATGATCAAGACAGAAATCTTGTGAGCCTTACAAGCTTAATTCCTCTCTCACT 2219
Db      2175 CACTGGGAACGATCCGCAAGAAATATTTCTCAAACTCTACTCTATTTCTCAAAATGGGG 2234
QY      2220 TGGGAGTCTTCTGTCTATGACTATTTTGAAGAAATGTTAGCTCTGGGATCTTCTCATG 2279
Db      2235 ATTCAATATGCTGTGTATGAGATGACATGCCCAATGAAATTTGTGGGAATCCCTGAGC 2294
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Db      2295 TAGGCAATAGGGAGGAGAGTCTGATTTGGCCCACTCGTTACAAATATGACTCTGGGTGCG 2354
QY      2340 CACAAGTTTAGTATTAATACACCATGATGTATGTCGAAGATCATTTACAGAGAGTGA 2399
Db      2355 CCAACGAGCTGGCTTATCTTCATCAGACATGCGCAACAGGTATCATTTACAGAGATGTCA 2414
QY      2400 AGTGTCCAAATCTCTTTGCAAAAGACTTTAGAGCTGTGTTGACAGATTTTGAATAG 2459
Db      2415 AGTCCACAATATCTTGTGATGATGAGAAATCAGGCTGTGTGAGATTTTGGTTTG 2474
QY      2460 CGAAAAGCTTGTGTGT--CAAAGTCAATCTTCAATTAACGTATGCGACCATAG 2516
Db      2475 CTAAAGATCTTCAAGGCTGCCCGAGAGGTGATTTCTGATTAATCTGCAACCATG 2534
QY      2517 GTTAATAGACCCCGATAGTCTGCACTTCAAGGCTCACTGAGAAATCCGATGTCTACA 2576
Db      2535 GCTATATGCTCCAGAGATAGCTTATTCATCCAGGGTACCGAGAAAGATGACATTTACA 2594
QY      2577 GTTATGAATATGCTCTTCTTGAAGTTGTAAACCGAAGAAAGCCGTGATGACGAATCC 2635
Db      2595 GCTTCGTGTGTGTTTAACTGAGACTCATTAACAGGAGGCGCCAGTGAAGCAGAATTC 2653

RESULT 3
US-10-101-464A-880
; Sequence 880, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their use in the modification of Plant Cell Signaling
; FILE REFERENCE: 11000.102062
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 880
; LENGTH: 4017
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-880

Query Match      7.1%; Score 224.8; DB 3; Length 4017;
Best Local Similarity 45.7%; Pred. No. 2.2e-61;
Matches 1081; Conservative 0; Mismatches 1252; Indels 35; Gaps 7;

QY      294 TTAATTTGACATTTGAATCTTGAATGAGAAATCTCACTGCTATTTGAGATCTCAAGA 353
Db      718 TGAATTTATCGCAAAATCTTTTGTGGGGAACCTTCCGACTTATTTTCAGACTCGCAG 777
QY      354 GTCTCTTTCATTAATGATTCGAGATATGCTGTGTGGAACAATCCCGATGAGATG 413
Db      778 AGCTGGAATATCTGATATCTGAGATACATTTCTGTGTTGATTTCTGCGAGCATG 837
QY      414 GTGACTGTTCTTCTTTCGAAAACCTTAAGCTTATCTTCAATGAATTAAGTGTGACATAC 473
Db      838 GGAACGCGCAAGCTTCAAGTACTGAACTGTGTCGCAATCTGTAACGAGACATATCC 897
QY      474 CGTTTTCATTTGAAATGGAACAATTTGAGAGCTGATTTCTGAAAGATTAACCAATT-- 531
Db      898 CAACATTTCTGGGAAATCTCAGCAATCTCAGCAATTAATTTGTCGGGATCAATCCCTTGG 957
QY      532 -GATAGAGCGGATCCCTTCAACATTTCAAGATTTCAAAACCTGAAATTTCTGCACTTGG 590

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Db 958 CCCCCGCTGATTCCTCCAGAGCTGGGAAAGTAGCAAAAGTTACAAATCTATGGGCTA 1017
Qy 591 CACAGAAATAACTCAGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTTCTTCACT 650
Db 1018 CTTCTGTAAATTTTGTGGGTGCTATTCGGGATTTCTATGGCAATCTGCTCTTTGACGA 1077
Qy 651 ATCTTGGGTTCGAGAAACAATTAGTCGTAACATTTCTCCAGATTTGTCTCACTGA 710
Db 1078 ATCTGATCTTTCTGAAATCAGCTCTCGGAATTTATCCAGAGCCATCAGAAAGTTA 1137
Qy 711 CTGCTCTTGTGATTTTGAAGTAAACAACAGTTGACTGTGATTAACCTGAGCGA 770
Db 1138 ATCAAAATGATACAGATTGAGCTCTATCATTAACAATTACAGGAAGATTCCTGAGACT 1197
Qy 771 TAGAAATTCACATCGCTTCAGGTTTGGACTGTCTCAATCAGCTAAGTGTGAGA 830
Db 1198 GGGCTAATCTTGTCTCTCAGACATTTGATGCTCAACAATATGCTTTAACGGACCA 1257
Qy 831 TCCCTTTGACATCGGCTTCCTGCAAGTTGCAACATTATCATTTGCAAGCAATCACTCT 890
Db 1258 TACTGAGCAGTTGGGCAAGGTGGCACTTTCGTCTTGAACCTGTGAGAAATATTTGG 1317
Qy 891 CTGGGAAGATTTCCATCAGTATGTGTCTCATGCAAGCCCTTGCAGCTTTAGATTTAGTG 950
Db 1318 TAGGACACATTCGGAGGCTATGGGTATTTCTCCAACTGTCTGAGCTCAAGCTGTTTA 1377
Qy 951 GCAACTGTGTAGTGAATCTATTCTCCGATTCGGAATCTTACTTTACCGAGAAAT 1010
Db 1378 CGAATTAACCTTAATGTAGTCTGCTTCTGAAATTTGGGGAAATTTCCGGCTTACAAAGC 1437
Qy 1011 TGTATTTGACAGTAAACAAGCTGATCTGATGAGCCCAATGATGAGCTTGAACATGCTCA 1070
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Qy 1071 AACTCCATTACCTGGAATCAATGATATATCATCTCAGGGTCAATATACCAAGAGCTTG 1130
Db 1498 AGGTGCAAACTTGAATATCTTTTAAACAACATTCACCTGGGCAAGTCTCTTTCGAATACG 1557
Qy 1131 GGAAGCTTACTGACTTGTGATCTGAATGAGCCCAATGATCTGGAAGAGCTTATAC 1190
Db 1558 GTGCATGTTTGAAGCTTCAAAAGGTGGAATTAAGCCCAATGAGCTATGAGGACAAATGC 1617
Qy 1191 CTGATCATCTGAGCTCTTGCACAATCTTAAACAGCTTAAATGTTTCATGGGAAACAATTTA 1250
Db 1618 CTATGTCATTTCTGGGGTCTCCCTCAGCTTATATATCTGAACTGATTAACAACAAGTTGG 1677
Qy 1251 GTGGCACTAATCCCGGAGCAATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGCCA 1310
Db 1678 AAGGCTCGATTTCTTCTGAATTAAGAAATGCAAGAAATCTATCAGCGCTATGATATCCG 1737
Qy 1311 GCAACAATATCAAGGTCCAAATCCCGTTGAGCTATCGATGAGTACTGATGATCAT 1370
Db 1738 GTAAACGTTTCTCCGGGACCTTACTCTTGAAGATGGGCTTGTGGCTAATCTTTCTGTA 1797
Qy 1371 TGGATCTTTCCAAACAACAAGATTAATGAAATCAATCTTCTTCCCTTGTGATTTGGAGC 1430
Db 1798 TTGATGGTACCAACAATCAATTCACAGGTCTCTTCCAGCCCACTTTGGGTTCGCTGAACA 1857
Qy 1431 ATCTTCTCAAGATGAATTTAGTAAATATCATATTAATGTTAGTTCCAGGGGACTTTG 1490
Db 1858 AATTTAGTAAAGTTCATCTTCTCAGAAATCAAGTTCTCCGGTACCTTCTCAGTACATAC 1917
Qy 1491 GAATCTAAGAAAGCATGATGAATAATAGATCTTTCAATATGATATCTTGGCCCAATTC 1550
Db 1918 TGTCAATGAGATGAGCTTAACAGACTAATCTGTCAAAATTAACAAGTTTCCGGGCCCTAATTC 1977
Qy 1551 CAGAAAGCTTAAACAATTAACAAGCAATTAATTTGCTGAGACTGGAATTAATTAATCACTGA 1610
Db 1978 CTAAAGAGCTTAGGGGAGCTGCCAGTTCTGACATATCTGGAATCTTTCTGTTAATGCCCTGA 2037
Qy 1611 CTGCTAATGTTGGTTCATTAGCCCACTGTCTCACTCTCATGTAATGAATGATCTCATA 1670

Db 2038 CAGAGAAATCCCTCCTGAATTTGGGCAATTTGAAGCTTAAACAGTTTCAATCTTTCGATA 2097
Qy 1671 ACAACCTCGTAGGTGATATCCCTAAGAACATTAATCTTCAAGATTTTCCAGACAGCT 1730
Db 2098 ATCAGCTAATCTGGCATTTGTTCTTCTGCTTTCAGTCTC---AGTTTTTACAGTCAAGTT 2154
Qy 1731 TCAATTTGGCAATCTTGTCTTTTGGGATGTTGGCTTAACTCACCGGTGATGATTTCTGTC 1790
Db 2155 TAAATGGCAATCTCGGCTTTGAGCAATGATGCTTTAAAGGGTTTAAATCTGTTCT- 2213
Qy 1791 GAACTGTACAGATGTCAATCTCTAGACAGCTATTTCTGGAATAGCTATTTGGGGACTTG 1850
Db 2214 GACATGAGAAATAGCGGAGAAAAAGTTTACAGTTGGGCATGAGCTGCCAGACACTG 2273
Qy 1851 TGAATCTTCTCATGATCTTATATAGACAGCTTGCCGACCGCATTAATCTCTCTTTCTTG 1910
Db 2274 TTTGCTTTGGCTGGGTCATTTTGTGTATAGACTGGCTGTTGTTTATAGCAATACCTG 2333
Qy 1911 ATGATCACTTGAACAACAGTAACTTATTCGACACCGAAGCTGTATCTTCAATGA 1970
Db 2334 GAATTAACAATTAAGCTAAAGTTAAAGATTGTGGCGAAAGCAATTAAGTCTCCCTGATGCTG 2393
Qy 1971 ACATGGCACTCCAGCTTTACAGAGATATCATGAG-AATGACAGAAATCTAATGTGAGAG 2029
Db 2394 ACCACGTTTCAACGATTTGGGTTTCAAGAAATATGAATTTGATTCATGACAGGAA 2453
Qy 2030 TATATCATTTGGGACGAGCATCAACACTGATTAACAATGTTTGAAGATTTGAATTTGA 2089
Db 2454 AATGTATTTGAAGTGTGTGATCAGAAAGTTTACAGGCCACATCCGGGAATGAGAA 2513
Qy 2090 CCGGTTGCGATTAGCGGCT-----TTACTCTACAACCCACAGTCA 2131
Db 2514 ACTGTGGCCATCAAGAGGCTGTGGAACAATGAAATGCTGAAGGCTCTACATCTCGCAAT 2573
Qy 2132 ATGAACAGTTTGAACAGAACTCGAGATGCTAATAGATCAAGACAGAAATCTTTGTC 2191
Db 2574 GATTAATGATTAAGGAGGAAGTTGAAACTTTGGAAATTTTAGGCAATTAACAATAGTG 2633
Qy 2192 AGCTTCAAGCTTATTCCTCTCTCACTTGGGAGTCTTCTGTCTATGATCTAATTTGAA 2251
Db 2634 AACTCTGTGTGTGTGTGTGATGACATGACATCTTAATCTTTTGGTATACAGTACATGCC 2693
Qy 2252 AATGTAGCTCTTGGGATCTTCTTCAATGAGCCCTACAGAAAGAAAGACTTGAATGGGAC 2311
Db 2694 AATGGCAATTTGGGGATCTCTTCAATGGCC---CCAAAGCTGTGACCTTAATTTGGCT 2750
Qy 2312 ACAGGCTTAAATAGTATGATGAGTGAAGCAAGAGTTTATGCTTATCTACACATGACTGT 2371
Db 2751 ACAAGTTACAAATTTGAGTGAAGAGCTCAGGGTTTGGCTTATTTGATTCATGATGATGT 2810
Qy 2372 AGTCCAAAGATCAATTCACAGAGAGCTGAAGTCTCCAAACTTCTTGGCAAAAGACTTA 2431
Db 2811 GTATCTCTCATATCATCGACGATGGAAGTCCAAACAATTTCTGTAGATGCTGATTTT 2870
Qy 2432 GAGGCTGTGTTGACAGATTTTGAATTTGGAATGCGAAAAGCTT-----GTGTGTCAAAAGTCA 2485
Db 2871 GGTGCTGTGTGTGCTATTTTGGACTTGGCCAAAGGCTCTTCAAGAGCTATGGAAGGGAATC 2930
Qy 2486 CATACTTCAACTTAAGTATGAGGCAAGATGATGATTAATGATGACCCGAGATATGCTGCAGCT 2545
Db 2931 GATTTTATGTCTCAATTTGCTGATCTTATGTTATATAGCTTCAGAAATGATGATCACT 2990
Qy 2546 TCACGGCTCAGTAGAATTCGATGTCTACAGTTATGGAATAGTCTTCTTGAAGTTGTA 2605
Db 2991 CTCAAGGTGATATGAAAGTGAATCTACAGTTTGGAGTGTGCTTTAGAGCTTAGTG 3050
Qy 2606 ACCGAAAGAAAGCCGTTGATGACGAAT 2633
Db 3051 ACGGGCAAGCAGCGGTAATTCAGGAAT 3078

RESULT 4
US-10-101-464A-833

2030 TATATCATGGGACGAGCATCAAGCATGTATCAATGTGTTTGAAGATTGTAA 2089
2323 AATGTGATTGGAAGTGTGATCGAGAAAGTACAAAGCCACATCGGGAATGGAA 2382
2090 CCGGTGCGATTAAAGCGCT-----TTACTCTCAAAACCCACAGTCA 2331
2383 ACTGTGGCCATCAAGAGCTGTGGACAAATGAAATGCTGAAGGCTCTACATCTGCAAT 2442
2132 ATGAAACAGTTGAAACAGAACTCGAGATGCTAGTGCATCAAGCAGCAAAATCTGTG 2191
2443 GATTAATGATTCAAGGCAAGATTGAAACTTTGGGAAATATAGGCAATAAACAATAGTG 2502
2192 AGCTTCAAGCTTATTCCTCTCTCACTTGGGAGTCTGTCTTCTATGACTATTGGAA 2251
2503 AACTCTGGTGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2562
2252 AATGTGACCTCTGGGATCTTCTTCACTGAGCCCTACGAAAGAAAGACTCTTGATGGAC 2311
2563 AATGGAGTTTGGGGGATCTCTTCAAGGCC---CCAAAGCTGGTGAACCTTAATTGGCT 2619
2312 ACACGGCTTAAGATAGATATGATGAGCAGCAAGCTTACCTATCTACACCATGACTGT 2371
2620 ACACGTTACAAATGAGATGAGTGGAGCAGCTAGGCTTGGCTTATTTGATCATGATGTGT 2679
2372 AGTCAAGATCATTCACAGAGAGTGAAGTCTCCAAACATTTCTTGGACAAAGACTTA 2431
2680 GTACCTCTCTATCATCCATCGAGATGATGATGATGATGATGATGATGATGATGATG 2739
2432 GAGGCTCTGTTGACAGATTTTGGAAATGCGAAAGCTT-----GTGTGTCTCAAGTCA 2485
2740 GGTGCTGT 2799
2486 CATACTTCACTTACATGATGAGGAGCAGATAGTATACATCAAGCCGAGTATGCTGAGT 2545
2800 GATTTCTATGCTGCAATGCTGATCTTATGATATATAGCTCCAGATATGATACACT 2859
2546 TCAAGGCTCACTGAGAAATCCAGTGTCTACAGTATGAAATAGTCTTCTTGAAGTTTGA 2605
2860 CTCAAGGTGATGAGAAAGATGACATCTACAGTTTGGAGTGTGCTTCTTGAAGTGTG 2919
2606 ACCCGAAGAAAGCGGTTGATGACGAAT 2633
2920 ACCGGCAAGACGCGGTATTCAGGAT 2947

RESULT 5
US-09-353-585-4
Sequence 4, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q

1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3573 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: CE2
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-353-585-4
Query Match 6.9%; Score 220.2; DB 3; Length 3573;
Best Local Similarity 48.0%; Pred. No. 6.2e-60;
Matches 692; Conservative 0; Mismatches 743; Indels 6; Gaps 2;
283 TGTGTGCTCTTAATTTGTCAGATTTGAATCTTATGAGGAATCTCACTGCTATTGG 342
280 TCTTGAATATCTTGATCTTATGCAAGAAACATATCTATGATCACTTCCACTAGATGG 339
343 AGATCTCAAGAGTCTCTTGCATGATGTCGAGGATATCGCTGTGTGACAAATCCC 402
340 TAATCTCAAAATCTTGTCTATCTTGTGATGAAACAACAATCAATTTGAGGAACATACC 399
403 TGATGATGTTGTGACTGTTCTTCTTGGCAAACTTAACTTATCTTCAATGAATTAAG 462
400 ACCAATATCGGTTTACTAGCCAGCTTCAGATCATCCGATATTCACAAATCAATTA 459
463 TGTGATATCCGTTTTCATTCGAATGAGCAACTTGACAGCTGATTTGTAAGA 552
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523 TAACCAATGTATGAGACCGATCCCTTCAACACTTTGACAGATTTCAAACTGAAATTTCT 582
520 CAATTTCTTATAGTGTTCATCTCTGTTCAAGTGGGAATCTGAACAATGCTTTT 579
583 GGACTTGGCAGAAATTAATCACTGATGATGATGATGATGATGATGATGATGATGATG 642
580 GTATCTTAAATTAATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 639
643 TCTTCACTATCTTGGTGTGAGAGAAACAATAGTCGTAATATTTCTCCAGATTTG 702
640 TCTTACTGACTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 699
703 TCACTGACTGCTTGTGATTTTGAAGTAAAGCAACAGTTTGAAGTGTAGTATACC 762
700 GAATATGAACAATCTGCTTTTGTGTTTCTTATGAAATCAGCTTTGCTGCTATACC 759
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760 TGAAGAAATATGTTACTTAAGATCTCTTACTTACTTACTTACTTACTTACTTACTTAA 819
823 TGTGATATCCCTTTTGAATGAGGCTTCCGCAAGTTGCAACATTAATCATGTC---AAG 879
820 TGGCTTATTCCTGCTTCACTTGGGAAATTTGAACAACCTGCTTTTGTGTTTCTTATGG 879

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QY 880 CAATCAACTCTCTGGGAGATTCATCAGATGTCATGCAAGCCCTTGACGCTT 939
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QY 940 AGATCTAATGAGCACTGTTTGAAGTATCTATCTCCGATTCCTCGAATCTTACTT 999
DB 940 AGGTTTGAAGGAGAAATGCTTTATATGCTCTATCTCCGCTTCAATGGGAAATCTGAAAA 999
QY 1000 CACCGAATAATTTATTTGCAAGTAACAAGCTGACTGTTCAATTCACCTGAGCTTGG 1059
DB 1000 CTGTCTAGGTTGAATCTGTTATATATCAGCTTTCTGGCTCTATCTCGCTTCATTTGGG 1059
QY 1060 AAACATGTAAACCTCATCTACTGGAACCAATGATTAATCATCTCAACGGGTATATACC 1119
DB 1060 GAATCTGAACAATCTGTATGTTGATCTTTCAATTAACACAGCTTTCTGGCTCTATCTC 1119
QY 1120 ACCAGAGCTTGGAGGCTTACTGACTTGTGATCTGAATGTGGCAACAATGATCTGA 1179
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QY 1180 AGGACCTAATCTGATCATCTGAGCTCTTGCAAAATCTAACAAGCTTAAATGTTCAATG 1239
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QY 1240 GAACAGTTTATGTCGACTATACCCGAGATTTCAAAAGCTAGAAAGTATGATTAATCT 1299
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QY 1300 TAATCTGTCCAGCAACAATATCAAAAGTCCAGCTTGAAGCTATCTCTGATCTGTA 1359
DB 1300 AGATTTGAGTAATATCTCCATTAATGATTTATCTCGCTTCAATTTGGCAATATGAGCAA 1359
QY 1360 CTGAGCTTTTCTGCTTCTTATGAAATATCAGCTTCTGCTGCTGCTGCTGAGAAATAGG 1419
DB 1360 CTGAGCTTTTCTGCTTCTTATGAAATATCAGCTTCTGCTGCTGCTGCTGAGAAATAGG 1419
QY 1420 TGAATTTGAGACATCTCTCAAGATGAATCTGATGAGAAATCATATTAATCTGATGCTTC 1479
DB 1420 TTAACCTAAGGCTCTTAATGCTCTTGAATGAGTGAATGCTCTTAATGCTCTTAATGCT 1479
QY 1480 AGGCGACTTGGAAATCTAAGAAGCATCATGAAATAGATCTTCAAAATATGATATCTC 1539
DB 1480 TGCTTATCTCGGAATTTGAAACAATTTGCTAGTGAATCTTGTATATATATAGCTTTC 1539
QY 1540 TGGCCCAATTCAGAAAGCTTAACCAATTAACAACATATATTTGCTGAGCTGAGAAA 1599
DB 1540 TGGCTCTATCTGAGAAATAGTTAAGTCTCTTAATGCTCTTGAATTTGAGTGA 1599
QY 1600 TATAACCTGACCTG---TAATGTTGCTCATTAAGCAACTGTCTCAGTCTCATGTAAT 1656
DB 1600 GAATGCTCTTAATGCTTAATGCTCTTAATGCTCTTAATGCTCTTAATGCTCTTAATGCT 1659
QY 1657 GAATGATCTCATTAACAACCTGAGTATCTCCCTAAGAACATTAATCTTCAAGAT 1716
DB 1660 GAATCTTGTATTAATATCAGCTTTCTGCTCTATTTCTGAGAAATATAGTTACTTAAGATC 1719
QY 1717 T 1717
DB 1720 T 1720

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RESULT 6
US-09-353-585-1
; Sequence 1, Application US/09353585
; Patent No. 6287865
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; Jones, David A
; Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses
; thereof
; NUMBER OF SEQUENCES: 15

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/62, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1754..5012
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1677..1753
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-353-585-1
Query Match 6.9%; Score 220.2; DB 3; Length 6471;
Best Local Similarity 48.0%; Pred. No. 9.4e-60;
Matches 692; Conservative 0; Mismatches 743; Indels 6; Gaps 2;
QY 283 TGTGTGCTCTTAATTTGTGCAATTTGAATCTTGAATGAGAAATCTCACTGCTTATGG 342
DB 1964 TCTTGAATCTTGAATCTTGAAGAAACAATATCTATGATGATCTTCACTGAGATTTGG 2023
QY 343 AGATCTCAAGAGCTCTCTGCAATTTGATCTGCGAGGTATCGCTTGTGCAAAATCTCC 402
DB 2024 TAATCTCAAAATCTTGTCTATCTTGAATCTTGAACAACAATCTGAGATTTCAAGAAATACC 2083
QY 403 TGAATGATTTGTGACTGTTCTTTTGGCAAACTTATGACTTATCTTCAATGAATTAAG 462
DB 2084 ACCACAATCGGTTTACTAGCAAGCTTCAATCTCCCATATTTTCAACAATCAATTAATA 2143
QY 463 TGTGATATACCGTTTTCATTTTCAAGTTGAAGCAACTTGAAGCGCTGATCTGAAGA 522
DB 2144 TGAATTTATCTTAAAGAAATAGTTTACTTAAGTCTTACTAAGCTATCTTTGGGTAAT 2203
QY 523 TAACCAATGATAGGACGATCTTCAACACTTTCACAGATTTCCAAACCTGAAATTTCT 582

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Db 2204 CAACCTTTCTAGTGTCCATCTCCTGCTGAGGGGAATCTGAACAATGCTTTT 2263
QY 583 GGACTTGGCAGAAATACTCACTGCTGAGATACCAAGCTTATTAAGTGAATGAGT 642
Db 2264 GATCTTTTACAAATATCAGCTTTCTGGCTCTATTCGGAAGAAATTAAGTACCTAGATC 2323
QY 643 TCTTCAGATCTTGGTGGCGAGGAACAATTAGTGGTAACTTTCTCCAGATTGTG 702
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QY 703 TCACTGACTGCTCTTGTGATTTTGAAGTAAACAAGTTGACTGGTATATACC 762
Db 2384 GAATATGAAACAACCTGCTTTTGTCTTATGAAATACAGCTTCTGCTCTATTTCC 2443
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QY 823 TGGTGAAGATCCCTTTTGACATCGGCTTCTGCAAGTTGCAACATTTATCATTCG--AAG 879
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QY 880 CAATCAACTCTCTGGGAAGATTCATCAGTGAATGCTCTATGTCATGCAAGCCCTGCACTT 939
Db 2564 AAATCAGCTTTCTGGCTCTATTCCTGGAAGAAATAGTTTACCTAAGATCTCTAATGCTCT 2623
QY 940 AGATCTAAGGGCAACTTGTGATGATCTATTCCTCCGATTTCTGGGAATCTTACTTT 999
Db 2624 AGGTTTGAAGAGATCCTTTAATGAGCTCTATTCCTGCTTCATTTGGGGAATCTGAAAA 2683
QY 1000 CACCGAAGAAATGATTTGACAGATTAACAAGCTGACTGTTCAATTCACCTGAGCTTG 1059
Db 2684 CTGTCTAAGTTGATCTTGTATATATACGCTTCTGGCTCTATTCCTGCTTCATTGGG 2743
QY 1060 AAACATGTCAAAATCCTATTACTGGAATCATATGATATCATATCATCGGCTATATACC 1119
Db 2744 GAATCTGAACAACCTTGTCTATGTTGATCTTTACAAATACAGCTTCTGCTCTATTTCC 2803
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Db 2804 TGTCTTCAATGGGGAATCTGAACAATGCTGATGTTGATCTTTACATATATCAGCTTTC 2863
QY 1180 AGGACCTATACCTGATCATCTGAGCTCTTGCAAAATCTAAACAGCTTAAATGTTCAAG 1239
Db 2864 TGGCTCATTCCTGCTTCATTTGGGGAATCTGAACAATCTGCTAAGTTGATCTCTCAAA 2293
QY 1240 GAACAAGTTTATGTCATATACCCCGAGCTTTCAAAGCTAGAAAGTATGATCTTACT 1289
Db 2924 TAAATCAGCTTTCTGGCTCTATTCCTGGAAGAAATAGTTACTGATCTCTTACTTATCT 2983
QY 1300 TAACTCTCCAGCAAAATATCAAAAGTCCAAATCCCGGTTGAGCTATCTCGTATCGGTA 1359
Db 2984 AGATTAGTATATACCTCATTAATGATTTATTCCTGCTTCATTTGGCAATATGAGCA 3043
QY 1360 CTATAGATACATTTGATCTTTCAACAACAAGATTAATGAAATCAATCTCTTCTCCCTGG 1419
Db 3044 CTGGCTTTTGTGTTCTTATGAAAAATCAGCTTGTAGCTCTGCTCTGGAAGAAATAG 3103
QY 1420 TGATTTGAGACATTTCTCAAGATGAACCTGAGTGAAGAAATCATATACCTGTGTAGTCC 1479
Db 3104 TTACCTAAGGCTCTCTTATGCTCTTGAATGAGTGAAGAAATGCTCTTAAATGCTCTATTC 3163
QY 1480 AGGCACTTTGGAAATCTAAGAAAGCATATGAGAAATGATCTTCAATATATGATCTC 1539
Db 3164 TGTCTTCTTGGGAATTTGAACAATGCTGTAGGTTGAATCTTTTAATATACGCTTTC 3223
QY 1540 TGGCCCAATTCAGAGAGCTTAAACAATTAAGAAATATTTTGTGAGACTGAAAA 1599
Db 3224 TGGCTCATTCCTGAAGAAATAGTTACCTAAGTCTCTTAATGCTCTGTTGAGTGA 3283
QY 1600 TAATAACCTGACG--TAATGTTGTTCTTATGACCAAGCTCTCAGCTCATGATTT 1656
Db 3284 GAATGCTCTTAATGCTCTATTCCTGCTCAATGGGAAATTTGAACAATGCTGTAGGTT 3343
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QY 1657 GAATGATCTCATACAACTCTGATGATATCCCTAAGAAACAATTAATCTCAAGATT 1716
Db 3344 GAATCTTGTTAATATACAGCTTCTGCTCTATTCCTGAAGAAATAGTTACTTAAGATC 3403
QY 1717 T 1717
Db 3404 T 3404

RESULT 7
US-09-180-439-7
; Sequence 7, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; CURRENT FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 4123
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-180-439-7

Query Match 6.9%; Score 217.6; DB 3; Length 4123;
Best Local Similarity 48.2%; Pred. No. 4.8e-59;
Matches 678; Conservative 0; Mismatches 724; Indels 6; Gaps 2;

QY 292 TCTTAATTTCTCAGATTGTAATCTTGATGGAAGAAATCTCACCTGCTATTTGAGATCTCAA 351
Db 950 TCTTGAATCTTGAACAACAATATCTCTGTACATTTCCACCTGAGATTTGATATCTCAC 1009
QY 352 GAGTCTTGTCAATGATCTGAGAGTAATGCTGTGTCGACAAATCCCTGATGAGAT 411
Db 1010 AAATCTTGCTATCTTGACTTGAACACCAATCAGATTTTCAGAAACAATTCACACAAAT 1069
QY 412 TGGTACTGTTCTTCTTTGCAAACTTAGACTTAATCTTCAATGAATTAAGTGTGACAT 471
Db 1070 CGGTTCACTGACCAAGCTTCAAGATCAATCCGATATTTAAATCATTTAATGAGCTTAT 1129
QY 472 ACCGTTTTCGATTTCCAGTGAAGTGAAGCACTTGAGCAGCTGATTTCTGAAGATTAACCAAT 531
Db 1130 TCTTGAAGAAATAGTTTACTTAAGTCTCTTACTAAGCTATCTTGGGTATCAACTTCT 1189
QY 532 GATAGACGAGATCCCTTCAACACCTTTCACAGATTTCCAAACCTGAAATTCGAGACTTGGC 591
Db 1190 TAGTGTCTTATTCCTGCTTCATTTGGGCAATGAGCAATGACCAATCTTCTTTTATTTCTTTA 1249
QY 592 ACAGATTAACCTGAGTGTGAGATACCAAGACTTATTTACTGAAATGAAGTCTTCAGTA 651
Db 1250 TGAATAATCAGCTTTCTGGCTTTATTTCTGAAAGAAATAGTTACTTAAGTGTCTTACTAA 1309
QY 652 TCTTGGGTCGAGAAACAATTAATGCTGTAACATTTCTCCAGATTTGTGTCACTGAC 711
Db 1310 GCTATCTTTGATATACCAATCTTATGTTGTTCTTATTCCTGCTTCAATTTGGGGAATCGAA 1369
QY 712 TGGTCTTGTATTTGAGCTAAGAAACAACAGTTGACTGTAGTATACCTGAGACGAT 771
Db 1370 CAATCTGCTTTTGTATCTTTTACAAATATACAGCTTTCTGCTCTATTTCTGAAGAAAT 1429
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PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 878
LENGTH: 3432
TYPE: DNA
ORGANISM: Pinus radiata
US-10-101-464A-878

Query Match 6.3%; Score 199.6; DB 3; Length 3432;
Best Local Similarity 45.2%; Pred. No. 3e-53;
Matches 1043; Conservative 0; Mismatches 1229; Indels 36; Gaps 7;

QY 344 GATCTCAAGAGTCCTTGTCAATGATCTGAGAGTATCGCTTGTGCAAAATCCCT 403
DB 562 GAGCTCTTCAAGCTTAAAGCATCTGATCTTGTGAAATAAATTAAAGCGGTCCG 621
QY 404 GATGAGATGTTGTAAGTCTTCTTGTGCAAACTTAACTTATCTTCAATGAATTAAGT 463
DB 622 CTGCGCTTCCGCGGCTGCGGGAATTCAGTCTTAATCTCTCTCAATCTTCTCAAT 681
QY 464 GGTGACATACCGTTTGTGATTTGGAAGTGAAGCACTTGAGCACTGATTTGGAAGAT 523
DB 682 ACTACAAATTCGCGCTTGTGATGATCTTCAAAATCTTGTGCAATTTGGCTTAC 741
QY 524 AACCAATTTGATAGAACCGATCCCTTCAACATTTTCAAGATTTCCAACTGAAATTTCTG 583
DB 742 AATCTCTCACTGGAACGTATCCTCTGAGCTGGAATTCGAAGAGCTGCAGAAATCTA 801
QY 584 GACTTGCCACAGAAATAACTGATGTTGAGTATCCAAAGACTTATTTACTGGAATGAAGTT 643
DB 802 TGGCTGCGGAGCTGCAATCTCTGCGAAGAAATCCGAGACCTTGGCAATCTCTCCGAG 861
QY 644 CTTCAGATATCGGCTTGTGCGAGAAACACTTACGCTTAACATTTTCCAGATTTGTGT 703
DB 862 CTAAACAACTTGGATTTATGATGATGATCCGTTTGTCCGTTGATTTCCGAGAGTATCAG 921
QY 704 CAATGATCTGTTGTGATTTTGAAGTAAAGAAACAAGTTTGAAGTATGATTAATCT 763
DB 922 AAGCTGGAACAAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 981
QY 764 GAGACGATAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 823
DB 982 GTGCGCATGCGGCGAGCTTAAAGCAATTAAGAGGTTTATGATGATGATGATGATGAT 1041
QY 824 GGTGAGATCCCTTTTGAATCGGCTTCTGCAAGTGAACATTAATGATGCAAGGCAAT 883
DB 1042 GGTTCATTTCTGCGGAGCTGAGAGCTGATGATGATGATGATGATGATGATGATGAT 1101
QY 884 CAATCTTGGGAAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 943
DB 1102 AATCTGTTGGGCAAAATATCCAGGCTTGGGTTGTTACGAGTCTCAAGAGATTAAG 1161
QY 944 CTAAAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003
DB 1162 CTCTTCTCAATAGTTTAAACGAGTCTTGTGCGGAGAACCTCGGCAAAATTTGAGATCTT 1221
QY 1004 GAGAAATTTGATTTGACAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1063
DB 1222 CTAGCATGATATGACAGACATCTGATATCGGAAAGGCTTCTCGGATCTATGCAAA 1281
QY 1064 ATGCAAAATCTCAATCTGGAATCAATGATTAATCATCTACAGGATCATATACCA 1123
DB 1282 AACAAAAGCTTGAATTTCTAGCATTTTCAACATGAGCTCGGTGGAATTTACTGAA 1341
QY 1124 GAGCTTGGGAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
DB 1342 AGCTTGGGAACCTGACGAGCTTAAACAGAGTCCGCTAGGAGCAACAAATTTAACGGC 1401

QY 1184 CTTATACCTGATCATCTGAGCTCTTGCAAAATCTAAACAGCTTAATGTTTCATGGGAAC 1243
DB 1402 TCGGTACCCAGATTATTTCTGGGAGCTTCTCAGCTCTCACTGCTGGAGCTCAAGAACAT 1461
QY 1244 AAGTTTAGTGCACTATACCCGAGCATTTCAAAAGCTGAAAGTATGACTTACTTAAT 1303
DB 1462 TATTTGAAGGATTTATTTCTCCCGCATTTGCCGAGCTTAAATCTCATATGCTCTGTC 1521
QY 1304 CTGTCCAGCAACATATCAAAAGGTCCAATCCGCTTGAAGTATCTGATTCGTAATCTTA 1363
DB 1522 ATCAGGCGCAATATTTTACCGGACAGCTGCTTACAGAAATCTGATGATGCAAGAACCT 1581
QY 1364 GATACATTTGATCTTTTCAACAAAGATTAATGATGATGATGATGATGATGATGATGAT 1423
DB 1582 AGGAGATTAATGCTGATGATTAATTTACTCATCTGATGATGATGATGATGATGATGAT 1641
QY 1424 TTGAGCATCTTCTCAAGATGAACCTGATGAATATATATATCTGATGATGATGATGAT 1483
DB 1642 CTGCAACTGCTCGGAAAGCTGAGCTTATGATGATGATGATGATGATGATGATGATGAT 1701
QY 1484 GACTTTGGAATATTAAGACATCATGAAATGATCTTCAATATATGATATCTGATGAT 1543
DB 1544 CCAATTTCCAGAAAGCTTAAACCAATTAACAGAAATATTTGCTGAGACTGGAATAAT 1603
QY 1762 TCGATTTCTGCGAGATGCTGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1821
DB 1604 AACCTGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
QY 1822 CTCTTCAACCGGCGGATGCTTCCGAGCTGATGATGATGATGATGATGATGATGATGAT 1881
DB 1664 TCTCATTAACAACCTCGAGGTG-ATATCCCTAAGAACATATATCTGCAAGATTTTAC 1722
QY 1882 TCGGACAACTGTTGCTGCGGAGCTTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1941
DB 1723 AGACAGCTTATTTGCAATCTGCTTGTGCGGATGATGATGATGATGATGATGATGATGAT 1782
QY 1942 AGTTTCTGGAATATCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2001
DB 1783 TTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1842
QY 2002 TCTGAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2061
DB 1843 G--GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900
QY 1901 CTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1960
DB 2122 AACTTTGCAAAATGAGAGGAAATCTGTGACAAATCTTCTGAGATGATGATGATGAT 2181
QY 1961 CTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2020
DB 2182 TTTTCAACAG--TTGGGATTCAGTGAATACAG-----ATCTGATGATGATGATGAT 2226
QY 2021 AGTGAAGATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2080
DB 2227 GATGAAGATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2286
QY 2081 AATTTGAACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2131
DB 2287 AATGATGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2346
QY 2132 ATGAACAGATTTGAACAGAACTGAGATGATGATGATGATGATGATGATGATGATGAT 2191
DB 2347 GATTAATGATTTTCAAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2406
QY 2192 AGCTTACAGCTTATTCCTCTCTCACTTGGGAGTCTTCTGTTCTTATGATGATGATGAT 2251
DB 2407 AAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2466

2252 AATGATAGCTCTGGAGATCTTCTTCAATGAGCCCTACGAGAAAAAGACTCTTGAATGGAC 2311
2467 AATGGAGTCTGGAGATCTTCTTCAATGAGCT--AAGCTAGTCTTGAATGGCCC 2523
2312 ACAAGGCTTAAGATACATATGATGACGACGAAAGTTTACCTATCTACACATGACTGT 2371
2524 ATAGATACAGATGCTCCCTTGGAGAGCTCAGGGGGTGGCATATCTTCAATGGTGT 2583
2372 AGTCCAGAGATCTTACAGAGAGCTGAGTGGTCCCAACTTCTCTTGGACAAAGCTTA 2431
2584 GATACCATCATTTGTTACAGAGAGCTGAAATCCAAATATATTTTGGTGGATGAGATAT 2443
2432 GAGGCTCGTTTGCAGATTTTGGATATAGCGAAAGCTTG-----TGTGTGCAAAATCA 2485
2644 GGGGCTCATGTTGCTGATTTTGGTGTGCGAAGTTTCTGCAAGCTTGGGTAGTGAAGCT 2703
2486 CATACTTCAACTGATGATGAGGACGATAGATGTTACATAGACCCGATATGCTGCACT 2545
2704 GATTTATGACTGCAATGCTGGGTCTATGGCTACATAGCTCAGAGATGCTCACT 2763
2546 TCACGCTCACTGAGAAATCCGATGCTACAGTTATGAAATAGTCTTCTTGAAGTTTA 2605
2764 CTCAGATGATGATGAAAAAGTGAATCTATATGTTTGGAGTGTGATCTTGGAGCTGTA 2823
2606 ACCGAGAGAAAGCCGTTGATGACGAAT 2633
2824 ACTGCAAGCGGCGGAGTATGACGACT 2851

RESULT 10

US-09-180-439-1

Sequence 1, Application US/09180439

Patent No. 6225532

GENERAL INFORMATION:

APPLICANT: Dixon, Mark S

APPLICANT: Hatzixanthis, Kostas

APPLICANT: Jones, David A

APPLICANT: Jones, Jonathan DG

TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof

FILE REFERENCE: 620 - 53

CURRENT APPLICATION NUMBER: US/09/180,439

CURRENT FILING DATE: 1998-12-06

EARLIER APPLICATION NUMBER: PCT/GB97/01249

EARLIER FILING DATE: 1997-05-08

EARLIER APPLICATION NUMBER: GB 9609681.3

EARLIER FILING DATE: 1996-05-09

EARLIER APPLICATION NUMBER: GB 9619924.5

EARLIER FILING DATE: 1996-09-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3979

TYPE: DNA

ORGANISM: Lycopersicon esculentum

US-09-180-439-1

Query Match 6.2%; Score 195.4; DB 3; Length 3979;

Best Local Similarity 48.2%; Pired. No. 7,8e-52;

Matches 615; Conservative 0; Mismatches 656; Indels 6; Gaps 2;

423 CTTCTTGGAAAATTAGACTTATCTTCAATGATTAAGTGGTGAATACCGTTTTCG 482
937 CTTTCTCGAATCTTGAATCTTAGCAACAATATCTGTGATACATTCACCTGAGA 996
483 TTTCGAAGTTGAACAATGAGCAGTGAATTTCTGAAGATTAACAATGATGAGACGA 542
997 TTGGTATCTCACAAAATCTGTCTATCTTGAATGAAACCAATCAGATTTCAAGAACAA 1056
543 TCCCTTCAACATCTTCAACAGATTTCAAACTGAAATTTCTGGAGCTTGGACAGAAATTAAC 602
1057 TTCCACACCAAAATCGGTTCACTAGCCAAAGCTTCAAGATCATCCCATATTTTAACAATCAT 1116
603 TCAGTGTGATGATACCAAGACTTATTTACTGAATGAATGTTCTTCAAGTATCTTGGGTTC 662

1117 TAATGGCTTATCTCTGAAAGAAATAGTATACCTAAGTCTCTTACTAAGCTATCTTTGG 1176
663 GAGGAAACAACATTATGCTGTAATCTTCTCAGATTTGTCTCACTGACTGCTTTGGT 722
1177 GTATCAACTTCTTATGATGTTCTATCTCTGATTTAGTGGCAATATAGCAACTTGTCT 1236
723 ATTTAGCGTAAGAAACAACAGTTTGAATGATGATGATGATGATGATGATGATGATGAT 782
1237 TTTATTTCTTATGAAATTCAGCTTCTGCTTTATCTCTGAGAAATAGTTTACTTA 1296
783 CTGCTTCCAGGTTTGGATTTGATCTCTTCAATGATGATGATGATGATGATGATGATGAT 842
1297 GGTCTTCTTACTAAGCTATCTTGGATATCACTTTTATGATGATGATGATGATGATGAT 1356
843 TCGGCTTCTG--CAAGTTGCAACATTATCATGCAAGGCAATCACTCTCTGGAGAGA 899
1357 TGGGGAATCTGAACAACCTTCTTTTGTATCTTATCAATATCAAGCTTCTGCGCTCTA 1416
900 TTCCATCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
1417 TTCTGAGAAATAGGTTACTAGGTCATCTAAGCTATCTTATGATGATGATGATGATGAT 1476
960 TGAATGATCTATCTCTCGATTTCTGAAATCTTCACTTTCAACGAGAAATGATTTATTC 1019
1477 TTAGTGTTCATCTCTGCTTCACTTGGGATCTTAACAACCTTGTCTAGGTTGATCTTT 1536
1020 ACAATTAACAAGCTGACTGTTCAATTCACCTGAGCTTGGAAACATGTCAAACTCAT 1079
1537 ACAATTAACAAGCTTCTGCTCTATCTCTGAGAAATAGGTTACTTCAAGCTCTTACT 1596
1080 ACCTGGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
1597 ACCTGAATTTGGTGAATAGCTCTTAATGCTCTATCTTCTTATTTGGGAAATCTTA 1656
1140 CTGACTTGTGTTGATCTGAATGCTGGAATGCTGCAACATGATGGAAGCACTTATCTATC 1199
1657 ACACTTGTCTAGGTTGATCTTACATATATAGTTTCTGCTCTATCTCTGAGAAATA 1716
1200 TGAATCTTGAACAATCTTAACAGCTTAATGCTTCAATGGAACAAAGTTTATGTCAC 1259
1717 TAGGTTACTGAAGTCTCTTACTTACTTCAATTTGGTGAATGCTCTTAAATGCTCTTA 1776
1260 TACCCGAGATTTCAAAAGCTAGAAATGATGATGATGATGATGATGATGATGATGATGAT 1319
1777 TTCTGCTCTATTTGGGAAATCTGAACAATGTTTATGTTGATCTTTTACAAATATCAGC 1836
1320 TCAAGATCCAAATCCCGGTTGAGCTATCTGTAATCGTAATGATGATGATGATGATGAT 1379
1837 TTCTGCTCTATTTGGGAAATCTGAACAATGTTTATGTTGATCTTTTACAAATATCAGC 1896
1380 CCAACAACAAGATTAATGAAATCTTCTCTTCTGTTGATGATGATGATGATGATGATGAT 1439
1897 GTATTAATCTCTTATGCTCTATCTCTGTTTCAATTTGGGAAATCTGAACAATGTTT 1956
1440 AGATGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1499
1957 TGTGATCTTTTACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2016
1500 GAAGCATCTGAAATATGATCTTTCAATATGATGATGATGATGATGATGATGATGATGAT 1559
2017 GTTCTCTTACTGAACATTTTGGGAAATGATGATGATGATGATGATGATGATGATGATGAT 2076
1560 TTAACCAATTAACAACATTAATTTGCTGAGACTGGAATAATTAACCTGACTG--TA 1616
2077 TGGGGAATCTTAACAACCTTGTAGGTTGATCTTATCAATATATCAGCTTCTGCGCTCTA 2136
1617 AGTGTGCTCATTAAGCAATGCTGAGTCTGAGTCTGATGATGATGATGATGATGATGATGAT 1676
2137 TTCTGCTCTATTTGGGAAATGAGAAATCTGCAAACTGTTTCTGAGTATGAGATC 2196
1677 TCGTAGATATCTCT 1693

Db 2197 TCATTGGGGAAATTCCT 2213

RESULT 11

US-09-180-439-2

/ Sequence 2, Application US/09180439

/ Patent No. 6225532

/ GENERAL INFORMATION:

/ APPLICANT: Dixon, Mark S

/ APPLICANT: Hatixanthia, Koelae

/ APPLICANT: Jones, David A

/ APPLICANT: Jones, Jonathan DG

/ TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof

/ FILE REFERENCE: 620 - 53

/ CURRENT APPLICATION NUMBER: US/09/180,439

/ EARLIER FILING DATE: 1998-12-06

/ EARLIER APPLICATION NUMBER: PCT/GB97/01249

/ EARLIER FILING DATE: 1997-05-08

/ EARLIER APPLICATION NUMBER: GB 9609681.3

/ EARLIER FILING DATE: 1996-05-09

/ EARLIER APPLICATION NUMBER: GB 9619924.5

/ EARLIER FILING DATE: 1996-09-24

/ NUMBER OF SEQ ID NOS: 10

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 2

/ LENGTH: 3979

/ TYPE: DNA

/ ORGANISM: Lycopersicon esculentum

US-09-180-439-2

Query Match 6.2%; Score 195.4; DB 3; Length 3979;

Best Local Similarity 48.2%; Pred. No. 7.8e-52;

Matches 615; Conservative 0; Mismatches 656; Indels 6; Gaps 2;

QY 423 CTCTTTGCAAACTTAGATTTATCTTCATGATTAATGATGATACCGTTTCCA 482

Db 937 CTTTTCGGAATCTTGATCTTAGCAACAATATCTGTGATCCATTCACCTGAGA 996

QY 483 TTTCGAAGTTGAACAACCTGAGCAGCTGATTCGAAGATAACCAATTGATGAGCGA 542

Db 997 TTGGTATCTCACAATCTTGTCTATCTTGAACCAACCAATGATTTCAAGAACAA 1056

QY 543 TCCCTTCAACCTTTCACAGATTCACAACTGAAATTTGCACTTGACAGAAATTAAC 602

Db 1057 TTCCACCAACAATCGGTTCACTAGCAAGCTTCAGATCATCCGATTTTAACATCAT 1116

QY 603 TCGTGTGAGATACCAAGACTTATTTACGGAATGAAGTTCTTCAGTATCTGGGTGC 662

Db 1117 TAAATGCTTATCTCGAAGAAATAGTTAAGTCTCTTACTAAGCTATCTTTGG 1176

QY 663 GAGAAACAACCTTAGTGTGATACATTTCTCCAGATTTGTGCAACTGATGCTTTGGT 722

Db 1177 GTATCAACTTTCTTAGGTGTTCTATCTCTGCTTATGGGCAATATGACCAACTGTCT 1236

QY 723 ATTTTGAAGTAAGAAACACAGTTTGAAGTGTGATTAAGTGTGAGAGATGAATTTGA 782

Db 1237 TTTTATTTCTTTATGAAGAAATCAGCTTTCTGCTTTATCTCGAAGAAATAGTTACCTTA 1296

QY 783 CTGCTTCCAGGTTTGGATGCTTCACATGACGTAAGTGTGAGATGATCCCTTTGACA 842

Db 1297 GGTCTCTTACTAAGCTATCTTTGATATCAACTTTCTTATGTTGTTCCATTCGCTTCAT 1356

QY 843 TCGGCTTCTCTG---CAAGTTGCAACATTTATCTTGAAGCAATCAACTCTCTGGAGAGA 899

Db 1357 TGGGGAATCTGAACAACCTTCTTTTGTATCTTTTACATTAATCAGCTTTCTGGCTCTTA 1416

QY 900 TTTCATCAGTATGTTGTTCTCATGCAAGCCCTTGAGTCTTGAATCTAAGTGGCACTTGT 959

Db 1417 TTCTGAAGAAATAGTTAAGTCACTTAAGTCACTTAAGTATCTTTGGTATCAACTTTC 1476

QY 960 TGAAGTGAATATTTCCCTCCGATTTCTGGAAATCTTATTTCCACCGAAGAAATGATTTGC 1019

Db 1477 TTATGTTTCAATTCCTGCTTCAATGGGGAATTAACAACCTGTCTAGGTGATCTTT 1536

QY 1020 ACAGTAACAAGTGAAGTGTTCATTTCCACTGAGCTGGAAACATGTCMAATCCATTT 1079

Db 1537 ACAATATATAGCTTTCTGGCTATTTCTCGAAGAAATAGTTATCTTAAGTCTCTACTT 1596

QY 1080 ACTCGAATCAATGATATATCATCTCAAGGCTATATACCACAGACTTGGAGCTTA 1139

Db 1597 ACCTAATTTGGGTGGAATGCTTAAATGGCTTATTCCTTCTTCAATGGGGAACTTA 1656

QY 1140 CTGACTGTTTGAATCTGAATGAGCCAAATGATGTCGGAAGGACCTATACCTGATCATC 1199

Db 1657 ACAACTTGCTAGCTTGGATCTTAAATATATAGCTTTCTGCTCTATTTCTGAAGAAA 1716

QY 1200 TGAGCTCTTGCACAAACTTAACAGCTTAATGTTCAATGGGAACAAGTTAGTGGCACTA 1259

Db 1717 TAGTTAACCAAGGCTCTTACTTACTGATTTGGGTGGAATGCTTAAATGGCTCTTA 1776

QY 1260 TACCCGAGATTTCAAAGCTAGAAAGTATGACTTAACCTTAATCTGTCCAGCAACAATA 1319

Db 1777 TTCTGCTTCAATGGGGAATCTGMAACAATGTTTATGTTGATCTTTACMAATATCAGC 1836

QY 1320 TCAAGGTCCAAATCCGGTTGAGCTATCTGATCGTAACTTAAGATTTGATCTT 1379

Db 1837 TTCTGCTTATTTCTGAAGAAATAGTTAAGCTTGAAGTTCTTACTGAATATATTTGG 1896

QY 1380 CCAACAACAAGATTAATGGAATCATTCCTTCTCCCTGGTGAATTTGAGACATCTTCTCA 1439

Db 1897 GTATTAATCTCTTAATAGGCTATTTCTGCTTCAATGGGGAATCGAACACTTGTCTTA 1956

QY 1440 AGATGAACCTTGAATGAATATATATACCTGATGATTTCCAGGCACTTTGGAATCTTA 1499

Db 1957 TGTGATCTTAAATTAATACACTTTCGCTCTATCTCGAAGAAATAGTTACTCTGA 2016

QY 1500 GAGCATCATGGAATATAGATCTTCAATATATATATCTCTGSCCAATTCGAAAGAGC 1559

Db 2017 GTTCTCTTACTGAATATTTTGGTATATACCTCTTAATGCTCTATTTCTGCTTCAT 2076

QY 1560 TTAACCAATTAACAACATATTTTCTGAGACTGGAATAATTAACCTGACTG---TA 1616

Db 2077 TGGGGAATCTAAACAACCTTGTAGGTTGATCTTAAATATATCAGCTTCTGGCTCTTA 2136

QY 1617 ATGTTGTTATTAAGCACTGCTCAGTCTCATCTGATTTGAATGATATCTCATTAACACC 1676

Db 2137 TTCTGCTTCAATTTGGCAATATGAGAAATCTGCAAACTGTGTTCTCAGATTAAGCATC 2196

QY 1677 TCGAGTGTATTCCT 1693

Db 2197 TCATTGGGGAATTCCT 2213

RESULT 12

US-09-228-986-5

/ Sequence 5, Application US/09228986

/ Patent No. 6359198

/ GENERAL INFORMATION:

/ APPLICANT: Strabala, Timothy

/ APPLICANT: Nieuwenhuizen, Niels

/ TITLE OF INVENTION: Compositions Isolated from Plant Cells

/ TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

/ FILE REFERENCE: 11000/1020

/ CURRENT APPLICATION NUMBER: US/09/228,986

/ NUMBER OF SEQ ID NOS: 130

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 5

/ LENGTH: 3340

/ TYPE: DNA

/ ORGANISM: Pinus radiata

US-09-228-986-5

Query Match 5.5%; Score 173.2; DB 3; Length 3340;

Best Local Similarity 45.7%; Pred. No. 1.1e-44;

Matches 1015; Conservative 0; Mismatches 1133; Indels 72; Gaps 9;

QY 294 TTAATTGTCAGATTGAATCTTGATGAGAGAAATCTCAGCTGATTTGAGATCTCAGA 353
 DB 477 TGACTCTCTCTTAACACACTCAGCGGAAACATTCGCCACACATATGCTTCTCCCA 536
 QY 354 GTCTCTTGTCATTTGATCTGCGAGTAATGCTTGTCGACAATTCCTGATGAGATTG 413
 DB 537 ACCTAATATGATGTCCTTGGAATTAACAATTTGACGGGAAACATTCGCCAGCTGTGG 596
 QY 414 GTGACGTGTTCTTTGGCAAACTTAGACTTATCTTCATGAAATTAAGTGTGACATAC 473
 DB 597 GAAACATATCTCTTTGACGATCTTATCTTTGATCAGGTAACCTTCAGGGAGTGTC 656
 QY 474 CGTTTTCGATTTGAGATTGAAAGCACTTGAGCAGCTGATTTGAAAGATTAACCAATGA 533
 DB 657 CTTCGCAATTTGGTAGGCTTAAGCAGCTCATCGTTCTTGATCTGTTTGGGAAACATCTCA 716
 QY 534 TAGGACCGATCCCTTGACACTTTCACAGATTCCAAACCTGAAATTTCTGACTTGGCAC 593
 DB 717 CGGATGATATCCGTCTTGCTGTCACACAGCAATCTTGAACTATTGATATAGGTG 776
 QY 594 AGAATTAATCTCAGTGTGAGATACCAAGACTTATTAAGTGAATGAATTTCTTCA----- 648
 DB 777 ATTAACCAATTAAGTTGGCACAATTCGTCATTTGTGTACCAAGAAAGACCAACCAAGTTAA 836
 QY 649 -GTATCTGGGTTGCGAGGAAACAAGTATAGTGGTAACTTTCTCCAGATTTGTGCAAC 707
 DB 837 TGTATCTCGTCTGGGTCTTAATCAGTATAGTGACGCTTCTTCAATCCCTCTTCAATT 896
 QY 708 TGACTGTCTTTGGTATTTTGAAGTAACAACAAGTTGACTGTGATATACCTGAGA 767
 DB 897 GTACCAAGTTACAAGAGATTGCTTACATTAACCAAGCTCAGCGGAATGTGCTATAG 956
 QY 768 CGATAGGAATTTGACTGCTTCCAGSTTTTGAATTTGTCTCAATCAGCTAATCTGTG 827
 DB 957 AGTTGGTAAATTTGACACATCTCAGCGCTTTCTTTTGGCGGAAATTAATTTAAGCG 1016
 QY 828 AGATCCCTTT----TGACATCGGCTTCTGTCAGTTGCAAC-----AT 866
 DB 1017 GCACACCATGAGATGCCCATTTCTTACTGTCTTGTAGTACTGTTCTGATCTCAATATG 1076
 QY 867 TATCATTTGCAAGGCAATCACTCTGCGAAGATTCATCAGTATG--TCTCATGC 923
 DB 1077 TTAGCTTATCTGAGATTAATCTTCACTGGGCAATTCGCTTTCTATAGGCACTCTCCA 1136
 QY 924 AAGCCTTGCACTTATGATCTAAGTGGCACTTTGATGATCTATTTCTCCGATTC 983
 DB 1137 AAAAATCTTACCAATTTAGACTTGGTAGCAACAAATTAAGCTGAGAAATCTCCGCGCTA 1196
 QY 984 TCGGAATCTTACTTTCAACGAGAAATTTGATTTGACAGTAAACAGCTGACGTGTCAA 1043
 DB 1197 TTGGAATTTTAACTAGCTTACATCTCTTATTTAGAGAGTAATTTTTCAGGGCTCA 1256
 QY 1044 TTTCACCTGAGCTTGGAAACATGTCAAAATCTCATTAACCTGAACTCAATGATATATC 1103
 DB 1257 TCCCATCTTCACTTATTAATGCTTACAGAAATTTGAGAGGTTATATGATTTCCAAATAT 1316
 QY 1104 TCAAGGCTATATACCAAGAGCTTGGAAAGTTACTGACTTTGATCTGAATGTGG 1163
 DB 1317 TACAGGAAACATTTCCAAATGGAATTTGGGACGCTAAAGAGCTTAGCTTCTTATCTTT 1376
 QY 1164 CCAACATGATCTGAAAGGCTATACCTGATCATCTGAGCTTTGCACAAAATCTTAAAC 1223
 DB 1377 CTGGAATTAATTTGTGTGAAAAATCCGTGATTTTGTGGCAACCTTCAGCAATTAAGAT 1436
 QY 1224 GCTTAATTTCAATGGAACAAAGTTAAGTGCATATACCCCGAGATTTCAAAAGCTAG 1283
 DB 1437 ATTATATCTTATATCAATCAGTTATCAAGAGATTAATTAATGCAATTTAGGAAATGTG 1496
 QY 1284 AAGATATGACTTAACTTCTGTCCAGCAACAATATCAAAAGTCCAAATCCGGTTGAGC 1343
 DB 1497 TGAATTAATCTACTGATGATCTATATCAACAAGGCTTGTGTGGGACATATCTCAAGAGC 1556

QY 1344 TATCTGTATCGGTAACTTAGATACA---TTGATCTTTTCAACAACAAGATAAATGAA 1400
 DB 1557 TCGCAGGCTTGGAATTTTAACTTATGCTTATTTCACTTGTCAACAATTAATTAAGTGGC 1516
 QY 1401 TCATTCCTTCTTCCCTTGATGATTGGACATCTTCAAGATGAACCTGAGTAGAAATC 1460
 DB 1617 ATGTACTTTAGAACATGGAAGATGATGATAGCTTCAACGCAATGATATTTCCGCAATC 1676
 QY 1461 ATATATCGTGTATGTTCCAGCGGACTTTGGAAATCTAAGACATCATGAAATGATC 1520
 DB 1677 AAATTAATCGCTACATTTCAAGATATGTTGGAAGCTGGAAGAGATGACATATCTGATC 1736
 QY 1521 TTTCATATATGATATCTCTGCGCCATTCAGAAAGCTTAAACCATTAACAGAACTAA 1580
 DB 1737 TTTCTTACATGACTTGAAGTCCATTCAGTGTCAATCATGATGAACCTTCAATGCTTC 1796
 QY 1581 TTTTGTGAGACTGGAATAATATACCTGAC---TGTAAATGTTGTTCTATAGCAACT 1637
 DB 1797 AAGACCTAGATCTCTCTCCAAACAATTTGCGGGTGAATACCTATATCAGTCAAAATC 1856
 QY 1638 GTCTCAGTCTCACTGATTTGAATGATATCTCATTAACAACCTCGAGTGAATCCCTAAG 1697
 DB 1857 TCACAAATGCTCAATCACTTGAATTTTCTTTTAAACAAGTTGTCAAGGAAATCCCTAAG 1916
 QY 1698 ACATATACTTCTCAAGATTTTTCACAGACGCTTCAATGSCAATCCGTGCTTTGGCGTA 1757
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 QY 1758 GTTGGCTAAATCTACCGTGTATGATTTCTGTGAACGTGACAGTGCATCTAGAG 1817
 DB 1977 CTGGGTAAATCTACACCGGTGCTATGCTATTAACATAAAGTGTGGAATCTCAAAA 2036
 QY 1818 CAGCTATTTCTGGAATAGATATTTGGGGACTTGTGATCTCTTCAATGCTTAAATAGAG 1877
 DB 2037 GAGTATCATATCTGTTGTGTTGTAGCAATTTGTATGTTGTGTTCTTTCATATAT 2096
 QY 1878 CTGCGCAGCGCATATCTCTCTCTTCTTGATGATCACTTGAACAACAGTAATCT 1937
 DB 2097 TGTGAGAAAGAAAT-----TGTAGGAATAATTTCAAGAGACATTTGTCTCATC 2145
 QY 1938 ATTTGACACCGAAGCTGTCTCATCTTCAATATGAAACATGACATCCAGTTTACAGAGATA 1997
 DB 2146 ATTAATATGAGGACATCGAAGAAATCTCTATGCA-----GAGC 2183
 QY 1998 TCATGGAATGACAGAGATCTAAGTGAAGAATATCAATGAGGACAGACATCAAGCA 2057
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 DB 2244 AAGTATCAAAAGGATTTTGAATGATGCAACAATGTTGTCTCAAGCTTCTCAATCTAC 2303
 QY 2118 ACNACCACAGTCATGAAACAGTTTGAACAAGACTCGAGATGCTAAGTAGCATCAAGC 2177
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 QY 2295 AGACTTTGATTTGGGACACAGCGCTTAAGATAGCATATGCTGACAGCAAGTTAGCTT 2354
 DB 2484 GTTGTGTAATTTGAATCAAGGTGAATATAGCAATATAGCAATATCGCCAAAGGATACAT 2543
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 DB 2544 ATCTCATATATATGCTTTGTGCAAGTATTCATTTGTAATTTGAAACCAACAAATGTCT 2603
 QY 2415 TCTTGACAAAGACTTAGAGGCTCGTTTGACAGATTTTGAATAGCAAAAGCTTGTGTG 2474

Db 2604 TGTGGGTGAAGATGACTGATATTATAGACTTGGCATGTGCTACTATATGTTTTG 2663

RESULT 13

US-10-101-464A-5

Sequence 5, Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT APPLICATION NUMBER: US/101,464A

PRIOR FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 3340

TYPE: DNA

ORGANISM: Pinus radiata

US-10-101-464A-5

Query Match 5.5%; Score 173.2; DB 3; Length 3340;

Best Local Similarity 45.7%; Pred. No. 1.1e-44;

Matches 1015; Conservative 0; Mismatches 1133; Indels 72; Gaps 9;

Db 294 TTAATTTGTCAGATTGGAATCTTGATGAGAGAAATCTCACCTGCTATTGAGATCTCAGA 353

477 TGACTCTCTCTTAACACCTCAGCGAACAATTCGCCACAACATGCTTCTCCCA 536

354 GTCCTCTTCAATGATCTGCGAGTAATGCTTGTCTGACAAATCCCTGATGAGATTG 413

537 ACCTAATATGATGCTCTTGGGAATTAACAATTTGACGGGAACATCCCGACTGCTGG 596

414 GTACCTGTTCTTCTGCAAACTTGAATCTTATCCTTCAATGAAATTAAGTGAGACTAC 473

597 GAAACATATCTCTTGGCACTACTTATCTTGAATCAAGGTAACTTCAGGGCAGTGTCC 656

474 CGTTTTCGATTTGGAATGGAAGCACTTGAGCAGCTGATTTGGAAGATTAACCAATTGA 533

657 CTTCCGAATGGGATGAGCTTAAGCAGCTCATCGTCTTGATCTGTTGGGAACAATCTCA 716

534 TAGACCGATCCCTTCAACACTTTCACAGATTTCCAAACTGAAATTTCTGACTTGGCAC 593

717 CGGAGATGCAATCCGCTCTTCTTCCAACTGCAACCAATCTTGAATTTGGAATTAAGTG 776

594 AGAATAACCTCAGTGGGAGATACCAAGACTTAATTTACTGGAATGAAGTTCTTCA----- 648

777 ATAAACCAATTAAGTTGGCCACATTCCTGCAATTTGTTACCAAGAAACACCACTGTTAA 836

649 -GATCTTGGGTTGCGAGAAACAATTAGTCGGTAACATTTCTCCAGATTTGTGCAAC 707

837 TGTATCTCGGTGCGGTGCTAATACAGCTAAGTGCAAGTTCTTCTCAATTCCTTCAATT 896

708 TGACTGCTCTTTGGTATTTTGAAGTAAGAAACAAGATTGACTGTTGATGATACCTGAGA 767

897 GTACCAAGTTACAGAGATGCTTACCAATTAACAGCTCAGGGGAATGCTGCTATGG 956

768 CGATAGGAATTTGACATGCTCCAGGTTTGTGACTGTCTCAATCAGCTAATCTGCTG 827

957 AGTTGGTAATTTGACATCTCCAGCGGCTTTTCTTTGGCGGGAATTAATCTTAATTAAGC 1016

Qy 828 AGATCCCTT-----TGACATCGGCTTCTGCAAGTTGCAAC-----AT 866

1017 GCAACACATGAGATGCCCATTTCTACTGCTCTTGTAGTAAGTGTCTGATCTCAATATG 1076

Qy 867 TATCATTTGCAAGCATTCACACTCTTGGGAAGATTTCTATCAGTATGG-----TCTATGC 923

1077 TACACTTATCTGGAATTAATCTTACAGGGCAATTTGCGTTTCTATAGGCACTCTCCCA 1136

Qy 924 AAGCCCTTGACATCTAGATCTTAAGTGGCACTTGTGAGATCTAATCTCCCGATTG 983

1137 AAAAATCTTACCTTTAGACTTGGTGAAGCAATTAAGTGAAGAAATCTCCCGCTTA 1196

Qy 984 TCGGAATCTTACTTACCCAGAAATGATTTGCAAGTAACAAGCTGACTGTTCAA 1043

1197 TTGGAATTTAAGTACCTTAATCTTAAATTAAGGATTAATTTTACAGGGCTCAA 1256

Qy 1044 TTCCACTGAGCTTGGAAACATGTCAAAATCTCATTCCTGGAACCTCATGATATATC 1103

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Qy 1104 TCAGGGTCAATATACCAAGAGCTTGGGAAGCTTACTGACTGTTGATCTGAATGTGG 1163

1317 TACAGGAAACATTTCCAAATGGAATTTGGCAGCTTAAGAGCTTATAGTCTTATATCTTT 1376

Qy 1164 CCAACAATGATCTGGAAGACCTATACCTGATCTGAGCTTTCACAAATCTTAACA 1223

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Qy 1461 ATATTAATGATGATGTTCCAGGCGACTTGGAAATCTTAAGAACATCATGGAATATGATC 1520

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1737 TTTCTTAATTAATGATGGAAGGTCCAAATTCAGATGATCAATGATTAAGTCTTC 1796

Qy 1581 TTTTGTGAGACTGGAATAATTAACCTGAC---TGTATATGTTGATCTTAATGCAACT 1637

1797 AAGACCTAGATCTCTCTCCAAACAATTTGCGGTGAATTAATTAATCACTGACCAATC 1856

Qy 1638 GTCTAGCTCACTGATTAATGATATCTCAATTAACAACCTCGTAGGTATATCTTAAGA 1697

1857 TCAATATGCTCACTCACTTAATTTTCTTTTAAACAAGTTGTAGGGGAAGTCCCTAAG 1916

Qy 1698 ACAATAATCTTCAAGATTTTCAACAGACGTTCAATGGCAATCTCGGTCTTTGGGCTA 1757

1917 AAGAGATTTTCAAAAATTAATGGCGCAACAGATTTTAAGGAAATCTTGTATATGTCAC 1976

Qy 1758 GTTGGCTAAATCTACCGGTCAATGATTTCTCGTGAAGCTGAGAGTGAATCTTAAG 1817

1977 CTGGGAAATCTACACCGGTCTATGCTATTAACAATTAAGATTTTGAATCTCAAAA 2036

Qy 1818 CAGCTATTTTGGAAATAGCTATTTGGGGGACTTGTGATCTCTTCAATGCTTAATAGCAG 1877

2037 GAGTTATCATACAGGTGTTGTTGTGAGCAATTTGTATATGTTGTTCTTGGCAATAT 2096

Qy 1878 CTGGCGAGCGCATTAATCTCTCTCTTTCTTGTGATGATCATTTGACAAACAGTAATCT 1937

Db 2097 TGTGGAGAAAGAT-----TGTAAGGAAATTTTACAGAGACATTTGGTCCATC 2145
 Oy 1938 ATTGCACACCGAAGCTGTCATCCTTCATATGACATGGACATCCACGTTTACGAGATA 1997
 Db 2146 ATTAATATGGGGCATTCGACAGAAATCTCCATSCA-----GAGC 2189
 Oy 1998 TCATGAGAAATGACACAGAAATCTAACTGAGAAATATATCATTTGGGCAACGAGATTCAGCA 2057
 Db 2184 TCGTATTTCGACCAATGAAATTTATGTATGACCAACTTTTATGGAATTTGTAGTTTGGAA 2243
 Oy 2058 CTGTATACAAATGTGTTTTTGAAGATTTGTAAACCGGTGGCATTTAAGCGGCTTTACTCTC 2117
 Db 2244 AAGTGTACAAAGGCAATTTTGAATGATGACAAATGGTTGCTGTCAAGCTTCTCAATCTAC 2303
 Oy 2118 ACAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAATGATCAAGC 2177
 Db 2304 AAAATGAAGGGGCTTCMAAAGATTTTGTATGAGAAATGCAAAATTTTGGGTAGAGTTAGAC 2363
 Oy 2178 ACAGAAATCTTGTGAGCCCTACAAAGCTTATTCCTCTCTCAGTTGGGGAGTCTTCGTTCT 2237
 Db 2364 ACCGGAATTTGATTTGGGTCATACCTTCTATTCAGATCTCMAATCAAACTTTGATAT 2423
 Oy 2238 ATGACTATTTGGAAAAATGATGCT--CTGGGATCTTCTTATGCGCCCTACGAAGAAA 2294
 Db 2424 TTCCATTTATGCGCAAAAGGAAGCTCAGAAAAAGTGTATATCCGATGATGAGAACAA 2483
 Oy 2225 AGACTCTGATTTGGGACACACGGCTTAATGATGCAATATGGTGCAGACAAAGTTTAGCT 2354
 Db 2484 GTTGTTAATTTGATTCAAAGGTTGAATATGACAAATGAAATGCGCCMAAGCATGATAT 2543
 Oy 2355 ATCTACACCATGACGTGATGTCMAAGATCATTTCCAGAGACGTGAAGTCGTCAAACTTC 2414
 Db 2544 ATCTCCATCATCATTTGCTTTGTGCAAGATTCATTTGATTTGAAACCAACAAATGTGT 2603
 Oy 2415 TCTTGGACAAAGACTTAGAGGCTGTTTGACAGATTTTGAATGACGAAAGCTTGTGTG 2474
 Db 2604 TGTGGGTGAAGATATGACTCATATTTAAATAGACTTTGGGATGCTACTATATGTTTGG 2663

 RESULT 14
 US-09-180-439-5
 ; Sequence 5, Application US/09180439
 ; Patent No. 6225532
 ; GENERAL INFORMATION:
 ; APPLICANT: Dixon, Mark S
 ; APPLICANT: Hatzixanthos, Kostas
 ; APPLICANT: Jones, David A
 ; APPLICANT: Jones, Jonathan DG
 ; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
 ; FILE REFERENCE: 620 - 53
 ; CURRENT APPLICATION NUMBER: US/09/180.439
 ; CURRENT FILING DATE: 1998-12-06
 ; EARLIER APPLICATION NUMBER: PCT/GB97/01249
 ; EARLIER FILING DATE: 1997-05-08
 ; EARLIER APPLICATION NUMBER: GB 9609681.3
 ; EARLIER FILING DATE: 1996-05-09
 ; EARLIER APPLICATION NUMBER: GB 9619924.5
 ; EARLIER FILING DATE: 1996-09-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 3541
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 ; US-09-180-439-5

	Query Match	5.4%	Score 170.2,	DB 3;	Length 3541;
	Best Local Similarity	48.0%;	Pred. No. 1.1e-43;		
	Matches 518,	Conservative 0;	Mismatches 558;	Indels 3;	Gaps 1.
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Db	865	CTTTTCCATTTCACCTCCCTCTTTTCTCGAGAACTTGATCTTAGCAACAACAATATCT	924
Qy	606	GTGGAGAGATCCAGAGACTTATTTACTGGAATGAAGTCTTCAGATCTTGGGTGCGAG	665
Db	925	CTGGTACCATTCACCTGAGATTGGTAATCTCAAAATCTGTCTATCTTGACTGAACA	984
Qy	666	GAAACAACCTTAGTCGGTAACTATTTCTCCAGATTGTGTCAACTGACTGTCCTTGTGATT	725
Db	985	CCAACTCAATTTCCAGGAACAATTTCCACACAATGCGTTCACCTACCAAGCTTCACATCA	104
Qy	726	TTGACGTAGAGAAACAACAGTTTGACTGGTAGATACCTGAGACGATAGAGAAATTCACGTG	785
Db	1045	TCCGATATTTTAACAATCATTTAATATGCTTATTCCTGAGAAATAGGTTACCTTAAGGT	110
Qy	786	CCCTTCAGGTTTGGACTTGTCTCAACAATCAAGCTAATCTGTGAGATCCCTTTGACATCG	845
Db	1105	CTCTTACTAGACTATCTTTGGGGTATCAACTTTCCTTAGTGTTCTATTCCTGCTTCATTGG	116
Qy	846	GCTTCCTG---CAAGTTGCACATATATCAATTGCAGAGCAATCACTCTCGGGAAGATTC	902
Db	1165	GCAATATGACCAACTGTGCTTTTATTTATTTCTTAGAAATATAGCTTCTCGCTTTATTC	122
Qy	903	CATCAGTATTTGTCTCAATGCAAGCCCTTCGAGCTTAGATCTAAGTGGCAACTGTTTGA	962
Db	1225	CTGAAGAAATAGTTACTCAATGAAGTCTCTTACTAAGCTATCTTTGATATCAACTTTCTTA	128
Qy	963	GTGATCTATTTCTCCGATTTCTCGAAATCTTACTTTCAACGAGAAATGTATTGGACA	102
Db	1285	GTGGTTCATTCCTGCTTCATTTGGGGAAATCGAACAACCTGTCTTTTGTATCTTTTACA	134
Qy	1023	GTAACAACCTACTGCTTCAATTTCCACCTGAGCTTGGAAACAATGCAAACTCCACTTACC	108
Db	1345	ATTAATCAGCTTCTTGCTCTTATTCCTGAAGAAATAGTTTACTTAAGTCTCTTACTTACC	140
Qy	1083	TGGAACCTCAATGATATATCATCTCAAGGGTCAATATCAACAAGAGCTTGGGAAGCTTACTG	114
Db	1405	TAGATTGAAAGAGATGCTCTTAATGAGCTCTATCTGCTTCAATTGGGAAATCTGAACA	146
Qy	1143	ACTTGTTTGATCTGAATGTGGCCCAACATGATCTGGAAGAGACTTATCTGTATCATCTCA	120
Db	1465	ACTGTCTAGGTTGATCTTTACAAATATCAAGCTTTCGGCTCTATTCCTGAAGAAATAG	152
Qy	1203	GCTCTTGGCAAAATCTAAACAGCTTAAATGTTCATGAGGAACAAGTTTATGTGCACTATAC	126
Db	1525	GTTACTTGAGTCTCTTACTATCTATATTTGGGTAATACCTCTTATTTGGAATTTATTC	158
Qy	1263	CCCGAGCACTTCAAAAGCTAAGAAAGTACTTACTTAAATCTGTCCAGCAACAATATCA	132
Db	1585	CTGCTTCAATTCGGCAATATGAGAAATCTGCAAGCTGTCTTCTCATGTATTAACAATCTCA	164
Qy	1323	AAAGTCCAATCCGGGTGAGCTATCTGATCTCGTAATCTTGATATCAATTTGATCTTTTCCA	138
Db	1645	TTGGGGAATTTCTTCAATTTGTGTGCAATTTAACAATCACTGAACTGTGTGTATATGCGCA	170
Qy	1383	ACAAACAAGATTAATGAAATCAATCTTCTTCTCCCTGTGTGATTTGGAGCAATCTTCCAMA	144
Db	1705	GAAACAATTTGAAGGAAAAAGTTCGCAATGTTGGGTAATATCAGTGACCTTGTGTTT	176
Qy	1443	TGAACTTGAGTAGAATATATTAATCTGTGTAGTTCACGGGCACTTTGGAAATCTTAAGA	150
Db	1765	TGTCAATGTCACTAAATAGTTCAGTGAGAGCTCCCTTTCATCTAATTTTCCAAATTTAACAT	182
Qy	1503	GCATCATGGAATATGATCTTTCAAATATATGATCTCGGCCCAATTCAGAAAGACTTA	156
Db	1825	CACATTAATAATCTGATTTTGGCAGAAACAATCTGGAGGAGCAATACACAAATGTTTTG	188
Qy	1563	ACCAATTAACAACATATATTTTCTGAGACTGGAATAATATTAACCTGACTGTAAATGTT	1621
Db	1885	GCATATATTAGAGCTCGAGGTTTTTGTATGCAAGATTAACAACCTTCTGTGGAGCTCT	1943

RESULT 15
US-10-101-464A-837

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; Sequence 837, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higinis, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704.302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228.986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162.866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 837
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-837

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Query Match 5.2%; Score 164.2; DB 3; Length 2691;

Best Local Similarity 48.1%; Pred. No. 8.3e-42;

Matches 497; Conservative 0; Mismatches 533; Indels 3; Gaps 1;

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QY 679 CGGTACATTTCTCCAGATTGTGTCAACTGACTGCTCTTGGATTGTGACGTAAGAA 738
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QY 739 CAACAGTTGACTGTGATGATTAACCTGAGACGATAGAAATTGCACTGCTTCCAGTTT 798
DB 525 TAATAGTTTACAGGGAGTATACCACTTCTATCGGCACAGCGCTTGGCAACGAT 584
QY 799 GGACTGTCTCAATCAGTAAGTGTGAGATCCCTTTGACATGGGCTTCCG---CA 855
DB 585 GAATCTTGAGAGAACCGATTGAGGGGTCTATCCAGCAAAATTCGGCGCTGGTCCA 644
QY 856 AGTGCACATTTATTCATTCGAGGCAATCACTCTGGGAAGATTCCATCAGTATGG 915
DB 645 CTGGAATCTCTCAGTTGATACAGCAATCTGAGTGAAGCATCCCACTTCTCGC 704
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DB 945 CTACTTCACGACAATATGATTAAGTGAAGACATCCAACTTTCTGTCAACTGCACTTC 1004
QY 1216 TCTAAACAGCTTAATGTTTCATGGAACAAGTTAGTGCACTAATCCCGAGACTTCA 1275
DB 1005 GCTCTCGCATTTGGGGGCTAGCGGAACAATGAGTTCATCCCTTCGGTATGGG 1064
QY 1276 AAAGCTAAGAAATGATGACTTAATCTGTCTCAGCAACAATATCAAGGTCCATCC 1335

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DB 1065 TTTGATGAAAAACATATCATTTTATGATTATTCACAAACTCTCTCACTGGCCATATCC 1124
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DB 1125 TCCACACCTATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1184
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DB 1185 AGGTAGCATTCCTCCCATTTATTTATTCACAAATGATGATGATGATGATGATGATGATGAT 1244
QY 1456 AATCATATACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1515
DB 1245 CAACAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1304
QY 1516 AGATCTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1575
DB 1305 TGATTTATCAAAATTAACATTTTCACTGATGATGATGATGATGATGATGATGATGATG 1364
QY 1576 CATTAATTTGCTGAGACTGGAATAATAAAGTGTGATGATGATGATGATGATGATGATG 1635
DB 1365 TCTTACTGCTGATCTATCAAGCAAAATTCAGTGAATCTCTCCGCTAGTATTAAG 1424
QY 1636 CTGCTCAGTCTCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1695
DB 1425 TCACTGGAATTTCAAGCTCTATATCTATATTAATTAATTAATTAATTAATTAATTA 1484
QY 1696 GAACAATTAACCTTC 1708
DB 1485 TAATATTAAGTTTC 1497

```

Search completed: September 3, 2006, 18:19:03
Job time : 413 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:14:32 / Search time 1881 Seconds
(without alignments)
11772.388 Million cell updates/sec

Title: US-10-519-135-1
Perfect score: 3176
Sequence: 1 gttctctctcatgagact.....acttctcataagttcttgc 3176

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
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- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3176	100.0	3176	12	AD132613 Thale cre
2	3136.2	98.7	3176	2	AAT62124 Arabidops
3	3136.2	98.7	3176	14	AED28148 Arabidops
4	2930	92.3	2930	8	ADA68568 Arabidops
5	1486.6	46.8	2750	13	ADK30336 Plant ful
6	1161.8	36.6	3089	14	AED28154 Arabidops
7	1117.6	35.2	2901	12	AD132621 Thale cre
8	1112.8	35.0	3100	14	AED28152 Arabidops
9	1102	34.7	9295	2	AAT62125 Arabidops
10	1074.6	33.8	2751	12	AD132619 Arabidops
11	1050.8	33.1	2766	12	AD132617 Thale cre
12	1044.4	32.9	2796	8	ADA71018 Arabidops
13	1035.2	32.6	3000	12	AD132615 Arabidops
14	1015.4	32.0	2533	13	ADK59740 Plant ful
15	995.8	31.4	1872	13	ADK27817 Plant ful
16	940.4	29.6	1859	13	ADK13059 Plant ful
17	915.4	28.8	2895	8	ADA71317 Maize gene
18	901.2	28.4	2315	12	AD132656 Maize tra

19	758.6	23.9	2523	13	ADK60773	Adx60773 Plant ful
20	680	21.4	1798	13	ADK60599	Adx60599 Plant ful
21	625	19.7	650	6	ABO65951	Abog65951 Arabidops
22	552.4	17.4	1688	14	ABE67281	Abe67281 Rice geno
23	543.4	17.1	1456	13	ADK35156	Adx35156 Plant ful
24	533.8	16.8	4356	3	AAA79736	Aaa79736 Pinus rad
25	530.8	16.7	1273	12	AD132633	Ad132633 Maize tra
26	515.6	16.2	522	10	ABK57642	Abk57642 Arabidops
27	489	15.4	501	10	ADK81647	Adk81647 Arabidops
28	488.6	15.4	1346	12	AD132631	Ad132631 Bread whe
29	410.4	12.9	1416	13	ADK28952	Adk28952 Plant ful
30	371.2	11.7	1079	13	ADK37065	Adk37065 Plant ful
31	340.4	10.7	1121	13	ADK61629	Adk61629 Plant ful
32	339.6	10.7	584	13	ACN54994	Acn54994 Cotton an
33	306.8	9.7	683	12	AD132648	Ad132648 Maize tra
34	306.8	9.7	683	12	AD132655	Ad132655 Maize tra
35	299.2	9.4	636	12	AD132623	Ad132623 Bread whe
36	275	8.7	6240	10	ADB84162	Adb84162 Gene exp
37	269.8	8.5	556	12	AD132654	Ad132654 Maize tra
38	267.4	8.4	4686	8	ADA71282	Ada71282 Rice gene
39	265.8	8.4	558	12	AD132652	Ad132652 Maize tra
40	263.8	8.3	549	12	AD132628	Ad132628 Bread whe
41	260.4	8.2	719	12	AD132630	Ad132630 Bread whe
42	248.4	7.8	3375	6	ABZ12862	Abz12862 Arabidops
43	241.6	7.6	3330	8	ADA70802	Ada70802 Rice gene
44	241.6	7.6	3330	11	ACL26733	ACL26733 Rice abio
45	237.6	7.5	634	12	AD132651	Ad132651 Maize tra

ALIGNMENTS

RESULT 1	AD132613	standard; DNA; 3176 BP.
ID	AD132613	
XX	AD132613;	
AC	XX	
XX	XX	
DT	22-APR-2004	(first entry)
XX	XX	
DE	Thale cress transpiration efficiency-related ERECTA DNA.	
XX	XX	
KM	plant; transpiration efficiency; ERECTA; breeding; genetic engineering;	
KW	thale cress; ds; gene; chromosome 2.	
XX	XX	
OS	Arabidopsis thaliana.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	77..3007
FT	FT	/tag= a
FT	FT	/product= "Thale cress transpiration efficiency-related ERECTA protein"
XX	XX	
XX	XX	
PN	W02004005555-A1.	
XX	XX	
PD	15-JAN-2004.	
XX	XX	
PF	02-JUL-2003; 2003WO-AU000854.	
XX	XX	
PR	02-JUL-2002; 2002AU-0003339.	
XX	XX	
PA	(AUSU) UNIV AUSTRALIAN NAT.	
XX	XX	
PI	Masle J, Farquhar GD, Gilmore SR,	
XX	XX	
DR	WPI; 2004-091390/09.	
XX	XX	
DR	P-PSDB; AD132614.	
XX	XX	
PT	Selecting plant having enhanced transpiration efficiency, useful for	
PT	producing plants with enhanced transcription efficiency comprising	
PT	selecting plant expressing a genetic marker linked to the ERECTA locus in	
PT	the genome of the plant.	
XX	XX	

PS Claim 3; SEQ ID NO 1; 209pp; English.
XX
CC The invention relates to a novel method for selecting a plant having
CC enhanced transpiration efficiency comprising detecting a genetic marker
CC for transpiration efficiency, where the marker comprises a nucleotide
CC sequence linked genetically to an ERBCTA locus in the genome of the plant
CC and selecting a plant that comprises or expresses the genetic marker. The
CC method of the invention may be useful for selecting a plant having
CC enhanced transpiration efficiency. The isolated ERBCTA gene or allelic
CC variant or protein-encoding region may be useful in the preparation of a
CC genetic construct for modulating the transpiration efficiency of a plant.
CC Furthermore, the ERBCTA genes may be useful for producing plants having
CC enhanced transpiration efficiency by both traditional plant breeding and
CC genetic engineering approaches. The current sequence is that of the thale
CC cress ERBCTA DNA of the invention which is located on chromosome 2.
XX
SQ Sequence 3176 BP; 896 A; 660 C; 667 G; 953 T; 0 U; 0 Other;
Query Match 100.0%; Score 3176; DB 12; Length 3176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCTTCATGAGAGACTTGAAGCTTTAAAGTATATCTAAAACGCACTGCTTTTA 60
DB 1 GTTCTCTTCATGAGAGACTTGAAGCTTTAAAGTATATCTAAAACGCACTGCTTTTA 60
QY 61 AGACTGTGTGGAAGAAATGGCTCTGTGTAGATATGTTCTTCTGGGTTTCTCTCTG 120
DB 61 AGACTGTGTGGAAGAAATGGCTCTGTGTAGATATGTTCTTCTGGGTTTCTCTCTG 120
QY 121 CTGAGCTTAGTACTGCTGCTGACTTGCAGAGAGAGCAAGTGTGAGATTAAGAA 180
DB 121 CTGAGCTTAGTACTGCTGCTGACTTGCAGAGAGAGCAAGTGTGAGATTAAGAA 180
QY 181 GTCAATTCAAGATGGAACATGTTCTTTATGACTGACAACTTCACTTTTGGATTA 240
DB 181 GTCAATTCAAGATGGAACATGTTCTTTATGACTGACAACTTCACTTTTGGATTA 240
QY 241 TTGTGTCTGGAGAGTGTGCTTGTGAAATGTCACTCAATGTGTGCTTAAATT 300
DB 241 TTGTGTCTGGAGAGTGTGCTTGTGAAATGTCACTCAATGTGTGCTTAAATT 300
QY 301 GTCAATTTGATCTGTGATGAGAAATCTCACTGCTAATTTGAGATCTCAAGACTCTT 360
DB 301 GTCAATTTGATCTGTGATGAGAAATCTCACTGCTAATTTGAGATCTCAAGACTCTT 360
QY 361 GTCAATTTGATCTGTGAGAGTAAATCGCTGTCTGACAAATCCCTGATGAGATTGGTGA 420
DB 361 GTCAATTTGATCTGTGAGAGTAAATCGCTGTCTGACAAATCCCTGATGAGATTGGTGA 420
QY 421 TTCTTCTTTGAAACCTTGAAGCTTAATCCTTGAATTAAGTGTGACATACCGTTTC 480
DB 421 TTCTTCTTTGAAACCTTGAAGCTTAATCCTTGAATTAAGTGTGACATACCGTTTC 480
QY 481 GATTTCGAAGTTGAAGCACTTGAAGAGCTGATTTCTGAAGATTAACCAATTTGATGAGACC 540
DB 481 GATTTCGAAGTTGAAGCACTTGAAGAGCTGATTTCTGAAGATTAACCAATTTGATGAGACC 540
QY 541 GATCCCTTCAACACTTTCAAGATTTCCAAACCTGAAATTTCTGACCTTGGCAAGATTA 600
DB 541 GATCCCTTCAACACTTTCAAGATTTCCAAACCTGAAATTTCTGACCTTGGCAAGATTA 600
QY 601 ACTAGTGTGAGATCCAGAACTTATTTACTGGAATGAAGTTCTTCAAGATTTGGGTT 660
DB 601 ACTAGTGTGAGATCCAGAACTTATTTACTGGAATGAAGTTCTTCAAGATTTGGGTT 660
QY 661 GCGAGAAACAACTTACGCTTAACTTTCTCAAGATTTGTCACTGACTGCTTTTG 720
DB 661 GCGAGAAACAACTTACGCTTAACTTTCTCAAGATTTGTCACTGACTGCTTTTG 720
QY 721 GTATTTTGAAGTAAAGAAACAAAGTTTGAAGTGTGATACCTGAGAGATGAAATTTG 780
DB 721 GTATTTTGAAGTAAAGAAACAAAGTTTGAAGTGTGATACCTGAGAGATGAAATTTG 780

QY 781 CACTGCTTCCAGATTTTGGACTTGTCTTACATGACTAATCTGTGAGATCCCTTTTGA 840
DB 781 CACTGCTTCCAGATTTTGGACTTGTCTTACATGACTAATCTGTGAGATCCCTTTTGA 840
QY 841 CATGCGCTTCTCGAAGTTGCAACATTTATATTGCAAGGCAATCACTCTCTGGAAAGAT 900
DB 841 CATGCGCTTCTCGAAGTTGCAACATTTATATTGCAAGGCAATCACTCTCTGGAAAGAT 900
QY 901 TCCATGAGATTTGATGTCTATGCAAGCCCTTGAGCTTATGATCTAATGAGCAATGTT 960
DB 901 TCCATGAGATTTGATGTCTATGCAAGCCCTTGAGCTTATGATCTAATGAGCAATGTT 960
QY 961 GAGTGAATCTATTCCTCCGATTTCTCGGAAATCTTACTTTTCCAGAGAAATTTGATTTGA 1020
DB 961 GAGTGAATCTATTCCTCCGATTTCTCGGAAATCTTACTTTTCCAGAGAAATTTGATTTGA 1020
QY 1021 CAGTAAACAGCTGACTGTTCAATTTCCACTGAGCTTGGAAACATGTCAAATCTCCATTA 1080
DB 1021 CAGTAAACAGCTGACTGTTCAATTTCCACTGAGCTTGGAAACATGTCAAATCTCCATTA 1080
QY 1081 CCTGGAACCTAATGATATATCATCTACGGGTATATACACAGAGCTTGGGAAAGCTTAC 1140
DB 1081 CCTGGAACCTAATGATATATCATCTACGGGTATATACACAGAGCTTGGGAAAGCTTAC 1140
QY 1141 TGAATTTGATCTGATGTGCGCAACATGATCTGGAAGACCTTATACCTGATCATCT 1200
DB 1141 TGAATTTGATCTGATGTGCGCAACATGATCTGGAAGACCTTATACCTGATCATCT 1200
QY 1201 GAGCTCTTGCACAAATCTTAAACAGCTTAAATGTTTATGAGGAACAACTTTAGTGACATAT 1260
DB 1201 GAGCTCTTGCACAAATCTTAAACAGCTTAAATGTTTATGAGGAACAACTTTAGTGACATAT 1260
QY 1261 ACCCGAGCAATTTCAAAAGCTAGAAAGTATGACTTACCTTATCTGTCAGCAACAATAT 1320
DB 1261 ACCCGAGCAATTTCAAAAGCTAGAAAGTATGACTTACCTTATCTGTCAGCAACAATAT 1320
QY 1321 CAAAGGTCCAATCCCGTTGAGCTATCTGATCGTAACTTAACTTGAATCTTTG 1380
DB 1321 CAAAGGTCCAATCCCGTTGAGCTATCTGATCGTAACTTAACTTGAATCTTTG 1380
QY 1381 CAACACAAATTAATGAAATCATCTCTTCTTCTGTTGGATTTGGAGCATCTTCCAA 1440
DB 1381 CAACACAAATTAATGAAATCATCTCTTCTTCTGTTGGATTTGGAGCATCTTCCAA 1440
QY 1441 GATGAATCTGATGAAGAAATATATTAATCTGATGATTCAGGGGCACTTGGAAATCTAAG 1500
DB 1441 GATGAATCTGATGAAGAAATATATTAATCTGATGATTCAGGGGCACTTGGAAATCTAAG 1500
QY 1501 AAGCATCATGAAATATGATCTTTCAAAATTAATGATCTCTGAGCCAAATTCAGAAAGACT 1560
DB 1501 AAGCATCATGAAATATGATCTTTCAAAATTAATGATCTCTGAGCCAAATTCAGAAAGACT 1560
QY 1561 TAAACCAATTAAGAAACATTAATTTTGTGAGACTGGAAGAAATTAACCTGATGTAATGT 1620
DB 1561 TAAACCAATTAAGAAACATTAATTTTGTGAGACTGGAAGAAATTAACCTGATGTAATGT 1620
QY 1621 TGGTTCAATTAAGCAACGTCTCAGCTCTCACTGATTAAGATTAATCTAATAACAACCTCGT 1680
DB 1621 TGGTTCAATTAAGCAACGTCTCAGCTCTCACTGATTAAGATTAATCTAATAACAACCTCGT 1680
QY 1681 AAGTGAATATCCCTTAAGAAACATTAATCTTCAAGATTTTCCAGAGACAGCTTCAATTTGCAA 1740
DB 1681 AAGTGAATATCCCTTAAGAAACATTAATCTTCAAGATTTTCCAGAGACAGCTTCAATTTGCAA 1740
QY 1741 TCTGTGTCTTGGCGGATGTTGGCTAAATCTACCGGTGATGATTTCTGTGAACTGTACG 1800
DB 1741 TCTGTGTCTTGGCGGATGTTGGCTAAATCTACCGGTGATGATTTCTGTGAACTGTACG 1800
QY 1801 AGTGTCAATCTTAAGACAGCTAATCTTGAATTAAGTATTTGGGGGCACTTGGATCTTCT 1860
DB 1801 AGTGTCAATCTTAAGACAGCTAATCTTGAATTAAGTATTTGGGGGCACTTGGATCTTCT 1860

QY	1861	TATGGCTTAATAGAGCTTGCAGCCGCAATATCTCTCTCTTCTGTAGATCACT	1920
Ds	1861	CATGGCTTAATAGAGCTTGCAGCCGCAATATCTCTCTTCTGTAGATCACT	1920
QY	1921	TGACAAACCACTAATCTTATTCGACACCCAACTCGTCATCCCTCATATGACATGGCACT	1980
Ds	1921	TGACAAACCACTAATCTTATTCGACACCCGACTCTCATCTTATGAAACATGGCACT	1980
QY	1981	CCAGCTTTACGAGGATATCATGAGATGACAGAAATCTAAGTAGAAGATATCATTTGG	2040
Ds	1981	CCAGCTTTACGAGGATATCATGAGATGACAGAAATCTAAGTAGAAGATATCATTTGG	2040
QY	2041	GCACGGAGCATCAAGCACTGTATACAAATGTGTTTGAAGAAATTTGAACCCGGTTGGAT	2100
Ds	2041	GCACGGAGCATCAAGCACTGTATACAAATGTGTTTGAAGAAATTTGAACCGGTTGGAT	2100
QY	2101	TAAAGGGCTTACTCTCAACCCCAAGTCATGATAAGATTGTAAGACAGAACTCGAGAT	2160
Ds	2101	TAAAGGGCTTACTCTCAACCCCAAGTCATGATAAGATTGTAAGACAGAACTCGAGAT	2160
QY	2161	GCTAAGTAGCATCAAGCAGAGAAATCTTGTAGCCTACAACTTATTCCTCTCTCACTT	2220
Ds	2161	GCTAAGTAGCATCAAGCAGAGAAATCTTGTAGCCTACAACTTATTCCTCTCTCACTT	2220
QY	2221	GGGGAGTCTTCTGTCTATAGCATTTTGGAAAATGTATGCTCTGGGATCTTCTTCAATGG	2280
Ds	2221	GGGGAGTCTTCTGTCTATAGCATTTTGGAAAATGTATGCTCTGGGATCTTCTTCAATGG	2280
QY	2281	CCCTACGAAAGAAAAGACTCTTGTATGGGACACACGGCTTAAAGATAGATATGGGACGC	2340
Ds	2281	CCCTACGAAAGAAAAGACTCTTGTATGGGACACACGGCTTAAAGATAGATATGGTGCACG	2340
QY	2341	ACAAAGTTTACCTATCTTACACCAATGACTGTAGTCCAAAGATCATCTCACAGACGTAAG	2400
Ds	2341	ACAAAGTTTACCTATCTTACACCAATGACTGTATGTCMAAGATCATCTCACAGACGTGA	2400
QY	2401	GTCTGTCCAACTTCTTGGACAAAGACTTATGAGGCTGTTTGAACATTTTGGAAATAGC	2460
Ds	2401	GTCTGTCCAACTTCTTGGACAAAGACTTATGAGGCTGTTTGAACATTTTGGAAATAGC	2460
QY	2461	GAAAAGCTGTGTGTGTCAAAAGTCAATCTTCAACCTTACGTATGGGACAGATAGGTTA	2520
Ds	2461	GAAAAGCTGTGTGTGTCAAAAGTCAATCTTCAACCTTACGTATGGGACAGATAGGTTA	2520
QY	2521	CATAGACCCCGAGTATGCTCCGACTTCCAGGCTCACTAGAGAAATCCGATGTCTACAGTTA	2580
Ds	2521	CATAGACCCCGAGTATGCTCCGACTTCCAGGCTCACTAGAGAAATCCGATGTCTACAGTTA	2580
QY	2581	TGGAATAGTCTTCTTGAAGTTTATACCCGAGGAAAGCCGTATGATGACGAATCCAAATCT	2640
Ds	2581	TGGAATAGTCTTCTTGAAGTTTATACCCGAGGAAAGCCGTATGATGACGAATCCAAATCT	2640
QY	2641	CCACCATCTGATATATGTCAAAGACGGGGAACAATGAAGTGTGAAATATGGAGATCCAGA	2700
Ds	2641	CCACCATCTGATATATGTCAAAGACGGGGAACAATGAAGTGTGAAATATGGAGATCCAGA	2700
QY	2701	CATCAACATCGACGTGTAAAGATCTCGGTGTGTGAAGAAATTTTCCACTCGGCACTCCT	2760
Ds	2701	CATCAACATCGACGTGTAAAGATCTCGGTGTGTGAAGAAATTTTCCACTCGGCACTCCT	2760
QY	2761	ATGCAACCAAAAGACGCGGAATGATCGACCCACAAATGACACAGGTGACTCGTGTCTTCGG	2820
Ds	2761	ATGCAACCAAAAGACGCGGAATGATCGACCCACAAATGACACAGGTGACTCGTGTCTTCGG	2820
QY	2821	CAGTTTATATGCTATATCGGAACAACCACTGTGTGCGACTGACACGTACAGGAGCGCTGGCTGG	2880
Ds	2821	CAGTTTATATGCTATATCGGAACAACCACTGTGTGCGACTGACACGTACAGGAGCGCTGGCTGG	2880
QY	2881	TTCTGTCTACGCTCATGATAGTATGCAAAATCTCAAGACTCTCTCATTTCTGTCAATTGTCTTTC	2940
Ds	2881	TTCTGTCTACGCTCATGATAGTATGCAAAATCTCAAGACTCTCTCATTTCTGTCAATTGTCTTTC	2940
QY	2941	CATAGATGCTTCTGATGCTCAACTGTATTTCTTGGTTTGGACAAATATTTCTCGAAACAG	3000

ID	Accession	Gene Name	Location/Qualifiers	Score	DB	Length	Mismatches	Indels	Gaps
Db	2941	CATAGAGCTTCTATAGCTCAACGCTTCTTCGTTGGACAGTATTTCTCGAAGCAG		98.7%	3136.2	3176	0	3	0
Qy	3001	TGAGTAGTCTTTTCGTTAGAGAGAGAACTTTAAACGGTATCTTTTCGTTGCGTTAAAGCT	Location/Qualifiers	99.9%	Pred. No. 0		0		
Db	3001	TGAGTAGTCTTTTCGTTAGAGAGAGAACTTTAAACGGTATCTTTTCGTTGCGTTAAAGCT	/*tag= a						
Qy	3061	GTTTGAAAAAATTAATGCTCATGTGAATATATAGCATGCTGCTTATATATATAGCAAG	/note= "plant morphogenesis regulatory protein"						
Db	3061	GTTTGAAAAAATTAATGCTCATGTGAATATATAGCATGCTGCTTATATATATAGCAAG							
Qy	3121	TGTGTGGTGCAATATGCTTCAGACCTGGACCTTGACTTCTTAAGTCTTGCC							
Db	3121	TGTGTGGTGCAATATGCTTCAGACCTGGACCTTGACTTCTTAAGTCTTGCC							
RESULT 2									
ID	AA062124	standard; cDNA; 3176 BP.							
XX	AA062124;								
XX	AA062124;								
DT	10-JUN-1997	(first entry)							
DE	Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.								
XX	Plant; morphogenesis; regulation; short; stem; alteration; inflorescence;								
KW	extraneous; gene; expression; transformation; increase; control; form;								
XX	length; de.								
XX	Arabidopsis thaliana.								
OS	Arabidopsis thaliana.								
XX	Key								
XX	FT	51..2981							
XX	CDS	/*tag= a							
XX	FT	/note= "plant morphogenesis regulatory protein"							
XX	FT								
XX	JF09056382-A.								
XX	PD	04-MAR-1997.							
XX	XX								
XX	24-AUG-1995;	95JP-00216187.							
XX	PR	24-AUG-1995;	95JP-00216187.						
XX	XX								
XX	24-AUG-1995;	95JP-00216187.							
XX	PA	(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.							
XX	PA	(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.							
XX	WI	1997-206629/19.							
XX	DR	P-PSDB; AAM13408.							
XX	PT	DNA encoding plant morphogenesis regulatory protein - useful to yield							
XX	PT	plants with short stems or altered inflorescence.							
XX	PS	Claim 1; Page 6-10; 17pp; Japanese.							
XX	XX								
XX	XX	The present sequence encodes an Arabidopsis thaliana plant morphogenesis							
XX	CC	regulatory protein (MRP), which can be used to yield a plant with e.g.							
XX	CC	short stems or altered inflorescence. The MRP acts on a plant at a							
XX	CC	specific site for a specific period, and can therefore be used to							
XX	CC	regulate extraneous gene expression in a plant. The MRP's cDNA or genomic							
XX	CC	cDNA can be used to transform a plant to increase its MRP expression, and							
XX	CC	therefore control the form (particularly stem length) of the plant							
XX	SO	Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T; 0 U; 0 Other;							
Qy	Query Match	98.7%; Score 3136.2; DB 2; Length 3176;							
Qy	Best Local Similarity	99.9%; Pred. No. 0;							
Qy	Matches 3138; Conservative	0; Mismatches 3; Indels 0; Gaps 0;							
Db	1	CTTTTAAGATATCTTAATAACGAGCGCTTTTAAGCTGTGCTGAGAAATGGCTCTGT							
Db	1	CTTTTAAGATATCTTAATAACGAGCGCTTTTAAGCTGTGCTGAGAAATGGCTCTGT							

QY	87	TTAGAGATATTGTTCTTCTTGGGGTTTCCTCTGCTTGAAGCTTAGTACCTACTGTACTT	146
Db	61	TTAGAGATATTGTTCTTCTTGGGGTTTCCTCTGCTTGAAGCTTAGTACCTACTGTACTT	120
QY	147	CAGAGAGAGGAGCAACGTTGGCTGGAGATTGAAGACTCAATCAAGATGTGAACATGTTG	206
Db	121	CAGAGAGAGGAGCAACGTTGGCTGGAGATTGAAGACTCAATCAAGATGTGAACATGTTG	180
QY	207	TTTATGACTGGACAACTTCACCTTCGAGTTATGTGTGAGAGGTGTCTTGTG	266
Db	181	TTTATGACTGGACAACTTCACCTTCGAGTTATGTGTGAGAGGTGTGTGTGTG	240
QY	267	AAAAGTCACTTCAATGTGTGTCTTAATTGTGCAGATTGGAATCTTGATGGAGAA	326
Db	241	AAAAGTCACTTCAATGTGTGTCTTAATTGTGCAGATTGGAATCTTGATGGAGAA	300
QY	327	TCTCACTGTCTATTGGAGATCTCAAGAGTCTCTTGTCAATTGATCTGGAGGTATCGCT	386
Db	301	TCTCACTGTCTATTGGAGATCTCAAGAGTCTCTTGTCAATTGATCTGGAGAGTATCGCT	360
QY	387	TGTCGGACAAATCCCTGATGAGATTGGTGACTGTTCTTCTTGGAAAATTAGACTTAT	446
Db	361	TGTCGGACAAATCCCTGATGAGATTGGTGACTGTTCTTCTTGGAAAATTAGACTTAT	420
QY	447	CCCTCAATGAAATTAGGTGTGACATACAGGTTTTGCATTCGAAAGTTGAAGCACTTGAGC	506
Db	421	CCCTCAATGAAATTAGGTGTGACATACCGTTTTGCATTCGAAAGTTGAAGCACTTGAGC	480
QY	507	AGCTGATTTCTGAAGATAACCAATTGATPAGACCGATCCCTTCACACCTTTCACAGATTG	566
Db	481	AGCTGATTTCTGAAGATAACCAATTGATPAGACCGATCCCTTCACACCTTTCACAGATTG	540
QY	567	CAAACCTGAAAATTGTGACTGGACAGATPAACTAGTGGTGAATPACCAAGACTTA	626
Db	541	CAAACCTGAAAATTGTGACTGGACAGATPAACTAGTGGTGAATPACCAAGACTTA	600
QY	627	TTTATCTGAAATGAAAGTTCTTCAGTACTTGTGGGTTGCGAGAAAACAATTAATCGGTACA	686
Db	601	TTTATCTGAAATGAAAGTTCTTCAGTACTTGTGGGTTGCGAGAAAACAATTAATCGGTACA	660
QY	687	TTTTCTCCAGATTTGTGTGCACTGATCTGGTCTTGTGATTTTGAAGCTAAGAAAACAAGTT	746
Db	661	TTTTCTCCAGATTTGTGTGCACTGATCTGGTCTTGTGATTTTGAAGCTAAGAAAACAAGTT	720
QY	747	TGACTGTGAGTATACCTGAGACGATAGAGAAATTGCACTGCCCTTCAGAGTTTTGCACTTGT	806
Db	721	TGACTGTGAGTATACCTGAGACGATAGAGAAATTGCACTGCCCTTCAGAGTTTTGCACTTGT	780
QY	807	CCTACAAATCAGCTAACGTGTGAGATCCCTTTTGAATAGGGTCTCTGCAAGTTGGACAT	866
Db	781	CCTACAAATCAGCTAACGTGTGAGATCCCTTTTGAATAGGGTCTCTGCAAGTTGGACAT	840
QY	867	TATCATTTSCAAGGCAATCACTCTCTGGGAAAGATTCACATCAGTGAATGATCTCATGCAAG	926
Db	841	TATCATTTSCAAGGCAATCACTCTCTGGGAAAGATTCACATCAGTGAATGATGCTCATGCAAG	900
QY	927	CCCTTTCAGTCTTAGATCTAAGTGGCAACTGTGTAGTGAGATCTATTCCTCCGATTCGTG	986
Db	901	CCCTTTCAGTCTTAGATCTAAGTGGCAACTGTGTAGTGAGATCTATTCCTCCGATTCGTG	960
QY	987	GAAATCTTACTTTCACCGAGAAATTGTATTGTCACAGTAACTGATCTGATCTGATTC	1046
Db	961	GAAATCTTACTTTCACCGAGAAATTGTATTGTCACAGTAACTGATCTGATCTGATTC	1020
QY	1047	CACCTGAGCTTGGAAACAATGTCAAAATCCATTAACCTGGAACCTCAATGATATCATCTCA	1106
Db	1021	CACCTGAGCTTGGAAACAATGTCAAAATCCATTAACCTGGAACCTCAATGATATCATCTCA	1080
QY	1107	CGGGTCATATACCAACAAGCTTTGGGAAAGCTTACGACTGTTGTTGATCTGAAATGTGGCCA	1166
Db	1081	CGGGTCATATACCAACAAGCTTTGGGAAAGCTTACGACTGTTGTTGATCTGAAATGTGGCCA	1140

QY	1167	ACATGATCTGGAGAGACCTTACCCTGATCATCTGAGCTCTTGACAAATCTTAAACAGCT	1226
Db	1141	ACAATGATCTGGAGAGACCTTACCCTGATCATCTGAGCTCTTGACAAATCTTAAACAGCT	1200
QY	1227	TAAATGTTCAAGGGGAAACAAGTTTGTGGCACATAACCCGAGCATTTTCAAAAGCTAGAAA	1286
Db	1201	TAAATGTTCAAGGGGAAACAAGTTTGTGGCACATAACCCGAGCATTTTCAAAAGCTAGAAA	1260
QY	1287	GATGACTTACCTTAACTCTGTCTGACGACAAATATCAAAAGTCCAATCCGGTTGAGCTAT	1346
Db	1261	GTATGACTTACCTTAACTCTGTCTGACGACAAATATCAAAAGTCCAATCCGGTTGAGCTAT	1320
QY	1347	CTCGTATTCGGTAACCTTAGATCATTTGGATCTTTCCAAACACAGATTAATGGAATCATTC	1406
Db	1321	CTCGTATTCGGTAACCTTAGATCATTTGGATCTTTCCAAACACAGATTAATGGAATCATTC	1380
QY	1407	CTTCTCCCTGGTGGATTTGGAGACATCTTCGAAGATGAACCTTAGAGTAAGAAATCATATTA	1466
Db	1381	CTTCTCCCTGGTGGATTTGGAGACATCTTCGAAGATGAACCTTAGAGTAAGAAATCATATTA	1440
QY	1467	CTGGTGTAGTTCAGAGCGACTTTGGAAAATCTAAGAGCATCATGGAATAGATCTTTCAA	1526
Db	1441	CTGGTGTAGTTCAGAGCGACTTTGGAAAATCTAAGAGCATCATGGAATAGATCTTTCAA	1500
QY	1527	ATTAATGATATCTCTGGCCCAATTCGACAGAGCTTAAACCAATTACAGACATAATTTTGC	1586
Db	1501	ATTAATGATATCTCTGGCCCAATTCGACAGAGCTTAAACCAATTACAGACATAATTTTGC	1560
QY	1587	TGACACTGGGAAAAATATTAACCTGACTGATATGTTGGTCAATTAGCCACATGCTCAAGTC	1646
Db	1561	TGACACTGGGAAAAATATTAACCTGACTGATATGTTGGTCAATTAGCCACATGCTCAAGTC	1620
QY	1647	TCACTGTATTTGAATGTATCTTCATATAACAACCTCGTAGGTGATATCCCTAAGAACATTAAT	1706
Db	1621	TCACTGTATTTGAATGTATCTTCATATAACAACCTCGTAGGTGATATCCCTAAGAACATTAAT	1680
QY	1707	TCTCAAGATTTTCAACAGACAGCTTCAITGGCAAATCTCGGTCTTTGGCGGTATGTTGGCTAA	1766
Db	1681	TCTCAAGATTTTCAACAGACAGCTTCAITGGCAAATCTCGGTCTTTGGCGGTATGTTGGCTAA	1740
QY	1767	ACTCACCGTGTCATGATTTCTCGTGGAACTGAGACAGTGTCAAATCTTAAGACACTATATTC	1826
Db	1741	ACTCACCGTGTCATGATTTCTCGTGGAACTGAGACAGTGTCAAATCTTAAGACACTATATTC	1800
QY	1827	TTGGAATAGCTAATGGGGGACCTTGTGATCCCTTCATAGTCTTAAATAGACGTTGCCGAC	1886
Db	1801	TTGGAATAGCTAATGGGGGACCTTGTGATCCCTTCATAGTCTTAAATAGACGTTGCCGAC	1860
QY	1887	CGCATTAATCTCTCTCTTTTCTTGATGATCACTTGAACAAACAGTAACCTTATTTGCAAC	1946
Db	1861	CGCATTAATCTCTCTCTTTTCTTGATGATCACTTGAACAAACAGTAACCTTATTTGCAAC	1920
QY	1947	CGAAGCTCTGATCTCTTCATATGAACATGGGACCTTCCACGTTTACGAGAGATATCATTTGAAA	2006
Db	1921	CGAAGCTCTGATCTCTTCATATGAACATGGGACCTTCCACGTTTACGAGAGATATCATTTGAAA	1980
QY	2007	TGACAGAGAATCTTAAGTGAGAGATATATCATTTGGGACCGGAGCATCAAGCACTGTATACA	2066
Db	1981	TGACAGAGAATCTTAAGTGAGAGATATATCATTTGGGACCGGAGCATCAAGCACTGTATACA	2040
QY	2067	AATGTGTTTGGAGAAATTTGAACCGGTTGGATTAAAGCGGCTTTACTTCCACACCAC	2126
Db	2041	AATGTGTTTGGAGAAATTTGAACCGGTTGGATTAAAGCGGCTTTACTTCCACACCAC	2100
QY	2127	AGTCAATGAAACAGTTTGGAAAACAGAACTCGAGATGCTTAAGTACATAGCACAGAAATC	2186
Db	2101	AGTCAATGAAACAGTTTGGAAAACAGAACTCGAGATGCTTAAGTACATAGCACAGAAATC	2160
QY	2187	TTTGAGCGCTACAGACTTATTCCTCTCTCACTTGGGGAAGCTCTGTGTATATGACTATTT	2246
Db	2161	TTTGAGCGCTACAGACTTATTCCTCTCTCACTTGGGGAAGCTCTGTGTATATGACTATTT	2220
QY	2247	TGGAATAATGTAGCCTCTGGGATCTTCTTCACTGAGCCCTACGAAAGAAAAGACTTTGATTT	2306


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Db 2221 TGGAAATGTTACCTCTGGGATCTTCTTATGAGCCCTAGGAAAGAAAAGCTCTGATT 2280
QY 2307 GGGACACACGGCTTAAGATGATGATGTCAGACACAGGTTTATCTTATCTACACCATG 2366
Db 2281 GGGACACACGGCTTAAGATGATGATGTCAGACACAGGTTTATCTTATCTACACCATG 2340
QY 2367 ACTGTGTCCAAAGGATCATTCAGAGACGTCGTAAGTCGTCCAACTTCTTGGACAAAG 2426
Db 2341 ACTGTGTCCAAAGGATCATTCAGAGACGTCGTAAGTCGTCCAACTTCTTGGACAAAG 2400
QY 2427 ACTTAGAGGCTCGTTTGACAGATTTTGGAAATAGCGAAAAGCTTGTGTGTCAAGTCAC 2486
Db 2401 ACTTAGAGGCTCGTTTGACAGATTTTGGAAATAGCGAAAAGCTTGTGTGTCAAGTCAC 2460
QY 2487 ATACTTCAACTTACGTGATGGGACGATAGGTTACATAGACCCCGAGATAGTCTGCACTT 2546
Db 2461 ATACTTCAACTTACGTGATGGGACGATAGGTTACATAGACCCCGAGATAGTCTGCACTT 2520
QY 2547 CACGGCTCACTGAGAAATCCGATGTCTACAGTTATGGAATAGTCCTTGTGAGCTGTAA 2606
Db 2521 CACGGCTCACTGAGAAATCCGATGTCTACAGTTATGGAATAGTCCTTGTGAGCTGTAA 2580
QY 2607 CCCGAGAGAAAGCCGTTGATGACGAATCCATCTCCACCATGATATGTCAAGACGG 2666
Db 2581 CCCGAGAGAAAGCCGTTGATGACGAATCCATCTCCACCATGATATGTCAAGACGG 2640
QY 2667 GGAAACAATGAATGATGAGAAATGGCAGATCCAGACATCAGATGACGCTGTAAGATCTG 2726
Db 2641 GGAAACAATGAATGATGAGAAATGGCAGATCCAGACATCAGATGACGCTGTAAGATCTG 2700
QY 2727 GTGTGTGAGAAAGTTTCCAACTGGCACTCCTATGACCAAAAAGACAGCCGAATGATC 2786
Db 2701 GTGTGTGAGAAAGTTTCCAACTGGCACTCCTATGACCAAAAAGACAGCCGAATGATC 2760
QY 2787 GACCCACAATGACACGAGTACTGCTGTTCTCGGAGTTTATGCTATGCGAACAAACAC 2846
Db 2761 GACCCACAATGACACGAGTACTGCTGTTCTCGGAGTTTATGCTATGCGAACAAACAC 2820
QY 2847 CTGCTGCACTGACAGTCACGTCACGACGCTGCTGTTGCTGCTAGCTGATGATGATGCA 2906
Db 2821 CTGCTGCACTGACAGTCACGTCACGACGCTGCTGTTGCTGCTAGCTGATGATGATGCA 2880
QY 2907 ATCTCAAGACTCCTCATCTGTCGAATGCTCTCCAGTGCATGATGCTGATGCTCACTGT 2966
Db 2881 ATCTCAAGACTCCTCATCTGTCGAATGCTCTCCAGTGCATGATGCTGATGCTCACTGT 2940
QY 2967 TTTCTCGTTTGGACAAGTTATTTCTCAGAACAGTGAATGTTTTCGTTAGAGAGAA 3026
Db 2941 TTTCTCGTTTGGACAAGTTATTTCTCAGAACAGTGAATGTTTTCGTTAGAGAGAA 3000
QY 3027 TCTTTAAACGGTAATCTTTTCTGTTGCGTTAAGCTGTTAGAAAAATTAATGCTCATGTAA 3086
Db 3001 TCTTTAAACGGTAATCTTTTCTGTTGCGTTAAGCTGTTAGAAAAATTAATGCTCATGTAA 3060
QY 3087 AGATATATGACACGCTTATTTATTTATTAAGACAGTGTGTGTGTAATATGCTTCAAGAC 3146
Db 3061 AGATATATGACACGCTTATTTATTTATTAAGACAGTGTGTGTGTAATATGCTTCAAGAC 3120
QY 3147 TGGCACTTAGACTTCTTATTA 3167
Db 3121 TGGCACTTAGACTTCTTATTA 3141
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RESULT 3
AED28148
ID AED28148 standard; cdna; 3176 BP.
XX
AC AED28148;
XX
DT 01-DEC-2005 (first entry)
XX
DE Arabidopsis thaliana ERECTA protein encoding cdna.
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```
XX
KW Plant growth regulation; transgenic plant; crop improvement; transgene;
KW ERECTA; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS
FT 51..2981
FT /tag= a
FT /product= "Arabidopsis thaliana ERECTA protein"
XX
PN US2005223428-A1.
XX
PD 06-OCT-2005.
XX
PF 30-DEC-2004; 2004US-00027304.
XX
PR 01-APR-2004; 2004US-0558529P.
XX
PA (TORI/) TORI K U.
PA (SHPA/) SHPAK E D.
XX
PI Torii KU, Shpak ED;
XX
DR WPI: 2005-675788/59.
DR P-PSDB; AED28149.
XX
PT Modulating plant height and organ shape comprises expressing, in plants,
PT a transgene encoding an ERECTA-like protein lacking an active kinase
PT domain.
XX
PS Disclosure; SEQ ID NO 1; 72pp; English.
XX
CC The present invention relates to a method for modulating plant height and
CC organ shape. The method involves expressing a transgene in a plant, where
CC the transgene encodes an ERECTA-like protein lacking an active kinase
CC domain and where expression of the transgene modulates plant height or
CC organ shape. ERECTA protein contains leucine-rich repeat receptor-like
CC kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and
CC functional Ser/Thr kinase activity. The invention is useful for producing
CC transgenic plant and for enhancing the yield of a crop plant. The present
CC sequence is the Arabidopsis thaliana ERECTA protein encoding cdna.
XX
SQ Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T; 0 U; 0 Other;
XX
Query Match 98.7%; Score 3136.2; DB 14; Length 3176;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 27 CTTTAAAGTATATCTAAAAAGCAGTGGTTTAAAGACTGTGTGAGAAATGGCTCTGT 86
Db 1 CTTTAAAGTATATCTAAAAAGCAGTGGTTTAAAGACTGTGTGAGAAATGGCTCTGT 60
QY 87 TTAGAGATATGTTCTTCTTGGGTTCTCTTCTGCTGAGCTTAGAGCTAGTGACTT 146
Db 61 TTAGAGATATGTTCTTCTTGGGTTCTCTTCTGCTGAGCTTAGAGCTAGTGACTT 120
QY 147 CAGAGAGGAGCAACGTTGCTGAGATTTAGAAAGTCATTCAAAGATGGAACAATGTT 206
Db 121 CAGAGAGGAGCAACGTTGCTGAGATTTAGAAAGTCATTCAAAGATGGAACAATGTT 180
QY 207 TTTATAGCTGAGACAACTTACCTTCTTGGATTTATGTTGTGAGAGAGTGTCTTGTG 266
Db 181 TTTATAGCTGAGACAACTTACCTTCTTGGATTTATGTTGTGAGAGAGTGTCTTGTG 240
QY 267 AAAATGTCACTTCAATGTTGTGCTCTTAATTTGTGCAGATTGAATCTTGATGAGAAA 326
Db 241 AAAATGTCACTTCAATGTTGTGCTCTTAATTTGTGCAGATTGAATCTTGATGAGAAA 300
QY 327 TCTCACCTGCTATTTGAGATCTCAAGAGTCTCTTGTCAATTTGATCTGCAGGTAATGCT 386
Db 301 TCTCACCTGCTATTTGAGATCTCAAGAGTCTCTTGTCAATTTGATCTGCAGGTAATGCT 360
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OY	387	IGTCTGGGCAAAATCCCTGATGAGATTGGTGACCTGTTCTTCTTGGAAAACCTTAGCTTAT	446
Db	361	TGTCGGGCAAAATCCCTGATGAGATTGGTGACCTGTTCTTCTTGGAAAACCTTAGCTTAT	420
OY	447	CCTTCAATGAATTAATGAGTGATACATACCGTTTTCGATTTCGAAAGTTGAAGCAACTTGAGC	506
Db	421	CCTTCAATGAATTAATGAGTGATACATACCGTTTTCGATTTCGAAAGTTGAAGCAACTTGAGC	480
OY	507	AGCTGATTCTGAGAATAACCAATTGATAGACCGATCCCTTCAACACTTTCACAGATTTC	566
Db	481	AGCTGATTCTGAGAATAACCAATTGATAGACCGATCCCTTCAACACTTTCACAGATTTC	540
OY	567	CAAACTGAAAATTTCTGGACTTTGGCAACAGATTAACCTAGTGTGATACCAAGACTTA	626
Db	541	CAAACTGAAAATTTCTGGACTTTGGCAACAGATTAACCTAGTGTGATACCAAGACTTA	600
OY	627	TTTACTGGAAATGAAGTTCTTCAGTATCTTGGTTCGAGAAAACAATTAGTCGGTATCA	686
Db	601	TTTACTGGAAATGAAGTTCTTCAGTATCTTGGTTCGAGAAAACAATTAGTCGGTATCA	660
OY	687	TTTTCTCCAGATTTGTTGTCACATGACTGCTGTCCTTGGTATTTTGGACGTAAGAAACAAGTT	746
Db	661	TTTTCTCCAGATTTGTTGTCACATGACTGCTGTCCTTGGTATTTTGGACGTAAGAAACAAGTT	720
OY	747	TGACTGTGATATACCTTGAGACGATAGAAATTGCACTGCTCTCAAGTTTGGACTTGT	806
Db	721	TGACTGTGATATACCTTGAGACGATAGAAATTGCACTGCTCTCAAGTTTGGACTTGT	780
OY	807	CCTACAATCAGTAACTGGTGAGATCCCTTTTGATACGTGGCTCCTGCAAGTTGCAAGAT	866
Db	781	CCTACAATCAGTAACTGGTGAGATCCCTTTTGATACGTGGCTCCTGCAAGTTGCAAGAT	840
OY	867	TATCATTTGCAAGCAATCAACTCTCTGGGAAGATTCACATCAGTGATTTGATCTCATGCAAG	926
Db	841	TATCATTTGCAAGCAATCAACTCTCTGGGAAGATTCACATCAGTGATTTGATCTCATGCAAG	900
OY	927	CCCTTGCAGTCTTAGATCTAAGTGGCAACTTGTGATGATCTATTTCTCCGATTCTCG	986
Db	901	CCCTTGCAGTCTTAGATCTAAGTGGCAACTTGTGATGATCTATTTCTCCGATTCTCG	960
OY	987	GAAATCTTACTTTCACCCGAAATTGTAATTTGGCAGTAACAAGCTGACTGGTCAATTC	1046
Db	961	GAAATCTTACTTTCACCCGAAATTGTAATTTGGCAGTAACAAGCTGACTGGTCAATTC	1020
OY	1047	CACCTGACCTTGGAAACAATGTCAAACTTCATTACCTGGAATCTCATGATATATCACTCA	1106
Db	1021	CACCTGACCTTGGAAACAATGTCAAACTTCATTACCTGGAATCTCATGATATATCACTCA	1080
OY	1107	CGGGTCATATACACACAGAGCTTGGGAAGCTTACTGACTTGTGTTGATCTGAATGTGGCCA	1166
Db	1081	CGGGTCATATACACACAGAGCTTGGGAAGCTTACTGACTTGTGTTGATCTGAATGTGGCCA	1140
OY	1167	ACAAATGATCTGGAAGAAGCTATACCTGATCACTGAGCTCTTGGCACAAACTTAAACACT	1222
Db	1141	ACAAATGATCTGGAAGAAGCTATACCTGATCACTGAGCTCTTGGCACAAACTTAAACACT	1200
OY	1227	TAAATGTTCAATGGGAACAAGTTTAGTGCACTATACCCGAGCACTTTCAAAAGCTAGAAA	1286
Db	1201	TAAATGTTCAATGGGAACAAGTTTAGTGCACTATACCCGAGCACTTTCAAAAGCTAGAAA	1260
OY	1287	GTATGACTTAACTTAATCTGTCTCAGCAACAATATCAAAAGTCCAAATCCCGTTGAGCTAT	1346
Db	1261	GTATGACTTAACTTAATCTGTCTCAGCAACAATATCAAAAGTCCAAATCCCGTTGAGCTAT	1320
OY	1347	CTTCGATGGGTAACTTAGATATATTGATCTTTCACAACAAGAATAATGGAATCATATTC	1406
Db	1321	CTTCGATGGGTAACTTAGATATATTGATCTTTCACAACAAGAATAATGGAATCATATTC	1380
OY	1407	CTTCTCCCTTGGTATTTGGAGCACTCTCTCAAGTGAACTTGTAGTGAATAATCATATTA	1466
Db	1381	CTTCTCCCTTGGTATTTGGAGCACTCTTCTCAAGTGAACTTGTAGTGAATAATCATATTA	1440
OY	1467	CTGGGTGATTTCCAGCGCACTTTGGAAATCTAAGAAGCATCATGGAATAAGATCTTTGCA	1526

Db	1441	CTGGGTGATGTTCCAGGCGACTTTGGAAATTTAAGAGCATCATTGAAATGATCTTTCAA	1500
Oy	1527	ATAATGATATCTCTGGCCCAATTCAGAAAGCTTAAACAATTACAAGACATTAATTTTGC	1586
Db	1501	ATAATGATATCTCTGGCCCAATTCAGAAAGAGCTTAAACAATTACAAGACATTAATTTTGC	1560
Oy	1587	TGAGACTGGAAATAATTAACCTGACTGTAAATGTTGTTTATTAGCCAACTGTCTCACTC	1646
Db	1561	TGAGACTGGAAATAATTAACCTGACTGTGAATGTGTTCATTAGCCAACTGTCTCACTC	1620
Oy	1647	TCACGTAAATGAATGTATCTCATPACAACCTCGTAGGTGATATCCCTAAGACAATTAACCT	1706
Db	1621	TCACGTAAATGAATGTATCTCATPACAACCTCGTAGGTGATATCCCTAAGACAATTAACCT	1680
Oy	1707	TCTCAAGATTTTTCACGACAGCTTCAATTGGCAATCTGTGCTTTTGGTAGTTGGCTAA	1766
Db	1681	TCTCAAGATTTTTCACGACAGACTTCAATGGCAATCTGTGCTTTTGGTAGTTGGCTAA	1740
Oy	1767	ACTCACCGTGTCAATGATTTCTGTGAACTGTAGCAAGTGTCAATCTCTAAGACGCTAATTC	1826
Db	1741	ACTCACCGTGTCAATGATTTCTGTGAACTGTAGCAAGTGTCAATCTCTAAGACGCTAATTC	1800
Oy	1827	TTTGAATATGCTATTTGGGGGACTTGTGATCTCTTCAATGTGCTTAATPAGACGCTTGCAC	1886
Db	1801	TTTGAATATGCTATTTGGGGGACTTGTGATCTCTTCAATGTGCTTAATPAGACGCTTGCAC	1860
Oy	1887	CGCATTAATCCCTCCCTCTTTCTTGATGATCAGCTTGCAACAACAGTAACTTAATTCGACAC	1946
Db	1861	CGCATTAATCCCTCCCTCTTTCTTGATGATCAGCTTGCAACAACAGTAACTTAATTCGACAC	1920
Oy	1947	CGAAGCTGTCTATCTTCATATGAACATGGCACTCCACGTTTACGAGATATCATGAGAA	2006
Db	1921	CGAAGCTGTCTATCTTCATATGAACATGGCACTCCACGTTTACGAGATATCATGAGAA	1980
Oy	2007	TGAACAGAAATCTPAGTGAAGAAATTAATCAATTTGGGACCGAGATCAAGACCTGTATPACA	2066
Db	1981	TGAACAGAAATCTPAGTGAAGAAATTAATCAATTTGGGACCGAGATCAAGACCTGTATPACA	2040
Oy	2067	AATGTGTTTTGAAGAAATTTGTAAACCGGTTTCCGATTAAGCCGCTTTACTCTCACAAACCAC	2126
Db	2041	AATGTGTTTTGAAGAAATTTGTAAACCGGTTTCCGATTAAGCCGCTTTACTCTCACAAACCAC	2100
Oy	2127	AGTCAATGAACAGTTTGAACACGAACCTCGAGATGCTAAGTAGCATTCAGACAGAAATC	2186
Db	2101	AGTCAATGAACAGTTTGAACACGAACCTCGAGATGCTAAGTAGCATTCAGACAGAAATC	2160
Oy	2187	TTTGTAGCCTTAACAAGCTTATTTCCCTCTCTCACTTTGGGGAATCTTCTGTTATATGACTATT	2246
Db	2161	TTTGTAGCCTTAACAAGCTTATTTCCCTCTCTCACTTTGGGGAATCTTCTGTTATATGACTATT	2220
Oy	2247	TGAAAAATTTGAGACCTCTGGGAATCTTTTCATGTGCCCTAAGAAAAAAAAGACTCTTGATT	2306
Db	2221	TGAAAAATTTGAGACCTCTGGGAATCTTTTCATGTGCCCTAAGAAAAAAAAGACTCTTGATT	2280
Oy	2307	GGGACACACGGCTTAAAGATAGCATATGTGCAGACACAAGGTTTAGCTTATCTACACCATG	2366
Db	2281	GGGACACACGGCTTAAAGATAGCATATGTGCAGACACAAGGTTTAGCTTATCTACACCATG	2340
Oy	2367	ACTGTAGTCCAAAGATCATTTACAAGAGAGCTGAAGTGTCCAAACATTTCTTTGGACAAAG	2426
Db	2341	ACTGTAGTCCAAAGATCATTTACAAGAGAGCTGAAGTGTCCAAACATTTCTTTGGACAAAG	2400
Oy	2427	ACTTAAGAGGCTCGTTTACAGATTTTGGAAATPAGGAAAAACCTGTGTGTCCAAAGTCAC	2486
Db	2401	ACTTAAGAGGCTCGTTTACAGATTTTGGAAATPAGGAAAAACCTGTGTGTCCAAAGTCAC	2460
Oy	2487	ATACTTCAACTTAACGTATGGGACGATAGATTACATAGACCCCGAGATATGCTCGACATT	2546
Db	2461	ATACTTCAACTTAACGTATGGGACGATAGATTACATAGACCCCGAGATATGCTCGACATT	2520
Oy	2547	CACGGCTCACTGAGAAATCGATGTCTTACAGATTATGGAAATAGTCTTTGAGTTGTTAA	2606

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Db 2521 CACGGCTACTGAGAAATCCGATGCTCTACAGTTATGGAATAGTCTTCTTGAGCTGTAA 2580
Qy 2607 CCGAAGAGAAAGCGCTTGATGACGAATCAATCCACCACTGATATGTCGAAGACGG 2666
Db 2581 CCGAAGAGAAAGCGCTTGATGACGAATCAATCCACCACTGATATGTCGAAGACGG 2640
Qy 2667 GGAACAATGAAAGTATGGAATGGCAGATCCAGACATCAGATCGACGTGTAAGATCTCG 2726
Db 2641 GGAACAATGAAAGTATGGAATGGCAGATCCAGACATCAGATCGACGTGTAAGATCTCG 2700
Qy 2727 GTGTGTGAAAGAAAGTTTCCAACTGGCACTCCTATGCAACCAAGACACCGCAATGATC 2786
Db 2701 GTGTGTGAAAGAAAGTTTCCAACTGGCACTCCTATGCAACCAAGACACCGCAATGATC 2760
Qy 2787 GACCCCAATGACACCGAGTACCTGCTGCTGCGCACTTTATGCTATGCGAAACACAC 2846
Db 2761 GACCCCAATGACACCGAGTACCTGCTGCTGCGCACTTTATGCTATGCGAAACACAC 2820
Qy 2847 CTGCTGCACTGACAGTCAGCGACGCTGGCTGGTTCCTACGTCATGAGTATGCA 2906
Db 2821 CTGCTGCACTGACAGTCAGCGACGCTGGCTGGTTCCTACGTCATGAGTATGCA 2880
Qy 2907 ATCTCAAGACTCTCTCAATCTGTCATATGCTCTTCATGAGTCTTGATGCTCAACTGT 2966
Db 2881 ATCTCAAGACTCTCTCAATCTGTCATATGCTCTTCATGAGTCTTGATGCTCAACTGT 2940
Qy 2967 TTTCTGGTTTGGACAGTATTTCTTCAGAACAGTAGTATTTTCTGTTAGAGAGAA 3026
Db 2941 TTTCTGGTTTGGACAGTATTTCTTCAGAACAGTAGTATTTTCTGTTAGAGAGAA 3000
Qy 3027 TCTTTAAACGATATCTTTTCTGTCGTTAGAGTGTAGAAAATTAATGTCATGTA 3086
Db 3001 TCTTTAAACGATATCTTTTCTGTCGTTAGAGTGTAGAAAATTAATGTCATGTA 3060
Qy 3087 AGTATTATGACATGCTCTTATTTATTATTAACAAGTGTGCTGAATATGCTTCAAC 3146
Db 3061 AGTATTATGACATGCTCTTATTTATTATTAACAAGTGTGCTGAATATGCTTCAAC 3120
Qy 3147 TGGCACTTAGACTTCTCTATTA 3167
Db 3121 TGGCACTTAGACTTCCAAAAA 3141

RESULT 4
ADA68568
ID ADA68568 standard; DNA; 2930 BP.
XX
AC ADA68568;
XX
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 480.
XX
KW Plant; bacterial infection; fungal infection; viral infection; ds.
XX
OS Arabidopsis thaliana.
XX
PN MO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001MO-IB001105.
XX
PR 22-JUN-2001; 2001MO-IB001105.
XX
SY (SYGN ) SYNGENTA PARTICIPATIONS AG.
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX WPI, 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
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PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 480; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2930 BP; 828 A; 625 C; 616 G; 861 T; 0 U; 0 Other;
XX
Query Match 92.3%; Score 2930; DB 8; Length 2930;
Best Local Similarity 100.0%; Pred.No.0;
Matches 2930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 77 ATGGCTCTGTTAGAGATATTTGTTCTTGGGTTTCTCTTCTGCTTGAAGTTAGTACT 136
Db 1 ATGGCTCTGTTAGAGATATTTGTTCTTGGGTTTCTCTTCTGCTTGAAGTTAGTACT 60
Qy 137 ACTGTGACTTCAGAGAGGAGCAACGTTGCTGAGATTBAGAATTCATTAAGATGTC 196
Db 61 ACTGTGACTTCAGAGAGGAGCAACGTTGCTGAGATTBAGAATTCATTAAGATGTC 120
Qy 197 AACAAATGTTCTTATGACTGACCAACTCACCCTTTCGGATTATGTCGAGAGGT 256
Db 121 AACAAATGTTCTTATGACTGACCAACTCACCCTTTCGGATTATGTCGAGAGGT 180
Qy 257 GTGTCTTGTGAAAATGTCACCTTCAATGTTGTTGCTCTTAATTTGCAATTTGAATCTT 316
Db 181 GTGTCTTGTGAAAATGTCACCTTCAATGTTGTTGCTCTTAATTTGCAATTTGAATCTT 240
Qy 317 GATGAGAAATCTCACCTGCTATTTGAGATCTCAAGAGTCTTGTCAATTTGATCGCA 376
Db 241 GATGAGAAATCTCACCTGCTATTTGAGATCTCAAGAGTCTTGTCAATTTGATCGCA 300
Qy 377 GGTAAATGCTGTGCTGAGCAAAATCCCTGATGATGAGTACGTCCTTTGCAAAAC 436
Db 301 GGTAAATGCTGTGCTGAGCAAAATCCCTGATGATGAGTACGTCCTTTGCAAAAC 360
Qy 437 TTAGACTATCTTCAATGAATTAAGTGTGACATACCGTTTTCGATTTGCAAGTTGAAG 496
Db 361 TTAGACTATCTTCAATGAATTAAGTGTGACATACCGTTTTCGATTTGCAAGTTGAAG 420
Qy 497 CAACCTTGACAGCTGATTTCTGAAGATTAACAATTTGATGAGACCGATCCCTTCAACACTT 556
Db 421 CAACCTTGACAGCTGATTTCTGAAGATTAACAATTTGATGAGACCGATCCCTTCAACACTT 480
Qy 557 TCACAGATTCCAAACCTGAAAATTTCTGCACTTGGCAACAATAATCTAGTGTGAGTA 616
Db 481 TCACAGATTCCAAACCTGAAAATTTCTGCACTTGGCAACAATAATCTAGTGTGAGTA 540
Qy 617 CCAGACTATTTTACGGAATGAGTTCTTCAGTATCTTGGGTTGGAGAAAACAACCTTA 676
Db 541 CCAGACTATTTTACGGAATGAGTTCTTCAGTATCTTGGGTTGGAGAAAACAACCTTA 600
Qy 677 GTGGTAACTATTTCTCAGATTTGTGTCAACTGACTGCTGTTTGTATTTTGAAGTA 736
Db 601 GTGGTAACTATTTCTCAGATTTGTGTCAACTGACTGCTGTTTGTATTTTGAAGTA 660
Qy 737 AACAAAGTTTACAGTGTATTAACCTGAGAGATGAAATTTGACATGCTTCCAGGTT 796
Db 661 AACAAAGTTTACAGTGTATTAACCTGAGAGATGAAATTTGACATGCTTCCAGGTT 720
Qy 797 TTGACTTGTCTTACATCAGCTAACTGCTGAGATCCCTTTTGACATCGGCTTCGCA 856
Db 720 TTGACTTGTCTTACATCAGCTAACTGCTGAGATCCCTTTTGACATCGGCTTCGCA 856
```

D 721 TTGGACTTGTCTTACATCAATCACTAAGTGTAGATCCCTTTGGACATCGGCTTCCTGCAA 780
Q 857 GTTGCAACATTATCATTTGCAAGGCAATCACTCTCTGGGAAGATTCATAGATAGATTGCT 916
D 781 GTTGCAACATTATCATTTGCAAGGCAATCACTCTCTGGGAAGATTCATAGATAGATTGCT 840
Q 917 CTCATGCAAGCCCTTGCACTCTTATGATCTAAGTGGCAACTGTGTAGTGTATCTTCT 976
D 841 CTCATGCAAGCCCTTGCACTCTTATGATCTAAGTGGCAACTGTGTAGTGTATCTTCT 900
Q 977 CCGATTCTCGGAAATCTTACTTTTCAACCGAATAATTGATTGTGACAGTAAACAAGCTGACT 1036
D 901 CCGATTCTCGGAAATCTTACTTTTCAACCGAATAATTGATTGTGACAGTAAACAAGCTGACT 960
Q 1037 GGTTCATTCTCAGCTGAGCTTGGAAACATGCAAAATCTCATTAACCTGGAACCTCAATGAT 1096
D 961 GGTTCATTCTCAGCTGAGCTTGGAAACATGCAAAATCTCATTAACCTGGAACCTCAATGAT 1020
Q 1097 AATCATCTCAAGGCTCATATATACCAACAGAGCTTGGGAAGCTTACTGACTTGTGTATCTG 1156
D 1021 AATCATCTCAAGGCTCATATATACCAACAGAGCTTGGGAAGCTTACTGACTTGTGTATCTG 1080
Q 1157 AATGTGGCCAAATATGATCTTGGAAAGACCTTATACCTGATCATCTGAGCTCTTGCACAAA 1216
D 1081 AATGTGGCCAAATATGATCTTGGAAAGACCTTATACCTGATCATCTGAGCTCTTGCACAAA 1140
Q 1217 CTAAACAGCTTAAATGTTCAATGGGAACAAGTTTAGTGGCACTAATCCCGAGCATTTCAA 1276
D 1141 CTAAACAGCTTAAATGTTCAATGGGAACAAGTTTAGTGGCACTAATCCCGAGCATTTCAA 1200
Q 1277 AAGCTAGAAAGTATGACTTATCTGATCTGACGAAACAATATCAAAAGGTCCATCCG 1336
D 1201 AAGCTAGAAAGTATGACTTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1260
Q 1337 GTTGAAGTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1396
D 1261 GTTGAAGTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1320
Q 1397 GGAATCACT 1456
D 1321 GGAATCACT 1380
Q 1457 AATCATATTAACGATGATGATCTGACGAGCACTTGGAAATCTAAGAACATCATGGAATA 1516
D 1381 AATCATATTAACGATGATGATCTGACGAGCACTTGGAAATCTAAGAACATCATGGAATA 1440
Q 1517 GATCTTTCAAAATATGATCTCTGAGCCCAATTCAGAAAGCTTAAACAATTAACAAGAC 1576
D 1441 GATCTTTCAAAATATGATCTCTGAGCCCAATTCAGAAAGCTTAAACAATTAACAAGAC 1500
Q 1577 ATATATTTTGTGAGACTGGAATAATTAACCTGATCTGATGATGTTGGTCAATTAAGCCAA 1636
D 1501 ATATATTTTGTGAGACTGGAATAATTAACCTGATCTGATGATGTTGGTCAATTAAGCCAA 1560
Q 1637 TGTCTCAGTCTCACTGATTAATGAATGATCTCATTAACAACCTCGTAGTATATCCCTAAG 1696
D 1561 TGTCTCAGTCTCACTGATTAATGAATGATCTCATTAACAACCTCGTAGTATATCCCTAAG 1620
Q 1697 AACATTAACCTTCAAGATTTTCAACGACAGCTTCAATTTGGCAATCTCTGCTCTTGGGCT 1756
D 1621 AACATTAACCTTCAAGATTTTCAACGACAGCTTCAATTTGGCAATCTCTGCTCTTGGGCT 1680
Q 1757 AGTTGGCTTAAACCTCAAGCTGATGATCTCTGAGAACTGTAAGAGTGTCAATCTTGA 1816
D 1681 AGTTGGCTTAAACCTCAAGCTGATGATCTCTGAGAACTGTAAGAGTGTCAATCTTGA 1740
Q 1817 GCAAGTATTTTGGAAATAGCTAATGGGGAAGCTTGTGATCTCTCATGATCTTAAATGCA 1876
D 1741 GCAAGTATTTTGGAAATAGCTAATGGGGAAGCTTGTGATCTCTCATGATCTTAAATGCA 1800
Q 1877 GCTTGGCCGACCGCATATCT 1936
D 1801 GCTTGGCCGACCGCATATCT 1860

Q 1937 TATTGCAACCGAAGCTCGTATCTCTTCAATATGAAATGAGCACTCCACGTTTACGAGGAT 1996
D 1861 TATTGCAACCGAAGCTCGTATCTCTTCAATATGAAATGAGCACTCCACGTTTACGAGGAT 1920
Q 1997 ATCATGAAATGACAGAAATCTTAAGTGAAGATATATATCTTGGGACCGAGCATCAAGC 2056
D 1921 ATCATGAAATGACAGAAATCTTAAGTGAAGATATATATCTTGGGACCGAGCATCAAGC 1980
Q 2057 ACTGTATACAAATGCTTTTGAAGAAATGTAACCGGTGGCAATTAAGCGGCTTACTCT 2116
D 1981 ACTGTATACAAATGCTTTTGAAGAAATGTAACCGGTGGCAATTAAGCGGCTTACTCT 2040
Q 2117 CACAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAAGTATACATCAAG 2176
D 2041 CACAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAAGTATACATCAAG 2100
Q 2177 CACAGAAATCTTGTGAGCTTACAGCTTATCCCTCTCTCACTTGGGAGCTCTTCTGTTG 2236
D 2101 CACAGAAATCTTGTGAGCTTACAGCTTATCCCTCTCTCACTTGGGAGCTCTTCTGTTG 2160
Q 2237 TATGACTATTTGGAATAATGTTAGCTCTGAGGATCTCTTCAATGAGCTTACAGAAAGAG 2296
D 2161 TATGACTATTTGGAATAATGTTAGCTCTGAGGATCTCTTCAATGAGCTTACAGAAAGAG 2220
Q 2297 ACTCTGATTTGGGACACACGCTTAAAGATGATGATGATGATGATGATGATGATGATGAT 2356
D 2221 ACTCTGATTTGGGACACACGCTTAAAGATGATGATGATGATGATGATGATGATGATGAT 2280
Q 2357 CTACACCATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2416
D 2281 CTACACCATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Q 2417 TTGGAACAAGACTTAAAGGCTGTTTGAAGATTTTGAATTAAGCAAAAGCTTGTGTG 2476
D 2341 TTGGAACAAGACTTAAAGGCTGTTTGAAGATTTTGAATTAAGCAAAAGCTTGTGTG 2400
Q 2477 TCAAAAGTCAATCTTCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2536
D 2401 TCAAAAGTCAATCTTCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
Q 2537 GCTGCACTTCAAGGCTCACTGAGAAATCCGATGCTCACTGATGATGATGATGATGATGAT 2596
D 2461 GCTGCACTTCAAGGCTCACTGAGAAATCCGATGCTCACTGATGATGATGATGATGATGAT 2520
Q 2597 GAGTGTAAACCGGGAAGGAGCGTTGATGAGAAATCCAAATCTCCACCATCTGATTAAG 2656
D 2521 GAGTGTAAACCGGGAAGGAGCGTTGATGAGAAATCCAAATCTCCACCATCTGATTAAG 2580
Q 2657 TCAAAAGCGGGGAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2716
D 2581 TCAAAAGCGGGGAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Q 2717 AAAGATCTCGGTGTGTAAGAAATTTTCAACTGAGCACTCTTAATGACACCAAAAGCAG 2776
D 2641 AAAGATCTCGGTGTGTAAGAAATTTTCAACTGAGCACTCTTAATGACACCAAAAGCAG 2700
Q 2777 CCGAATGATGACCAACAATGACCAAGGTGATCGTGTCTGAGCACTTATGATGATGATGATGAT 2836
D 2701 CCGAATGATGACCAACAATGACCAAGGTGATCGTGTCTGAGCACTTATGATGATGATGATGAT 2760
Q 2837 GAAACAACCACTGCTGAGCTGACAGCTGACGACGCTGAGCTGATCTGATGATGATGATGAT 2896
D 2761 GAAACAACCACTGCTGAGCTGACAGCTGACGACGCTGAGCTGATCTGATGATGATGATGAT 2820
Q 2897 GAGTATGCAAAATCTCAAGATCTCTCATTTGCTCAATTTGCTCTTCAATGATGATGATGAT 2956
D 2821 GAGTATGCAAAATCTCAAGATCTCTCATTTGCTCAATTTGCTCTTCAATGATGATGATGAT 2880
Q 2957 GCTCAACTGTTCTTGGGTTTGAACAAGTATTTCTCAGAAAGTGA 3006
D 2881 GCTCAACTGTTCTTGGGTTTGAACAAGTATTTCTCAGAAAGTGA 2930

RESULT 5
AD30336
ID AD30336 standard; cDNA: 2750 BP.
XX
AC AD30336;
XX
DT 21-Apr-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 13156.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-Apr-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX
XX (LIU/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABAS/) TABASKA J E.
XX (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI WPI: 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 13156; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 2750 BP: 822 A; 572 C; 548 G; 808 T; 0 U; 0 Other;

Query Match 46.8%; Score 1486.6; DB 13; Length 2750;
Best Local Similarity 74.8%; Pred. No. 0;
Matches 1883; Conservative 0; Mismatches 619; Indels 15; Gaps 1;

QY 504 AGCAGCTGATTCGAGAATTAACCAATTGATAGACCGATCCCTTCAACACTTTCACAGA 563
DB 1 AGAATCTGATTTTGAACAACAACCAATTTGATGGACCAATTCCTTCAACTTGTCTGAGA 60
QY 564 TTCCAAACTGAAATTTCTGGACTTGGCAGACAGATAAATCACTAGTGAGATACCAAGAC 623
DB 61 TTCTGATTTGAAGATTTCTAGACCTGGCTCAAAATATCTTAGGGGAGAAATACCAAGGC 120
QY 624 TTATTACTGGAATGAAAGTTCTTCACTATCTTGGGTTGCGAGAAACAATCTAGTCGGTA 683
DB 121 TTATATATTTGGAAAGAAAGTTTGGCAATATCTAGGCTTGAAGGGAGAACAAATTTGGTTGGTT 180
QY 684 ACATTTCTCAGATTTGTGTCACTGACCTGGTCTTGGTATTTTGGATGAGAAACAGACA 743
DB 181 CACTATACCAAGACATGTGCAAGTTAACTGGGCTGTGTGATTTTGTGATGAGAAACATGA 240
QY 744 GTTTGACTGGTAGATATCTGAGACGATAGAGAAATTCAGCTGCTTCAGGTTTGGACT 803
DB 241 GCCTGACAGGAAGATTTCCAGAGAACATAGGCAATGTACTGCTTCAGGTCTTGATTT 300
QY 804 TGTCTTAACAATCAGCTAATCTGTGAGATCCCTTTTGCATCGGCTTCTGCAAGTTGCAA 863
DB 301 TATCTTAACAACCACTAATCTGAGAGATACCATTCATATTTGATTTCTTCAAGTAGACAA 360
QY 864 CATTATCATTTGCAAGGCAATCAACTCTCTGGGAAAGATTCATGATGATGTCCTCATTC 923
DB 361 CTGTGTCTTGGCAAGGCAATTAACCTCTGTGACATATTTCCACGGTGATGGTCTCATGTC 420
QY 924 AAGCCCTTGGAGCTTATGATCTAAGTGGCAACTTGTGATGATCTAATCTCCGATTC 983
DB 421 AAGCATTGCTGTCTGTGACCTTGAAGCTGCAACTTGTTAATGATGATGATCTCTATCT 480
QY 984 TCGGAAATCTTACTCTTCAACGAGAAATTTGATTGCAACAGTAAACAAGCTGATGTTCAA 1043
DB 481 TGGGAAATTTGACTTACACAGAAAAATTTGATCTGATGAGAAACAAGCTGATGCTTCA 540
QY 1044 TTCCACTGTAGCTTGGAAACATGTCAAAATCTCATTAACCTGGAATCTCAATGATATATC 1103
DB 541 TCCCCCAAGAGCTTGGAAATATGTCAAAAGCTTCACTATTTGGAATGGAATTAACCATTT 600
QY 1104 TCAAGGCTCATATACCAACAGAGCTTGGAGAGCTTACTGTTGATCTGAATGTG 1163
DB 601 TAAATGACATATATCCGCCGAGCTTGGAAAGCTTGAAGTCTGTGATCTTAATGTTG 660
QY 1164 CCAACAAATGATCTGGAAGACCTTATACCTGATCATCTGAGCTTGTGCAAAATCTAACA 1223
DB 661 CAAACAAACATCTTGAAGGGGCCAATTCCTAGTATCTAGCTCATGTAAATCTCAACA 720
QY 1224 GCTTAAATGTTCAATGGGAACAAGTTAGTGGCACTATCCCGAGACTTTCAAAAGCTAG 1283
DB 721 GCTCAATGATGCAATGGCAACAAATTTGAATGATCAATTCCTTTTGGCAAGTTTGG 780
QY 1284 AAGATATGACTTCACTTAATCTGTCCAGCAACAATATCAAAAGGTCNAATCCGGTTGAGC 1343
DB 781 AGAGCATGACCTCTTGAATCTTTCTTCCAAATCTTCAAGGCGCAATTCATATAGAAC 840
QY 1344 TATCTGTATCGGTAACTTATGATACATTTGATCTTTCCAAACAAGATTAATGATGATCA 1403
DB 841 TGTGCGGAGATTTGCAATTTGATGATATTTGCAATTTCAACATTAATCTAGTTGTTCCA 900
QY 1404 TTCTCTTCTTCCCTTGGTGTATTTGAGAGATTTCTCAAGATGAACCTGATGAGAAATCAT 1463
DB 901 TCCCTTCTTCCCTTGGTGTATTTGAGAGATTTCTTGAAGTTGAATCTTGAAGCAAAATTT 960
QY 1464 TAACTGTGTAGTTCCAGGCGCACTTGGAAATCTAAGAGCATCATGAAATATGATCTTT 1523
DB 961 TAAAGGAATTAATTTCCAGGCAAGATTTGGAATCTTGAAGTGTATGGAATATGATCTTT 1020
QY 1524 CAATTAATGATATCTGTGCGCAATTTCCAGAAAGCTTAAACAATTAACAAGATTAATTT 1583
DB 1021 CAATTAATCAACTCTGTGCTGATTTCTGATGATGATGATGATGATGATGATGATGAT 1080

QY	1584	IGCTGAGACTGGAAATAATAAACCCTGACTGCTGTAATGTTGTTCACTTACCAACTGTCTCA	1613
Db	1081	CCTTGAGACTTGGAAATAACAAATTGACTGGCGAGTGGCACTACCTTTCAAATTGCATTA	1140
QY	1644	GCCTCACATGTAATGGAATGATCTCATCAACAACCTGTAGTGAGATATCCCTTAAGAACATA	1703
Db	1141	GTCCTCTCTACTTAATGATGTCTCTATACAAACTATTTGGTGTATATCCCAACGAGTAA	1200
QY	1704	ACTTCTCAAGATTTTTCACACAGACAGCTTCATTTGGCAATCTGTCTTTGCCGTAGTTGGC	1763
Db	1201	ACTTTACACAGGTTTCCCTGTGACAGTTTCATTTGGAACCCCTGTCTTTGTGTATTTGGC	1260
QY	1764	TAAATCAACCGTGTATGATTTCTGTGCAACTGTACGAGTCAATCTCTAGACAGCTA	1823
Db	1261	TGAATTTCCGTCGTATGATGTCTCCCTTCAGACCGAGTTTACATTAATTAAGGCTGGCA	1320
QY	1824	TTCTTTGGAATAGCTAATTTGGGGGACCTGTGATCTCTCATATGTCTTAATPACAGCTTGC	1883
Db	1321	TTCTTGGAAATTACTTTGTGTGCTCCCTTGATGATCTTCTATAGGATATGCTGGACGTTGCC	1380
QY	1884	GACCGCATTAATCTCTCTCTTTTCTTGTAGATCACTTGACAAAACAGATACTTAATCGA	1943
Db	1381	GACCAATAGTCCCTCTCTCTTTCTGTANAGATCAATTTGACAAACAGATTAATTTCTGCC	1440
QY	1944	CACCGAGCTGCTCATCTCTCATATGAACATGGCACTCCACGTTTACGAGATATCATGA	2003
Db	1441	CCCCAAACCTAGTGAATTTCTTCATATGAATATGGCACTCAATGTGATATGAATATCATGA	1500
QY	2004	GAATGACAGAAATCTAGTAGGAATATCATATTGGGGACGGAGCACTCAAGCACTGAT	2063
Db	1501	GGATGACTGAAAACCTGAGTGAAGATATATATATGATATAGAACATCAAGTACAGTTT	1560
QY	2064	ACAAATGTGTTTTGAAGAATTGTAAACCGGTGCGATTAGCGGCTTTACTCTCAACAC	2123
Db	1561	ATTAATATGTTCTTAAGAATTGSCAACCGGTGGCTATCAAGAGATCTATTTCTACATATC	1620
QY	2124	CACAGCTAATGAACAGTTTGAACAGAACTCGAGATCTTAATGATCATCAAGCAAGAA	2183
Db	1621	CCCAATGATTAATAAGAAATTTGAAACTGAATCTGAGACGGTTGGCAGCATCAAGCACCGGA	1680
QY	2184	ATCTTTGAGCCCTAACAGCTTATTCCTCTCTCACTTGGGGAGTCTTCTGTCTATAGACT	2243
Db	1681	ATCTGTAGTCTCCAAAGTATATTCCTTGTCCCAATATGGGCATCTCTGTATTATGACT	1740
QY	2244	ATTTGGAAAAATGTGTAGCCTCTGGAGATCTTCTTCATGCGCCCTACAGAAAAAGACTCTTG	2303
Db	1741	ACATGGAATAATGGCAAGTCTATGGATCTTCTTCATGAGACCTACAGAAAGAAAAAGCTTG	1800
QY	2304	ATTGGGACACACGGCTTAAGATAGATATGTCGACACAAAGTTTACTATCTACACC	2363
Db	1801	ACTGGGACCTGTGCTTAATAAATAGACACTTGGAGCAGCAAAAGGCTTCTTATCTACACC	1860
QY	2364	ATGACTGTATGCCAGATTCATCTCACAGACGTGAATCGTCCCAACTTCTCTTTGGACA	2423
Db	1861	ATGATGTGTCTCTAAGATCACTCCACAAGATGTAAATCACTTAACATTTCTATTTGATG	1920
QY	2424	AAGACTTAGAGGCTGTTTGAACAGATTTTGGATATGCAAAAAAGCTTGTGTGTCAAGT	2483
Db	1921	CAGACTTTGAGGCTATCTCACTGATTTTGTGATTTGCCAAAGTCTGTGCCCTCAAGT	1980
QY	2484	CACATACTTCAACTTACGTGATGGGACAGATAGTTTACATAGAACCCCGAGTATGCTCGCA	2543
Db	1981	CCCAATACTTCTTACTTACATTAATATGGGCAAAATTTGGCTATATATAGACCCTGATATGCTGA	2040
QY	2544	CTTCAACGGCTCATCTAGAAATCCGATGTCTACAGTTATAGAAATAGTCTCTTATGATTTGT	2603
Db	2041	CTTCAAGTCTCATAGAAAGTGTAGTGTACAGTTAGGGAATGTTTTACTTGAATGGC	2100
QY	2604	TAAACCCGAAGAAACCGGTGATGACGAATCCAATCTCCACATCTGATTAATGTCAAAGA	2663
Db	2101	TBACTGGAAGGAAGACTGTGTGCAATGAATCCAACTTCCACATTTGATTTTGTTCAAAG	2160
QY	2664	CGGGAAACAATGAATGATGGAATATGGCAGATCCAGACATCATGACGTGTAAAGATC	2723

Db	2161	CAGCAACCAATGCACTGATGGAACAGTTGATCCAGCATTATTCGCGCATGCGAAGACC	2220
Oy	2724	TCGGTGTGTGTGAAGAAAGTTTCCMACTGGCACTCTATSCACCCAAAAGACAGCCGATG	2783
Db	2221	TAGAGAGCGTGTAAAAAGAGTTTATCAGGTTGCTGTATTATGACAAAGAGGACGACAGTG	2280
Oy	2784	ATCGACCCCAATGACACCAAGTAGTACTGTGTCTTCGCGCAATTATCTATC-----	2835
Db	2281	ATAGCGCGACATCTACGAAAGTGCACAGTGTACTCGGAAGCTGTGCTGTCAAAACACC	2340
Oy	2836	-----GGAACAACCACTGCTGCGACGTGCACGTACGAGCAGCGCTGGTTCGTGCT	2888
Db	2341	CACCAAGCAACTAGCTGCACTACCACTGCTTTAAATTCATCTGCCAAAGTGCATGCT	2400
Oy	2889	ACGTGATGATGATGACAAATCTCAAGACTCCTCATTTCTGTCATTTGCTCTTCATGAGTG	2948
Db	2401	ACGTGATGATGATGACAAACTCAAGACTCCAGACTTGGAAGTGCCTCCATATGAGCA	2460
Oy	2949	CTTCTGATGCTCAACTGTTTCTTCGTTTGAGCAAGTTATTCTCAGACAGTGAAGT	3005
Db	2461	CCTCAGATGCTCAACTCTTCTCTCAAGTTTGAGAGATTAATCTCTCAAAACAGTGAAGT	2517
RESULT 6			
ID	AED28154	standard; cDNA; 3089 BP.	
XX	AC	AED28154;	
XX	AD	01-DEC-2005 (first entry)	
XX	DE	Arabidopsis thaliana ERECTA paralog, ERL2 cDNA.	
XX	KM	Plant growth regulation; transgenic plant; crop improvement; transgene;	
XX	FT	ERL2; gene; ss.	
XX	OS	Arabidopsis thaliana.	
XX	FT	Key	Location/Qualifiers
XX	FT	CDS	186..3089
XX	FT		/*tag= a
XX	FT		/product= "Arabidopsis thaliana ERL2 protein"
XX	PN	US2005223428-A1.	
XX	PD	06-OCT-2005.	
XX	PF	30-DEC-2004; 2004US-00027304.	
XX	PR	01-APR-2004; 2004US-0558529P.	
XX	PPA	(TORI/) TORII K U.	
XX	PPA	(SHPA/) SHPAK E D.	
XX	PI	Torii KU, Shpak ED;	
XX	DR	WPI; 2005-675788/69.	
XX	DR	P-PSDB; AED28155.	
XX	PT	Modulating plant height and organ shape comprises expressing, in plants,	
XX	PT	a transgene encoding an ERECTA-like protein lacking an active kinase	
XX	PS	domain.	
XX	PS	Disclosure; SEQ ID NO 7; 72bp; English.	
XX	CC	The present invention relates to a method for modulating plant height and	
XX	CC	organ shape. The method involves expressing a transgene in a plant, where	
XX	CC	the transgene encodes an ERECTA-like protein lacking an active kinase	
XX	CC	domain and where expression of the transgene modulates plant height or	
XX	CC	organ shape. ERECTA protein contains leucine-rich repeat receptor-like	
XX	CC	kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and	
XX	CC	functional Ser/Thr kinase activity. The invention is useful for producing	

transgenic plant and for enhancing the yield of a crop plant. The present sequence is the Arabidopsis thaliana ERECTA paralog, ER12 cDNA.

Sequence 3089 BP; 866 A; 682 C; 653 G; 888 T; 0 U; 0 Other;

Query Match 36.6%; Score 1161.8; DB 14; Length 3089;

Best Local Similarity 65.2%; Pred. No. 0;

Matches 1760; Conservative 0; Mismatches 927; Indels 12; Gaps 3;

```
QY 150 AGGAGGAGCAACCTTGTGAGATTAAGAAGTATTCAAGATGTGAACATGTTCTT 209
DB 274 ACGAAGAGAAAGCCTTATGCGATAAGGCTTCATTCAGCAAGCGGCGATATGCTTC 333
QY 210 ATGACGACAACCTCACTTCCGATTAATGTGCTGGAGAGGTGCTTGAA 269
DB 334 TTGATTTGGACGATGTTCAATACCAAGCTTTGTCTTGAGAGGAGTCTTCTGTATTA 393
QY 270 ATGTCACTTCAATGTTGTGCTCTTAATTTGTCAATTTGAATCTTGATGAGAAATCT 329
DB 394 ACGTTACCTCAATGTTGTCTCTTAACTGTCAAACTGAACTTGGTGGAGATAT 453
QY 330 CACCTGCTATTGAGATCTCAAGATCTCTTGTCAATTTGATCTGGAGTATCGCTGT 389
DB 454 CATCTGCCCTTGAGATTTGATGATCTGCAATCAATAGACTTGCAAGAAATTAATTGG 513
QY 390 CTGGAAGAAATCCCGATGAGATTTGGTGAATGCTTCTTTGCAAACTTGACTATCT 449
DB 514 GTGTCAAAATTCAGATGATGATGAAAGTGTGTTCTCTGCTTAATGATGATTTCTCA 573
QY 450 TCAATGAATTAAGGTGACATACCGTTTTCATTTGATTTGAAAGTTGAACTTGAGAGC 509
DB 574 CCAATTTGTTGTTGAGACATACCGTTTTCATTTCAATCTTAAACTGAAAGGTGAGTTTC 633
QY 510 TGATTTGAAAGATTAACCAATTTAGAGCCGATCCCTTCAACCTTTCACAGATTTCAA 569
DB 634 TGAACCTTAAGAAATTAACGCTCACTGCTCAATATACAGCAACCTTCACTCAGATTTCAA 693
QY 570 ACCGGAATTTCTGGACTTGGCAGAGATTAACCTCAGTGGAGATTCGAAAGATTAATT 629
DB 694 ACCCTTAAGACCTTGACCTGCAAGAAACGACTTACCTGAGATACCAAGGTACTCT 753
QY 630 ACTGGAATGAAGTCTTCAGATCTTGGGTTGCGAGAAACAATTGAGCGGTAACTT 689
DB 754 ACTGGAATGAAGTCTTCAGATCTTGGGTTGCGAGAAATGTTAACTGGAGCATGT 813
QY 690 CTCCAGATTTGTCTCACTGACTGCTCTTGGTATTTGACGTAAAGAAACAAGTTGA 749
DB 814 CTCTGATATGTCTCAGCTGACGGGTCTGTGTACTTTGATGTGAGAGCAACAACCTTA 873
QY 750 CTGTGATATACCTGAGACAGATTAAGAAATTTGCACTGCTTCCAGTTTGGACTTGTCT 809
DB 874 CTGGAATCTATCCAGAGACATTTGGCAATTTGCAACAAGCTTTGAGATCTTGGATGATCTT 933
QY 810 ACAATCACTAATCTGTGAGATCCCTTTTTCATCTGCTTCCAGTTGCAACTTAT 869
DB 934 ATATCAATGATTAACCGAGATTAATCCCTAACAATTTGTTTCTCCAGTACTGTCTGT 993
QY 870 CATTGCAAGCAATCAACTCTCTGGGAAAGATTTCATGATGATTTGTCTCAATGCAAGCCC 929
DB 994 CACTTCAAGGAAACAATTTGACTGCGAGAAATTCGGAAGTATGTTGTCTGATGAGAGCTC 1053
QY 930 TTGAGCTTAAGATCTAAGTGAAGCACTTTGATGATGATCTATCTCCCAATCTTGGAA 989
DB 1054 TTGCTGATTTGATTTGATGATCAATGATTAATCTGGGCTTATTTCCACAATATCTTGGAA 1113
QY 990 ATCTTACTTTCAACCGAGAAATTTGATTTGACAGATTAACAAGCTGATGTTCAATTTCCAC 1049
DB 1114 ATCTGATTTCACTGAGAAACTGATATCTCAATGCAACAAGCTCACTGAGCAAAATTTCCAC 1173
QY 1050 CTGAGCTTTGGAACATGTCAAAATCTCAATTAATCTGGAATCTCAATGATTAATCTTCAAG 1109
DB 1174 CCGAGCTAAGCAATATGTCAAGCTCAAGCTAATTTTGGCAACTTAATGATTAATGATTAAGT 1233
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QY 1110 GTCAATATACCACAGAGCTTGGAGCTTACTGATGTTTGTGATCTGAATGTGGCCACACA 1169
DB 1234 GAAAGATCCCACTGAGCTTGGAGACTGGAAACAATTTGTTGCAAGCTGAATCTTGGCAACA 1293
QY 1170 ATGATCTGGAAGACCTTAATCTGATCATCTGAGCTCTTGGCAAACTTAACAGCTTAA 1229
DB 1294 ACAATCTTGAAGGCTGATTTCCATCAATGATTTGTTCTGTGTGCTTGAATCAATTTCA 1353
QY 1230 AATGTCATGGGAACAAGTTTATGAGCACTATACCAGGATTTCAAAAGCTGAAAGTA 1289
DB 1354 ATGTCAATGGAACTTCTTGAAGTGAAGCTGTACCACTGATTAATTCGGAATCTTGAAGCT 1413
QY 1290 TGAATTAACCTTAATCTGTCCAGCAACAATTAACAAGTCCCAATCCGTTGAGCTATCTC 1349
DB 1414 TGACTTATCTAAATCTTCTCTCAACAAGTTTCAAGGCAAAATTAATCTGAGCTTGGCC 1473
QY 1350 GATTCGTTAACTTGAATATGATTTCTTCAACAACAAGATTAATGATCATTTCTT 1409
DB 1474 ATATCAATCAATCTTGAATATGATTTCTGTGCAACAATTTCTGAGGCTCAATTTCAAT 1533
QY 1410 CTTCCTTGGTATTTGAGACATCTTCAAGATGAATGAACTTGAATGAATATATTAATCTG 1469
DB 1534 TAAACATTTGATCTTGAACATCTTCTCAATTTGAACCAATTTGAGCAAAATCAATCTGATG 1593
QY 1470 GTGATGTTCCAGGCGACTTGGAAATCTTAAGAAGCATCATGAAATATGATCTTCAAAAT 1529
DB 1594 GCACATTTGCTGCAAGATTTGGGAACCTCGGAAGCATCATGATCATGATGTCTCAATTTA 1553
QY 1530 ATGATATCTCTGCGCCCAATTTCCAGAAAGCTTAACCAATTTACGAACATTAATTTTCTGA 1589
DB 1654 ATTTTCTTGGCGGTGTTATTTCAACTGAACCTTGGCAGTTGCGAAGCATTAATCTCTCTGA 1713
QY 1590 GACTGGAATTAATTAACCTGACTGTATGT---TGTTCAATTAAGCACTGTCTGATCT 1646
DB 1714 TACTGAACAACAAGATTCATGAGGAAATCCCTATCACTTAATCACTTACTCTTCAATGCT 1773
QY 1647 TCACTGATTAATGATATCTCATTAACAACCTCTAGTGTATCTCTTAAGAAATTAAT 1706
DB 1774 TTGCAATCTGAACATCTCTCTTAATTAATTTCTGGAATTAATCCCACTTAAGAAATCT 1833
QY 1707 TCTCAAGATTTTGCAGAGACAGCTTCAATTTGCAATCTGCTCTTGGTATTTGCTTAA 1766
DB 1834 TTACAGTTTCTCCGCGCAGCTTCTTGGAAATCAATTTCTGCGGGAACCTGCGTTG 1893
QY 1767 ACTCAACGCTGATGATCTCTGTGCAAGCTTACGAGTTCATCTTGAAGCAGCTATTC 1826
DB 1894 GATCAATCTGTGCGCAATCTTAACCTTAAGTCAAGAT---ATTCAACAGAGTTGCCGTGA 1950
QY 1827 TTGGAATAGCTATTTGGGGGACTGTGATCTTCTCAATGCTTAATAGCAGTTGCCGAC 1886
DB 1951 TTGTATGTTCTCGGTTTCTGATCATCTCTCATATGATGATTAATTTGCGGTTTACAAGT 2010
QY 1887 CGCATTAATCTCTCTCTTCTTGTGATGATCACTTGAACAACCGATTAATTTGACAC 1946
DB 2011 CAAGAGAGAGAAACAGCTTTGAAAGGCTTCAAAACAC-----CTGAAGGCTCA 2064
QY 1947 CGAAGCTCTGATCTTCTCATATGAACAATGGCACTCCAGCTTTACGAGATTAATGAGAA 2006
DB 2065 CGAAGCTGATTTCTTCAATGACATGGCTTAATCAACAGTTGATGATATATGAGAG 2124
QY 2007 TGAAGAGAACTAAGTGAAGATATATCAATTTGGGACGAGCATCAAGCATGATATACA 2066
DB 2125 TTACAGAAACCTCGATGAGAAATATCATCTTGGATGATGATGATGATGATGATGATGATG 2184
QY 2067 AATGTGTTTGAAGAAATGTAACCGGTTGCAATTAAGCGGCTTAACTTCAACACCCAC 2126
DB 2185 AGTCACTCTCAAAACCTTCCGCACTATTTGCAATTAAGGCAATCTCAATCACTATCTCCA 2244
QY 2127 AGTCATGAAGACGTTTGAAGCAAGACTGGAATGCTAATGATGATCAATCAAGCAAGAAAT 2186
DB 2245 GCAACTTCTCGCGGTTTGAAGCAAGACTGGAATGCTAATGATGATGATGATGATGATGATG 2304
QY 2187 TTGTGAGCTTAACAAGCTTAATCTCTCTCTCACTTGGGAGTCTTCTGTTATGATTAAT 2246
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Db	2305	TAGTAAAGCTTGCAGGATACGCTTATCTCCCTTTGGGACCTCTCTTCTTACGACTTACA	2364
Qy	2247	TGAAAAATGTAGACCTCTGGGATCTTCTTCACTGGCCCTTACGAAGAAAAAGACTTGAT	2306
Db	2365	TGAAAAATGGCTCTCTTTGGGATCTTCTCCATGGGCTTGGAGAAAGGTGAAGCTTGACT	2424
Qy	2307	GGGACACACGGCTTAAAGTATGACTATAGTGTGACGACAAAGCTTGTAGCTATATCAACATG	2366
Db	2425	GGGAAACAAGCTGAAGATACCTGTTGAGCTGGCAAGGACTTGACATATCTTCAACATG	2484
Qy	2367	ACTGTAGTCCAAAGATCATCTTACACAGAGACGTGAAGTCTGCCAAGATCTCTTGGACAAAG	2426
Db	2485	ACTGGAACCTTAGATATTCATGAGACATCAAGTATCAACATACCTCTTATGAGGA	2544
Qy	2427	ACTTAGAGGCTTCGTTTGAACAATTTGGAAATAGCGAAAAAGCTTGTGTCTCAAAGTCAC	2486
Db	2545	ATTTTGAAGCCGCTTGTGCAATTTTGGGATTTGCCAAGACATACCAAGCCACCAAAACTT	2604
Qy	2487	ATACTTCAACTTACGTCGATGGGCAACGATAGGTTACATAGACCCCGAGATGCTGCACCT	2546
Db	2605	ATGCTTCAACTATGTCTTTGGAAACATTTGATATATTTAGACCCGAGATGCTGCACCT	2664
Qy	2547	CACGCGTCACTGAGAAATCCGATGTCTACAGTTATGGAATAGTCTCTTCTTGATGTTTAA	2606
Db	2665	CGCGTCTGAACGAGAAAGTCTGATATCTACAGTTTCGATATGTCTCTTCTTGAAGCTTAA	2724
Qy	2607	CCCCAAGAAAGCCGTTGATATGACCAATCCCATCTCCACATCTGTATATGTCAAAAGCGG	2666
Db	2725	CCGGCAAAAGGCTGTGATTAACGAGGCCAATTGCAATCAATGATATTTATCAAAAGGCGG	2784
Qy	2667	GGAACAATGAAGTGTGGAATATGGCAGATCCGACATCACATCGACGTGTAAGTCTCG	2726
Db	2785	ATGATTAACAAGTATGGAAGCTGTGATGCAAGAGTCTCAGTACTTGGATGACGAC	2844
Qy	2727	GTGTGTGTAAGAAAGTTTCCACTGTGCACTCTCTATGTGACCAAAAGACGCCGATGATC	2786
Db	2845	GACACATCAAAAGAAACATTTCAAGTACGCTCTCTTGTGTGACCAAGGAAATCTTTGGAGA	2904
Qy	2787	GACCACAAATGACACAGGTGACGTGTCTCGGACGTTTATGCTATCGGAACAACA	2845
Db	2905	GACCCACCATGACGAGAGGTCTGTAGGGTTCGTCTCACTTGTCCCGTCCACCTTCA	2963
RESULT 7			
AD132621			
ID	AD132621	standard; DNA; 2901 BP.	
XX	AC	AD132621;	
XX	DT	22-APR-2004 (first entry)	
XX	DE	Thale cress transpiration efficiency-related ERECTA homologue DNA SEQ 9.	
XX	KM	plant; transpiration efficiency; ERECTA; breeding; genetic engineering;	
XX	XX	thale cress; ds; gene.	
XX	OS	Arabidopsis thaliana.	
XX	Key	Location/Qualifiers	
XX	FT	1. 2901	
XX	FT	/*tag= a	
XX	FT	/product= "Thale cress transpiration efficiency-related	
XX	FT	ERECTA homologue protein - SEQ ID 10"	
XX	PN	MO200400555-A1.	
XX	BD	15-JAN-2004.	
XX	PF	02-JUL-2003; 2003WO-AU000854.	
XX	XX		
XX	PR	02-JUL-2002; 2002AU-00003339.	
XX	XX		

PA	(AUSU) UNIV AUSTRALIAN NAT.
PB	Masle J, Farquhar GD, Gilmore SR;
PI	WPI; 2004-09; 390/09.
XX	P-Psdb; ADI3622.
DR	
PT	Selecting plant having enhanced transpiration efficiency comprising for producing plants with enhanced transpiration efficiency comprising selecting plant expressing a genetic marker linked to the ERCTA locus in the genome of the plant.
PS	Claim 3; SEQ ID NO 9; 209pp; English.
XX	
CC	The invention relates to a novel method for selecting a plant having enhanced transpiration efficiency comprising detecting a genetic marker for transpiration efficiency, where the marker comprises a nucleotide sequence linked genetically to an ERCTA locus in the genome of the plant and selecting a plant that comprises or expresses the genetic marker. The method of the invention may be useful for selecting a plant having enhanced transpiration efficiency. The isolated ERCTA gene or allelic variant or protein-encoding region may be useful in the preparation of a genetic construct for modulating the transpiration efficiency of a plant. Furthermore, the ERCTA genes may be useful for producing plants having enhanced transpiration efficiency by both traditional plant breeding and genetic engineering approaches. The current sequence is that of the thale cress ERCTA homologue DNA of the invention.
CC	
SQ	Sequence 2901 BP; 824 A; 603 C; 613 G; 861 T; 0 U; 0 Other;
Query Match	35.2%; Score 1117.6; DB 12; Length 2901;
Best Local Similarity	64.0%; Pred. No. 0;
Matches 1741; Conservative	0; Mismatches 964; Indels 15; Gaps 3;
OY	131 GTAGCTACTGTGACCTTCAGAGGAGGAGCAACGTTGGAGATTAAAGAATCTTCAA 190
DB	64 GTTGCTTGCGCTATGACACAGGAAGGAAACCTCTGATGGGATTAAGGCTCTTTCAGC 123
OY	191 GATGGAACAATGTTCTTTATGACTGCAACATTCACCTTCTTGGAATTATGTGCTGG 250
DB	124 AACCTTAGGATATGCTTTTGGAATTGGAGCATGTTCACAACAGTGACTTGTTCTTGG 183
OY	251 AGAGGTGTGCTTGTGAAAATGTCACCTTCATGTTGTGCTCTTAATTTGTCAATTTG 310
DB	184 CGAGGTGTTTTCTGCGAACAGTTAGCATACCCTGTGCTCTCGAATTTGTCCAGTGTG 243
OY	311 AATCTGTGAGAGAATCTCACCGTCATTTGGAAGATCTCAGAGCTCTTGTCATAATTAT 370
DB	244 AATCTTGAGGGGAGATATCTCCAGACTATTTGAGAGACTTAGGAAATTTGCATCAATAGAC 303
OY	371 CTGGAGGTAATCGCTTGTCGCAAAATCCCTGATGAGATTGGTGACTGTTCTTTCTTGG 430
DB	304 TTGCAAGGTATTAATACGACAGTCAAAATTCAGATGAGATTGGAAATGTCGTTCTCTT 363
OY	431 CAAAATTAAGACTATCTCTTAATGAATTAAGTGTGATACCGCTTTGCATTTGCAAG 490
DB	364 GTTATATCGAATTTGTCGAGAATCTGTTAATGAGACATACTTTCTCAATCTCTTAA 423
OY	491 TTGAAGCAACTTGAGACAGCTGATTTCTGAAGATTAACCAATTGATAGACCGATCCCTTCA 550
DB	424 CTCAGACAGCTTGAATCTGTAATCTGAAGAACATACGCTCACAGGCTCTGTACACAGA 483
OY	551 ACACTTTCAAGATTTCCAACCTTGAAAATTTGTGACTTTGGACAGAAATCAAATCAATG 610
DB	484 ACCTTAACCCAGATTTCCAAACCTTAAGAGACTTGATCTTGTGCGCAATCATCTTAACGGGT 543
OY	611 GAGATACCAACACTTAATTTACTGGAATGAACATTTCTTGATCTTTGGTTGCGAGAAAC 670
DB	544 GAGATATGAATGCTTTTACTGGAATGAAGTTTTCAGATATCTTTGGAATTAACGAGGAAT 603
OY	671 AACTTAGTCGGTAACATTTCTCGAATTTGTCTCAACTGAAGTGGTCTTTGGTATTTTGAAC 730
DB	604 ATGTTGATCGGAACGTTATCTTTGATATGTGTGACGTAAACGGTTTGTGATCTTAT 663


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OY 731 GTAAGAAACAAGTTGACTGAGTAGTATACCTGAGACGATAGGAATGCACTGCCTTC 790
DB 664 GTGAGAGAAATATCTAATCTGGAACCATCCCGAGAGCATCGAAATGACAGACTTT 723
OY 791 CAGGTTTGGACCTTGTCTCAATCAGCTAACCTGAGATCCCTTTTGAATCGGCTTC 850
DB 724 CAATCTGTGACATCTTATTAATCAGATACAGGAGATTCCTTCAATATGGCTTC 783
OY 851 CTGCAAGTTGCAATTTATCTTGAAGGCAATACCTCTGAGGAAGATTCATCTGTC 910
DB 784 CTCCAATTTCTCTCTGTCACTTCAAGGAAACAGATTGACGGGTAAATTTCCAGAAATT 843
OY 911 ATTGATCTGACGAGCCCTTGGAGCTTATGATCTAAGTGGCAACTTTGAGTGACT 970
DB 844 ATTGATCTAATGACAGCTCTTGTCTTTTGGATTTGAGTACAAATGACCTTTGGTCT 903
OY 971 ATTCTCCGATTTCTCGGAAATCTTACTTTCACCGAGAAATTTGATTTGACAGTAAACAG 1030
DB 904 ATCCCAACCGAATCTGGCAATCTCTCATTTACCGGAAAGTTGATCTCCATGGCAATATG 963
OY 1031 CTGACTGTTCATTTCACTGAGCTTGGAAACATGTCAAAATCTCCATTAACCTGAACTC 1090
DB 964 CTCACTGTCTCAATCCCTCTGAGCTTGGGAATATGTACAGTCTCACTATTTTGCAGCTA 1023
OY 1091 AATGATATCATCTCAAGGGTCAATATACACGAGCTTGGGAAGCTTACTGACTGTTT 1150
DB 1024 AACGACAAATTAACCTAGTGGAACTATTCACCTGAGCTTGGAAAGCTGAGCAATGTTT 1083
OY 1151 GATCTGATGTTGGCCCAACAATGATCTGGAAGAGACTTATCTGATCTGAGCTTTCG 1210
DB 1084 GAATGATCTTGGCAACCAACCGTTAGTAGGGCCATACCATCCAACTTAATGTTCACTGT 1143
OY 1211 ACAATCTAAACAGCTTAAATGTTTATGAGGAACAAGTTTAGTGGCACTATACCCGAGCA 1270
DB 1144 GCAGCTTGAATCAATTCATGTTTCAATGAGGAACCTCTTGAAGTATATTTCCACTGGCG 1203
OY 1271 TTTCAAAAGTAGAAGTAGACTTACTTACTTATCTGTCAGCAACAATATCAAAAGTCCA 1330
DB 1204 TTTCGCAATCTCGAGAGCTTGAATCTTGAATCTTCTGTCGAAACAATTTCAAGGGAAA 1263
OY 1331 ATCCCGTTGAGCTATCTCGTATCGTAACTTGAATCATTTGATCTTTTCCAAACAAG 1390
DB 1264 ATACCAAGTTGAGCTTGGACATATATCAATCTTGACAACTAAGTCTGTGCGCAATAC 1323
OY 1391 ATTAATGGAATCATCTCTCTTCCCTTGTGATTTGAGACATCTTCTCAAGATGAACCTG 1450
DB 1324 TTCTCAGGGTCTATACCATTAACGCTTGGGATCTTGAAACACCTTCTCATATTAATCTT 1383
OY 1451 AGTAGAAATCATATPACTGCTGATGTTCCAGGAGCACTTGGAAATCTTAAGAACATCATG 1510
DB 1384 AGCAGAAACCATCTGTGTGACAAATTAACCTGACAGAGTTTGGAAACCTTGCAGACATTCAG 1443
OY 1511 GAATATGATCTTTCAATATATGATATCTGAGCCCAATTTCCAGAGAGCTTAAACAATTA 1570
DB 1444 ATGATTTGATATATCTTCAATCTGCTCCGAGTTATTTCCAACTGAACCTTGGCCAAATG 1503
OY 1571 CAGACATTAATTTTGTGAGACTGGAATAATTAATPACTGATGTTT---GGTTCA 1627
DB 1504 CAAATTTAAACTCTTAAATATTTGAACAACAACAAGCTTCATGGGAAATTTCCAGATCAG 1563
OY 1628 TTAGCCAACTGTCTCACTCTCACTGATATGAAATGATATCTATTAACAACCTCTGATGAT 1687
DB 1564 CTTAACGAAGCTGTCACTCTTGTCAATCTGAATGTCTCTTCAACAATCTCTCCGGGATA 1623
OY 1688 ATCCCTAAGACATAATCTTCAAGATTTTCAACAGACAGCTTCAATGGCAATCTGCT 1747
DB 1624 GTCCCAACCAATGAAAACTTCTACAGTTTGTCTCCAGCCAGCTTTGTGGAATTCATAT 1683
OY 1748 CTTTGGGTAAGTTGGCTAACTCAACGCTGATGATTTCTGTCGAACCTGTACAGATGTCA 1807
DB 1684 CTTTGTGGAACAGTGGTGTGATCTATTTGTGTCTTACCGAAATCTCGA-----GTA 1737

OY 1808 ATCTTAGACAGACTATTTCTTGAATAGCTATTTGGGGGACTTGTGATCTTCTCATGATGTC 1867
DB 1738 TTCTCCAGAGAGCTTGTGATCTGATCTTGTCTTGGGCTCATCTCTCTCATATGATAT 1797
OY 1868 TTAAATGACAGCTTGGCCGACCGATTAATCTCTCTCTTCTTGTGATGATCACTTGACAA 1927
DB 1798 TTCTTGGAGTTTAAACAATCTAATGACAGAGAAAGATTTCTACAAAGGCTC-----CTCA 1851
OY 1928 CCAGTAACTTATTCGACACCGAAGCTCTGTCATCTCTTCAATATGAACATGACATCCAGCT 1987
DB 1852 AAACAAGCTGAAAGGTTTAACCAAGCTATGATTTCTCAATGACATGGCAATTCATPACA 1911
OY 1988 TACAGGAATCATGAGAAATGACAGAGAAATCTAAGTAGAATATATTTGGGACCGA 2047
DB 1912 TTGATGATATCTATGAGAGTACGTAAGATCTTAAGGAAAGTTTAAATGATATGTGT 1971
OY 2048 GCATCAAGCACTGTATPACAAATGTGTTTGAAGAATTTGAACCGGTTGCAATTAACGG 2107
DB 1972 GCTTTAGCAGCGGTATPACAAATGTGCAATTAAGAAAGTTCCCGACCTATTTGCCATTAAGCGA 2031
OY 2108 CTTTACTCTACAAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAAT 2167
DB 2032 CTCTCAATCATGATTCGCAATTAATCTGCGGAAATTTGAGACAGAACTTGAACATTTGG 2091
OY 2168 AGCATCAAGCAGAAATCTTGTGAGCTTACAAAGCTTATTTCCCTCTCACTTGGGAGT 2227
DB 2092 AGCATTTAGCAGAAACATATGATGACCTTGTGATGATATGCTTGTCTCTCATGTGGCAAC 2151
OY 2228 CTTCTGTTCTATGATCTATTTGGAATTTGTAAGCTTGTGGATCTTTCATGAGCCCTACG 2287
DB 2152 CTTCTTTTCTATGATCAATATGAAATTTGATCACTTTGGGAACTTTCATGAGGCTATTG 2211
OY 2288 AAAAAAAGACTTGTATTTGGGACACAGCGCTTAATGATGATATGCTGACAGCAAGT 2347
DB 2212 AAAAAAGTGAAGTTGATTTGAGGACAGAAAGTTGAATATGCGGTTGAGACTGCAAGAA 2271
OY 2348 TTAGCTTATCTACACCATGACCTGATCTTCAAGGATCATTCACAGAGCGTAAGTGTCC 2407
DB 2272 CTAGCTTATCTTACCAAGATGATGATCTCTCTCAATATATTCACCTGATCAATCAAGTATCG 2231
OY 2408 AACATTTCTTTGGACAAAGACTTGAAGGCTGTTTGAACAGATTTTGAATAGCGAAAGC 2467
DB 2332 AACATCTCTTGTATGATGAAATTTGCAAGCAATTTATCTGATTTGGGATGCTTAAGAGC 2291
OY 2468 TTGTGTGTCAAAAGTCAATCACTTCACTTACGTATGAGGACGATAGCTTACATAGAC 2527
DB 2392 ATACCAAGCTTAGCAAAACCCATGCTCTGACTGTATGTTTGGGAACAATTTGTTATATAGAC 2451
OY 2528 CCCGAGTATGCTGCACTTCAAGGCTCACGAGTAATCCGATGTCTACAGTTATGGAATA 2587
DB 2452 CCAGATATGCTGTACTTCAAGATCAATGAAATCCGATATATACAGCTTCGGTATTT 2511
OY 2588 GTTCTTTTGTGATTTTAAACCGAAGAAAGCGTTGATGACGAATCCAATCTCCACAT 2647
DB 2512 GTTCTTTTGTGATTTTCACTGGAAGAAAGCAGTGATTAAGAACTTAACCTTGATCA 2571
OY 2648 CTGATATGTCAAAAGCGGGAAACAATGAAGTATGGAATGAGCAATCCAGATCAACA 2707
DB 2572 CTGATATTTGCAAAAGCGCTGATGATTAATCTGATGAGGAAGCAATGATCCAGAGTTACT 2631
OY 2708 TCGAGGTAAAGATCTGCTGTGTGGAAGAAAGTTTCCATCTGACATCCATGACCC 2767
DB 2632 GTGACTGTATGTGACTTGGACATATCAAGAAAGCAATTTCACTGCTCTTATATGACA 2691
OY 2768 AAAAGCAGCCGAATGATGACCCACCAATGACACAGTGATCTGTGTTCTCGGCACTTT 2827
DB 2692 AAGCGAAACCTTTAAGAGACCCACCAATGCTTGAAGTCTTGAAGGTTCTGCTCTCTTT 2751
OY 2828 ATGCTATCGGAACAACACC 2847
DB 2752 GTTCCCATCTCTGCAAGTAC 2771
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RESULT 8
ID AED28152 standard; cDNA; 3100 BP.
XX AC AED28152;
XX DT 01-DEC-2005 (first entry)
DE Arabidopsis thaliana ERECTA paralog, ERL1 cDNA.
XX KW Plant growth regulation; transgenic plant; crop improvement; transgene;
XX KM ERL1; gene; ss.
XX OS Arabidopsis thaliana.
XX PH Key Location/Qualifiers
XX FT CDS /*tag= a
XX FT /product= "Arabidopsis thaliana ERL1 protein"
XX PN US2005223428-A1.
XX PD 06-OCT-2005.
XX PF 30-DEC-2004; 2004US-00027304.
XX PR 01-APR-2004; 2004US-0558529P.
XX PA (TORI/) TORII K U.
XX PA (SHPA/) SHPAK E D.
XX PI Torii KU, Shpak ED;
XX WP1; 2005-675788/69.
XX DR P-PSDB; AED28153.
XX Modulating plant height and organ shape comprises expressing, in plants,
PT a transgene encoding an ERECTA-like protein lacking an active kinase
PT domain.
XX The present invention relates to a method for modulating plant height and
PS disclosure; SEQ ID NO 5; 72pp; English.
XX CC The present invention relates to a method for modulating plant height and
XX CC organ shape. The method involves expressing a transgene in a plant, where
XX CC the transgene encodes an ERECTA-like protein lacking an active kinase
XX CC domain and where expression of the transgene modulates plant height or
XX CC organ shape. ERECTA protein contains leucine-rich repeat receptor-like
XX CC kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and
XX CC functional Ser/Thr kinase activity. The invention is useful for producing
XX CC transgenic plant and for enhancing the yield of a crop plant. The present
XX CC sequence is the Arabidopsis thaliana ERECTA paralog, ERL1 cDNA.
SQ Sequence 3100 BP; 874 A; 647 C; 650 G; 929 T; 0 U; 0 Other;
Query Match 35.0%; Score 1112.8; DB 14; Length 3100;
Best Local Similarity 63.9%; Pred. No. 0;
Matches 1738; Conservative 0; Mismatches 967; Indels 15; Gaps 3;
QY 131 GTACTACTGTGACTTCAGAGAGAGGAGCAAGTTCGCGAGATTAAAGATCTTCAA 190
DB 263 GTTGCTTCGCGTATGAAACGAAGGGAAGCTCTGATGGCGATMAAAGGCTCTTACGC 322
QY 191 GATGTGAACAATGTTCTTTATGACGTGACCACTTCACTTCTTGAGATTATGTGTGG 250
DB 323 AACTTAGTAATATGCTTTTGGATTGGAGCATGTTCAACAAGTACTGTGTCTTGG 382
QY 251 AGAGGTGTCTTGTGAATAATGTCACCTTCAATGTGTGCTTAAATTGTGCAATTG 310
DB 383 CGAGGTCTTTCTCGCAACAAGTAACTACCTCGGTGTCTCTGAAATTGTGCAAGTCTG 442
QY 311 AATTTGATGGAATAATCTCACTGCTATTGGAGATCTCAAGAGTCTCTTGTCAATTGAT 370
DB 443 AATCTTGAGAGGAGATATCTCCAGCTATTGGAGACCTAACGAAATTGGCAATCAATGAC 502
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QY 371 CTCGAGGTATCGCTTGTCTGGACAATAATCCCTGATGAGATTGGTACTGTTCTTTG 430
DB 503 TTGCAAGGTAAATACTAGAGAGTCAAAATTCAGATGAGATTGGAACTGTGTTCTCTT 562
QY 431 CAAAACCTTAGCTTATCTTCAATGAATTAAGTGTGACATACCGTTTGCATTGCAAG 490
DB 563 GTTTATCTGTGATTGTCCGGAATCTGTATATAGAGACATACCTTCTTCAATCTTAA 622
QY 491 TTGAAGCAATTGAGAGCTGATTTGGAAGATAACCAATTGATAGAACCGATCCCTCA 560
DB 623 CTCAGAGCTTGAACCTGGAATCTGGAAGAACAAATCAGCTCACAGTCTCTTAACGCA 682
QY 551 ACACTTTCACAGATTCCAAACTGAAAATTTCTGACTTGGACAGATAAATCACTCAGTGT 610
DB 683 ACCTTAACCCAGATTCCAAACTTTAGAGACTGATCTTGCTGGCAATATCTAAGGGT 742
QY 611 GAGATACCAAGACTTATTTATCTGGAATGAAGTTCCTCAGTATCTTGGGTTGCAAGAAC 670
DB 743 GAGATATCGAGATTGCTTACTGGAATGAAGTTTTCAGATATCTTGGAATTACGAGGAAT 802
QY 671 AACTTAGTGGTAAACATTTCTCAGATTTGTGCAATGACGTGCTTGGTATTTTTCAG 730
DB 803 ATGTGACTGGAACGTATCTTCTGATATGTGTGACATAACGGTTTGTGTACTTTGAT 862
QY 731 GTAAGAAACAACAGTTTGAAGTGTAGATATCTGAGACATAGAAATTGACATGCTTC 790
DB 863 GTGAGGGAATAATATCTAATCTGAAACCATCCGGAAGAGCATGGAAATTCACAAGCTTT 922
QY 791 CAGGTTTGGACTTGTGCTTCAATCAATCAGCTAATCTGTGAGATCCCTTTTGCATCGGCTTC 850
DB 923 CAATCTCGACATATCTTATATCAGATTAACGAGAGATTCCTTCAATATTCGGCTTC 982
QY 851 CTGCAAGTTGCAACATATATATGCAAGGCAATCACTCTCGGGAAGATTCCATCAGT 910
DB 983 CTCGAGTTGCTACTCTGTACTTCAAGAAACAGATTCGCGGTAGCAATTCAGAAAGTT 1042
QY 911 ATTGCTCTCAATGCAAGCCCTTGGAGCTTATGATCTAATGTCGCAACTGTTGAGTGAATCT 970
DB 1043 ATTGCTATATGCAAGGCTCTGCGTTTGTGATTTGATGATGACAAATGAGCTTGTGGTCT 1102
QY 971 ATTCTCCGATTTCTCGGAATCTTACTTCAACCGAGAAATTGATTTGCACTAGTAACAG 1030
DB 1103 ATCCCAACCGAATCTTGGCAATCTCTCAATTCGGAAGTTGATCTCCATGCAATATG 1162
QY 1031 CTGACTGTGCAATTCACCTGACCTGGAACATGTCAAATCTCATCTGGAATCTC 1090
DB 1163 CTCAGTGTCAATCCCTCTGAGCTTGGAAATATGTCAAGCTCTCAAGCTATTGGCACTA 1222
QY 1091 AATGATATCATCTCAACGGGTCAATATPACCAACAGAGCTTGGGAAGCTTACTGACTGTTT 1150
DB 1223 AAGCAATTAATAGTAGGGAATATTCACCTGAGCTTGGAAAGCTGAGCAATGTGTT 1282
QY 1151 GATCTGAATGTGGCAACAATGATCTGGAAGACCTTACTGATATCTGAGCTCTTGC 1210
DB 1283 GAATCTGAATCTTGGCAACACCCGTTTATGTAGGGCCCTTACCATCAACATTAATGTTACGT 1342
QY 1211 ACAATCTAACAAGCTTAAATGTTCAATGGGAACAAGTTTGTGGCACTATATCCCGAGCA 1270
DB 1343 GCAAGCTTGAATCAATTCATATGTTCAATGGAACCTCTTGAGTGAATCTATTCACATGGCG 1402
QY 1271 TTTCAAAAGCTAAGAAATATAGCTTATCTTATCTGTCCAGACAATATCAAAAGTCCA 1330
DB 1403 TTTCGCAATCTCGGAGACTTGAATCTTATCTGAATCTTTCGTCGAACAATTTCAAGGGAAA 1462
QY 1331 ATCCCGGTGAGCTATATCTGATTCGGTAATCTGATATCATTTGATCTTTCACAACAAG 1390
DB 1463 ATACCAATGATGAGCTTGACATATATCAATCTTGACAACTAGATCTGTGTGCAATAAC 1522
QY 1391 ATAAATGAATCAATTCCTTCTCTGCTGATTTGGAGCATCTTCAAGATGAATCTTG 1450
DB 1523 TTCTCAGGGTCTATACCATTAAGCTTGGGCAATCTTGGAACCTTCTCAATTAATCTT 1582
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QY 1451 AGTAGAATCATATATACCTGGTGTAGTTCACAGCGACCTTGGAAATCTAAGAGCATCATG 1510
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QY 1628 TTAGCCCACTGTCTAGCTCTCACTGTATGTAATGTATCTCATAAACAACCTGTAGTGAT 1687
DB 1763 CTTAGCAACTGCTTCACTCTTGTCAATCTGAATGTCTCTTCAACATCTCTCCGGATA 1822
QY 1688 ATCCCTAAGAACATTAACCTTCAAGATTTTACACAGACAGCTTCATTTGCAATCTGTGT 1747
DB 1823 GTCCCAACAATGAAAACTTCTCACGTTTGTCTCACGCCAGCTTTGTTGAAATCCATAT 1882
QY 1748 CTTTGGGTAGTGTGGCTAACTCACCGGTGTCAATGATTTCTGTGCAATGTACAGATGTCA 1807
DB 1883 CTTTGTGGAAACCTGGGTGGATCTATTTGTGTCTTTACCGAAATCTCGA-----GTA 1936
QY 1808 ATCTTAGACACGCTATTTCTTGAATAGTATTGGGGGACCTTGTGATCTTCTCATGTGC 1867
DB 1937 TTCTCCAGAGGTGTCTTGTGATCTGATTTGTTCTTGGCTCATCTACTCTCATATGATAT 1996
QY 1868 TTAATAGCAGCTTGCACCGCATTAATCTCTCTTTCTTGAATGATGATCACTTGACAA 1927
DB 1997 TTCTTGACAGTTTAAACAATCAATGACAGAGAAGATTTCAACAAGGCTC-----CTCA 2050
QY 1928 CCAGTAACCTTATTCGACACCGAGCTGTGATCCTTCATATGTAACATGACACTCCAGCT 1987
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QY 1988 TACAGAGATATCATGAGATGACAGAGAAATCTAAGTAGAAGTATCATTTGGGACGGA 2047
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QY 2048 GCATCAAGCAGCTGTATCAAAATGTTTTGAAGAATTTGAACCGGTTGCGATTAAACGG 2107
DB 2171 GCTTCTAGCAGCGGTATCAATGTGCAATTAAGTTCCGACCTATTTGCCATTAAAGCGA 2230
QY 2108 CTTTACTCTACAAACCCACAGTCAATGAATAACGTTTAAACAGAACTCGAGATGCTAAGT 2167
DB 2231 CTCTACAAATAGTATCGCATTAACCTGGGAAATTTGAGACGAACCTTGAGACCATTTGG 2290
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QY 2288 AAGAAAAAGACTTGTGATTTGGGACACACGCGCTTAAGATAGATATGTGACACAAAGT 2347
DB 2411 AAGAAAGTGAAGCTTGGTTGGGAGACAAGGTTGAAGATACCGGTGAGCTGCACAAAGGA 2470
QY 2348 TTAGCTTATCTACACCATGACTGTAGTCCAAAGTCACTTACAGAGACGTGAAGTGCCTCC 2407
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RESULT 9
AAT62125
ID AAT62125 standard; DNA; 9295 BP.
XX
AC AAT62125;
XX
DT 10-JUN-1997 (first entry)
XX
DE Arabidopsis thaliana plant morphogenesis regulatory protein DNA.
XX
KW Plant; morphogenesis; regulation; short; stem; alteration; inflorescence;
KW extraneous; gene; expression; transformation; increase; control; form;
KW length; ds.
OS Arabidopsis thaliana.
XX
XX Location/Qualifiers
FH Key
FT exon
FT /tag= a
FT 1803..1881
FT 1882..2227
FT intron
FT /tag= b
FT 2228..2366
FT /tag= c
FT 2367..2467
FT intron
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FT 2468..2539
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XX 04-MAR-1997.
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XX 24-AUG-1995; 95JD-00216187.
PF
XX
XX 24-AUG-1995; 95JD-00216187.
PR
XX
XX (CHIK-) ZH CHIKU KANKYO SANGYO GIJITSU KENKYU.
PA (MTS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA
XX WPI; 1997-206629/19.
DR
XX
XX DNA encoding plant morphogenesis regulatory protein - useful to yield
PT plants with short stems or altered inflorescence.
PT
XX
XX Claim 6; Page 12-15; 17pp; Japanese.
PS
XX
XX The present sequence encodes an Arabidopsis thaliana plant morphogenesis
CC regulatory protein (MRP), which can be used to yield a plant with, e.g.
CC short stems or altered inflorescence. The MRP acts on a plant at a
CC specific site for a specific period, and can therefore be used to
CC regulate extraneous gene expression in a plant. The MRP's cDNA or genomic
CC DNA can be used to transform a plant to increase its MRP expression, and
CC therefore control the form (particularly stem length) of the plant
XX
XX Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T; 0 U; 0 Other;
SQ
Query Match 34.7%; Score 1102; DB 2; Length 9295;
Best Local Similarity 84.9%; Pred. No. 4e-312;
Matches 1376; Conservative 0; Mismatches 0; Indels 244; Gaps 3;
QY 1801 AGTGTCAATCTCTAGACACTATTTCTTGAATAGCTATTGGGGAGTGTGATCCTTCT 1860
DB 5881 AGTGTCAATCTCTAGACACTATTTCTTGAATAGCTATTGGGGAGTGTGATCCTTCT 5940
QY 1861 CATGTCCTTAATAGCAGCTTGGCCGACGATTAATCTCTCTCTTTCTTGATGATCACT 1920
DB 5941 CATGTCCTTAATAGCAGCTTGGCCGACGATTAATCTCTCTCTTTCTTGATGATCACT 6000
QY 1921 TGACAAAC----- 1928
DB 6001 TGACAAACGAGTCTACTCTCCAACCACTTACGAATGTTCTTCACTTCAATGTAATC 6060
QY 1929 -----CAGTAACCTTATTCGACACGGAAGCTCGT 1956
DB 6061 CAATAGTAAATCCTTAATTTCTGTGTGACATGTAATTTGACACCGAAGCTCGT 6120
QY 1957 CATCTTCATATGAACATGACATCCACGTTTACGAGATATCATGAGATGACAGAGAA 2016
DB 6121 CATCTTCATATGAACATGACATCCACGTTTACGAGATATCATGAGATGACAGAGAA 6180
QY 2017 TCTAAGTAGAAGATATATCATTTGGGCACGGAGATCAAGACGTGTATCAATATGTTTTT 2076
DB 6181 TCTAAGTAGAAGATATATCATTTGGGCACGGAGATCAAGACGTGTATCAATATGTTTTT 6240
QY 2077 GAAGAATTGTAACCGGTTGCGATTAAAGCGGCTTACTCTCAACCAACCAAGTCATGAA 2136
DB 6241 GAAGAATTGTAACCGGTTGCGATTAAAGCGGCTTACTCTCAACCAACCAAGTCATGAA 6300
QY 2137 ACAGTTTGAAGACAGACTCGAGATGCTAAGTAGACATCAAGACAGAAATCTTGAGCCT 2196
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QY 2197 ACAAGCTTATTCCTCTCTCACTTGGGAGTCTTGTGTTATGACTATTGGAAAAATGG 2256
DB 6361 ACAAGCTTATTCCTCTCTCACTTGGGAGTCTTGTGTTATGACTATTGGAAAAATGG 6420
QY 2257 TAGCCTCTGGAGATCTTCTTAT----- 2278
DB 6421 TAGCCTCTGGAGATCTTCTTATGTAAGTCTCATCGCAAAATAGAAAAATATTGTAAT 6480

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Qy	2279	-----GACCCTTACGAGAAAAAGACTC	2300
Dp	6481	CTTCGTGACATAACACTTCGCTGTGTGTTTTGTAAAGGCCCTTACGAAAGAAAAGACTC	6540
Qy	2301	TTGATTTGGGACACACGGCTTAAGATAGCATATGGGACGACCAAGGTTTACTTATCTAC	2360
Dp	6541	TTGATTTGGGACACACGGCTTAAGATAGCATATGGGACGACCAAGGTTTACTTATCTAC	6600
Qy	2361	ACCATGACTGTAGTCCAGAGATCATTTCAAGAGACGTGAAGTCGTCCAACTTCCTTGG	2420
Dp	6601	ACCATGACTGTAGTCCAGAGATCATTTCAAGAGACGTGAAGTCGTCCAACTTCCTTGG	6660
Qy	2421	ACAAAGACTTAGAGGCTCTGTTTGACAGATTTTGGAAATGCGAAAAAGCTTGTGTGTCA	2480
Dp	6661	ACAAAGACTTAGAGGCTCTGTTTGACAGATTTTGGAAATGCGAAAAAGCTTGTGTGTCA	6720
Qy	2481	AGTACATACTTCAACTTACGTGATGGGACAGATAGTTATAGACCCGAGATGCTC	2540
Dp	6721	AGTACATACTTCAACTTACGTGATGGGACAGATAGTTATAGACCCGAGATGCTC	6780
Qy	2541	GCACTTCACGGCTCACTGAGAAATCCGATGCTACAGTTATGAAATGCTCTTCTTGA	2600
Dp	6781	GCACTTCACGGCTCACTGAGAAATCCGATGCTACAGTTATGAAATGCTCTTCTTGA	6840
Qy	2601	TGTTAACCCGAGAAAGCCGTTGATGACGAATCCAACTCCACACTCT	2649
Dp	6841	TGTTAACCCGAGAAAGCCGTTGATGACGAATCCAACTCCACACTCTGATTTGTTCTT	6900
Qy	2650	-----	2649
Dp	6901	TCTTGCCATCTCTCTCGCTGCTCTGTTAGTCAAGTCCGTAATCTGTGTTTCATTGA	6960
Qy	2650	-----GATTAATGTCOAAGACGGGAAACATGAATGATGAAATGCGAGATC	2696
Dp	6961	TTCACTTACATCAGATTAATGTCOAAGACGGGAAACATGAATGATGAAATGCGAGATC	7020
Qy	2697	CAGACATACATCGACCGTGTAAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGGAC	2756
Dp	7021	CAGACATACATCGACCGTGTAAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGGAC	7080
Qy	2757	TCTATGACCAAAAGACAGCCGATGATCGACCACCAATCACCAGGTGACTGCTTC	2816
Dp	7081	TCTATGACCAAAAGACAGCCGATGATCGACCACCAATCACCAGGTGACTGCTTC	7140
Qy	2817	TGCGCAGTTTATGTCTATCGGAACAACCTGCTGCGACTGACACGTCAAGCAGCTGG	2876
Dp	7141	TGCGCAGTTTATGTCTATCGGAACAACCTGCTGCGACTGACACGTCAAGCAGCTGG	7200
Qy	2877	CTGGTTCGTGTACGTGATGATGATGCAAAATTCGAAGCTCTTCATTTCTGTCAATTGCT	2936
Dp	7201	CTGGTTCGTGTACGTGATGATGATGCAAAATTCGAAGCTCTTCATTTCTGTCAATTGCT	7260
Qy	2937	CTTCCATGAGTCTTCTGTGATGCTCAACTGTTCTTGGTTTGGACAAGTTATTTCTCAGA	2996
Dp	7261	CTTCCATGAGTCTTCTGTGATGCTCAACTGTTCTTGGTTTGGACAAGTTATTTCTCAGA	7320
Qy	2997	ACAGTGTACTTTTTCGTTAGGAGAGAACTTTAAACGGTATCTTTTCGTTGCGCTTA	3056
Dp	7321	ACAGTGTACTTTTTCGTTAGGAGAGAACTTTAAACGGTATCTTTTCGTTGCGCTTA	7380
Qy	3057	AGCTGTTGAAAAAATTAAATGCTCATCATGAAAGTATTTAGCACTGCTCTTATATTAGA	3116
Dp	7381	AGCTGTTGAAAAAATTAAATGCTCATCATGAAAGTATTTAGCACTGCTCTTATATTAGA	7440
Qy	3117	CAAGTGTGTGTGTGAATATGTCTTCAGACTGGCACTTGAAGCTTCTAATAGTTCTTGGC	3176
Dp	7441	CAAGTGTGTGTGTGAATATGTCTTCAGACTGGCACTTGAAGCTTCTAATAGTTCTTGGC	7500

RESULT 10
AD132619
ID AD132619 standard; DNA; 2751 BP.

XX	AC	AD132619;
XX	DT	22-APR-2004 (first entry)
XX	DE	Thale cress transpiration efficiency-related ERECTA homologue DNA SEQ 7.
XX	KW	plant; transpiration efficiency; ERECTA; breeding; genetic engineering;
XX	KM	thale cress; ds; gene.
XX	OS	Arabidopsis thaliana.
XX	FH	Key
XX	FT	location/Qualifiers
XX	FT	CDS
XX	FT	1..2751
XX	FT	/tag= a
XX	FT	/product= "thale cress transpiration efficiency-related
XX	FT	ERECTA homologue protein - SEQ ID 8"
XX	FT	/transl_except= (pos,334..339, aa;LEFLMKNNQLGPIPAT)
XX	PN	WO200400555-A1.
XX	PD	15-JAN-2004.
XX	PF	02-JUL-2003; 2003WO-AU000854.
XX	PR	02-JUL-2002; 2002AU-00003339.
XX	PA	(AUSU) UNIV AUSTRALIAN NAT.
XX	PI	Masle J, Farquhar GD, Gilmore SR;
XX	DR	WPI; 2004-091390/09.
XX	DR	P-PADB; ADI32620.
XX	PT	Selecting plants having enhanced transpiration efficiency, useful for
XX	PT	producing plants with enhanced transcription efficiency comprising
XX	PT	selecting plant expressing a genetic marker linked to the ERECTA locus in
XX	PT	the genome of the plant.
XX	PS	Claim 3; SEQ ID NO 7; 209pp; English.
XX	CC	The invention relates to a novel method for selecting a plant having
XX	CC	enhanced transpiration efficiency comprising detecting a genetic marker
XX	CC	for transpiration efficiency, where the marker comprises a nucleotide
XX	CC	sequence linked genetically to an ERECTA locus in the genome of the plant
XX	CC	and selecting a plant that comprises or expresses the genetic marker. The
XX	CC	method of the invention may be useful for selecting a plant having
XX	CC	enhanced transpiration efficiency. The isolated ERECTA gene or allelic
XX	CC	variant or protein-encoding region may be useful in the preparation of a
XX	CC	genetic construct for modulating the transpiration efficiency of a plant.
XX	CC	Furthermore, the ERECTA genes may be useful for producing plants having
XX	CC	enhanced transcription efficiency by both traditional plant breeding and
XX	CC	genetic engineering approaches. The current sequence is that of the thale
XX	CC	cress ERECTA homologue DNA of the invention.
XX	SQ	Sequence 2751 BP; 771 A; 622 C; 578 G; 780 T; 0 U; 0 Other;
OY	Query Match	33.8%; Score 1074.6; DB 12; Length 2751;
Dd	Best Local Similarity	64.0%; Pred. No. 2.3e-304;
	Matches 1717; Conservative %	0; Mismatches 904; Indels 60; Gaps 4;
OY	168	TGGAGATTAAAGAATCAATCTTCAAAGATGTGAACAATGTTCTTAAGACTGAGCAACTTCAC 227
Dd	2	TGGCGATTAAAGCTTCATTCAGCAACGTGGGAAATVATGCTTGATTTGGAGCATGTTC 61
OY	228	CTTCTTGGAATATTATGTCTGAGAGAGTGTGTTTGAAAATGTCACTTCATGTG 287
Dd	62	ATAACACAGACTTTTGTCTTCTTGAGAGAGTGTCTCTGTATTAACGTTAAGCTCATGTG 121
OY	288	TTGCTCTTAATTTGTCAAGATTGAATCTTGATGAGAAATCTCACCTGTATTGGAATC 347
Dd	122	TCTCTTAAATCTGTCAACCTGAATCTTGATGAGAGATATCATCTGCCCTTGGAATTT 181

xx Claim 3, SEQ ID NO 7, 209pp; English.

xs

xx The invention relates to a novel method for selecting a plant having

CC enhanced transcription efficiency comprising detecting a genetic marker

CC for transcription efficiency, where the marker comprises a nucleotide

CC sequence linked genetically to an ERGTA locus in the genome of the plant

CC and selecting a plant that comprises or expresses the genetic marker. The

CC method of the invention may be useful for selecting a plant having

CC enhanced transcription efficiency. The isolated ERGTA gene or allelic

CC variant or protein-encoding region may be useful in the preparation of a

CC genetic construct for modulating the transcription efficiency of a plant.

CC Furthermore, the ERGTA genes may be useful for producing plants having

CC enhanced transcription efficiency by both traditional plant breeding and

CC genetic engineering approaches. The current sequence is that of the thale

CC cress ERGTA homologue DNA of the invention.

CC

xx

xx Sequence 2751 BP; 771 A; 622 C; 578 G; 780 T; 0 U; 0 Other;

Query Match	33.8%	Score 1074.6;	DB 12;	Length 2751;
Best Local Similarity	64.0%;	Pred. No. 2.3e-304;		
Matches 1171; Conservative	0;	Mismatches 904;	Indels 60;	Gaps 4;

Oy	168	GGAGATTAAAGATCTCATTTCAAAGATGGAACATGTTCTTTATGACGTGGCAACCTTCAC	227
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Oy	228	CTTCTTGGGATTAATTTGTGTCTGGAGAGGTGTCTTGTGAAATATGTACCTTTCAATGTGG	287
Db	62	ATAACCAAGATTTTGTCTTGGAGAGGTGTCTTGTGAAACGTAAAGCTTCATGTGG	121
Oy	288	TTGCTCTTAATTTTGTGAGATTTGAATTTTGAATGAGAAATCTCACTGTCTATTGGAGATC	347
Db	122	TCTCTTTAATCTGTCAACCTGATTTGTGGAGAGATATCATCTGCCCTTGGAAATTT	181

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QY 408 AGATTGCTGCTGTTCTTCTTGCAAACTTAGCTTATCTTCAATGAATTAAGTGTG 467
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DB 302 ACATACCGTTTTCATCTTAATCTCAAAACAGCT----- 335
QY 528 AATTGATAGACCGATCCCTTCACACTTTCACAGATTCCAAACTGAAAAATTCGACT 587
DB 336 -----GACCTTAATCAGATTCCAAACTTAAGACCTTGACC 373
QY 588 TGGCAGCAATAACTCACTGCTGAGATCCAAACATTAATTACTGGAATGAATCTTTC 647
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QY 1368 CATTTGATCTTTCCAAACAAGATTAATGGAATCAATCTTCTTCCCTGGATTTGG 1427
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QY 1428 AGCATCTTCTCAAGATGAATTTGATGAAGAAATCATTAATCTGTGTAGTTCCAGGCACT 1487

DB 1214 AGCATCTTCTCATCTTAACTTGACAGAAATCATCTGAATGACACATTCCTGCAGAAAT 1273
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DB 1274 TCGGAACCTCCGAGGATTCAGATCATGTGATGTGATTAATTTTCTTCCGGGTGA 1333
QY 1548 TTCCAGAAAGCTTAAACCAATTAACAGAACATATTTTGTGAGACTGSAATAATTAAC 1607
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DB 1631 TCATCACTCTCATATGATATATTTCAATTCGGTTTACAGTCAAAAGCAGCAAAACAG 1690
QY 1905 TTCTTGATGATCATCTTGCAAAACAGTAATTAATTCGACACCGAAGCTGTCACTCTTC 1964
DB 1691 TCTTGAAGGCTCTTCAAAACAAC-----CTGAAGGCTCAAGAAAGCTGTATCTTCTC 1744
QY 1965 ATATGAACATGSCACTCCAGCTTTAGAGATATTCATGAGAAATGACAGAGAAATCTAAGT 2024
DB 1745 ACATGACATGAGGCTATTCACACGTTTGAATGATATCATAGAAATGACAGAAACCTGATG 1804
QY 2025 AGAATATATCATTTGGGCAAGAGCATCAAGCACTGATATCAATGATGTTTGAAGAT 2084
DB 1805 AGAATATCATATTTGATATGAGTATGCGTCTTTCAGACAGTTTACAGTGCACCTCCAAAAT 1864
QY 2085 GTAAACCGGTTTGCATTAAGCGGCTTTACTCTCAAAACCCAGCTCAATGAACAGTTTG 2144
DB 1865 CCGACCTATTTGCATTAACGAATCTAATCAGATATCCAGCAACTTCCGGAAGTTTG 1924
QY 2145 AAACAGAACTCGAGATGCTAATGATCAAGACAGAGAAATCTTGTGAGCTTCAAGCTT 2204
DB 1925 AAACAGAGCTCGAGACCATTTGGAGCATGACACAGAAACATATGATGCTTCACGAGT 1984
QY 2205 ATTCCCTCTCACTTGGGAGTCTTCTGTCTATGACTATTTGGAATAGTAGCTCT 2264
DB 1985 ACGCTTATCTCCCTTTTGGCACTCTCTTCTACGACTATCAGTGAAGAAATGGCTCTCTT 2044
QY 2265 GGAATCTTCTTCAATGCGCTTACGAAGAAAAAGCTTGAATTTGGGACACAGGCTTAAGA 2324
DB 2045 GGGATCTTCTCAATGGGCTCGGGAAGAGGTGAAGCTTGAAGCTGGGAAAAAGGCTGAAGA 2104
QY 2325 TAGCATATGTGACAGCAAGGTTTATAGCTTATCTAACAACATGACTGTATGACAAAGTCA 2384
DB 2105 TAGCTGTGAGGCTGCGCAAGAGCTTGCAATATCTTCAACATGACTGACACTAGAGATA 2164
QY 2385 TTCAAGAGAGCTGAAGTCTTCCAAACTTCTTGTGCAAAAGCTTAGAGGCTGTGTTGA 2444
DB 2165 TCCATGAGAGACTCAAGTCAATCAAACTATCTCTGTATGGAATTTGGAAGCCGCTTGT 2224
QY 2445 CAGATTTTGGAAATGCGAAAGCTTGTGTGTCAAGTCAATCTTCAATCTTAACGTGA 2504
DB 2225 CAGATTTTGGGATTTGCCAAGACATATCACGCCAACAAACCTTAATGCTTCAACCTATGTC 2284
QY 2505 TTGGCAGATAGGTTAATATAGACCCCGAAGTATGTCTGCACTTTCAGCGCTCACTGAAGAT 2564

Db 2285 TTGGAACATTTGATATATATGACCCAGATATGCTGACACTTGCCTGTAACGAGAAGT 2344
 Qy 2565 CCGATGCTACAGTTATGAAATAGTCTCTTGTAGTTGTTAACCCGAAGAAAGCCGTTG 2624
 Db 2345 CTGATATCTACAGTTTGGATATGTCCTTTTGAAGCTTCAACCGGAGAGGCTGTGG 2404
 Qy 2625 ATGACGAATCAATCTTCACCATCTGATTAATGTCMAAGCGGGAACAATGAATGATGG 2684
 Db 2405 ATAAACGAGCCAACTTGATCAATCAATGATCTATCAAAAGCGGATGATTAACAGTAAATGG 2464
 Qy 2685 AAATGCAATCCAGACATCAATCAACGATTAAGATCTCGGTGTGTGAAGAAATTT 2744
 Db 2465 AACCTGTGATGAGAGAGTCTCAGTCTGATGACCTGACATCAATCAAGAAATCAT 2524
 Qy 2745 TCCACGTCGACCTCTATGACCAAAAGACGCGGAATGATGACCAATGACAGG 2804
 Db 2525 TTGAGTACGCTCTCTTGTGACCAAGCAAAATCTTTGGAGAGACCAACATGAGAGG 2584
 Qy 2805 TGACTGCTGTCTCGGAGTTTATGCTATCGGAACAACCA 2845
 Db 2585 TCTCTAGGCTTCTGCTCTCACTGTCCCGTCTCCACCTCCA 2625

RESULT 11
 ADI32617
 ID ADI32617 standard; DNA; 2766 BP.

XX ADI32617;

XX 22-APR-2004 (first entry)

XX Sorghum transpiration efficiency-related ERECTA DNA.

XX plant; transpiration efficiency; ERECTA; breeding; genetic engineering;
 XX sorghum; ds; gene.

XX Sorghum bicolor.

XX Key Location/Qualifiers

XX FT CDS 1..2766
 FT /tag= a
 FT /product= "Sorghum transpiration efficiency-related
 ERECTA protein"

XX MO2004005555-A1.

XX 15-JAN-2004.

XX 02-JUL-2003; 2003MO-AU000854.

XX 02-JUL-2002; 2002AU-00003339.

XX (AUSU) UNIV AUSTRALIAN NAT.

XX Masle J, Farquhar GD, Gilmore SR;

XX MPI; 2004-091390/09.

XX P-PSDB; ADI32618.

XX Selecting plants having enhanced transpiration efficiency, useful for
 PT producing plants with enhanced transcription efficiency comprising
 PT selecting plant expressing a genetic marker linked to the ERECTA locus in
 PT the genome of the plant.

XX Claim 3; SEQ ID NO 5; 209pp; English.

XX The invention relates to a novel method for selecting a plant having
 CC enhanced transpiration efficiency comprising detecting a genetic marker
 CC for transpiration efficiency, where the marker comprises a nucleotide
 CC sequence linked genetically to an ERECTA locus in the genome of the plant
 CC and selecting a plant that comprises or expresses the genetic marker. The
 CC method of the invention may be useful for selecting a plant having
 CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic

CC variant or protein-encoding region may be useful in the preparation of a
 CC genetic construct for modulating the transpiration efficiency of a plant.
 CC Furthermore, the ERECTA genes may be useful for producing plants having
 CC enhanced transpiration efficiency by both traditional plant breeding and
 CC genetic engineering approaches. The current sequence is that of the
 CC sorghum ERECTA DNA of the invention.

XX Sequence 2766 BP; 716 A; 697 C; 646 G; 707 T; 0 U; 0 Other;

XX Query Match 33.1%; Score 1050.8; DB 12; Length 2766;

XX Best Local Similarity 63.4%; Pred. No. 2.3e-297;

XX Matches 1845; Conservative 0; Mismatches 882; Indels 185; Gaps 8;

Qy 112 TCTCTTCTGCTTGTAGCTTGTAGTACTCTGACTTGTGAGAGGAGGAGCAAGTTGCTTGA 171
 Db 24 TCTCTGTCGCCCTCTCTCTGTCGTCGCCGCCGCCGAGATGGGCGACGCTGATGA 83
 Qy 172 GATTAGAAGTCAATTCMAAAGATGTGAACAATGTTCTTTATGACTGTGACAACTTCACCTTC 231
 Db 84 GATCAAGAAGTCTCTCGCAAGCTCGCAACGTAAGTATGATTTGGGCGGCGAC----- 138
 Qy 232 TTGCAATTAATGCTGTGAGAGAGTGTCTTGTGAATAATGTACCTTCAATGTGTGC 291
 Db 139 ---GACTACTGCTCCTGGCGCGGCGCTCGTGCACAAAGTCAATTCGCCCTCGCTGC 194
 Qy 292 TCTTAATTTGTGATGATTTGATGATGAGAAATCTGACCGCTAATTTGAGATCTCAA 351
 Db 195 GCTCAACCTCTCTGAGCTCAACCTTGTGAGGCGAGATCTTCCAGCCGTGCGACGCTCAA 254
 Qy 352 GAGTCTCTTGTCAATTAATGATCTGCGAGATATGCTGTGTGCAAAATCCCTGATGAT 411
 Db 255 GAGCCTCGTCCATGATCTGAATCAATGAGGCTATCGGCGACATCCCTGATGATGAT 314
 Qy 412 TGGTGACTGTTCTTCTTGTGCAAACTTAGACTTATCTTCAATGAATTAAGTGTACAT 471
 Db 315 TGGTGATGTATCACTTAAGACGCTGACCTTCTTCAACAACTTGTGATGCGACAT 374
 Qy 472 ACCGTTTGTGATTTGCAAGTTGCAAGCACTTGAGCAGCTGATTTGAAATTAACCAAT 531
 Db 375 ACCATTTTCTATATCAAAAGTGAAGCACTTGAGAACTTGATTAAGAAACAACAGCT 434
 Qy 435 GATTGTGCGATCCCATCAATGTCACAGCTCCCAAAATTTGAATTTGATTTGGC 494
 Qy 532 GATGAGACCGATCCCTTCAACACTTTCACAGATTCGAAACCTGAAATTTGACTTGGC 591
 Db 495 ACATAAACAACCTGACCTGGGAGATACCAAGCTTATCTATCTGAAATGAGGTTCTCAAA 554
 Qy 652 TCTTGGGTTGCGAGAAACAATTAAGTGGTAAACATTTCCAGATTTGTCAACTGAC 711
 Db 555 TC----- 556
 Qy 712 TGGTCTTGTGATTTTGTAGCTAAGAAACAAGATTGTGACTGTGATATACCTGACGAT 771
 Db 557 -----TTGATGTGAAGAACATAGCTGACCGGGGTATACAGACCAAT 602
 Qy 772 AGGAATTTGCACTGCTTCCAGGTTTGTGACTTGTCTTCAATCACTAATCTGTGTAGAT 831
 Db 603 TGGGAACCTGTACAAGTTTCAAGTCTTGTGATTTGTCTTCAACCGCTTAACTGACCAAT 662
 Qy 832 CCGTTTGAACATCGGTTCTCGAAGTTGCAACATTAATGTCGAAGCAATCACTGTC 891
 Db 663 CCATTCAAACATTTGTTCTTCAAGTGTACACTACTTGTGCAAGGAAACAAGTTTAC 722
 Qy 892 TGGGAAGATTCATGATGATTTGTCTCATGCAAGCCCTTGTGACGTTGATTAAGTGG 951
 Db 723 CGGTCAATTTCTGTAGTATGATTTGTATGACAGGCTTCGCGTTCTGATGTAGTTA 782
 Qy 952 CAATTTGATGATGATCTATCTTCCGATTTCTCGGAATCTTACTTTACCGAAGAAAT 1011
 Db 783 CAACCAATTAATCTGTGCTATATCAATCAATTAATGAGCACTTGAACATCACTGAGAAAGCT 842

QY 1012 GATATTCACAGTAACAAGCTGACTGGTTCATTCACCTGAGGCTGGAAAACTGTCMAA 1071
DB 843 GTACATCCAAAGGCAATAAAGTTAACTGGGTGATACCAACAGAGTTAGAAATATGTCAC 902
QY 1072 ACTCCATTACCTGGAACTCAATGATATCATCTCAGGGGTCAATATACCAACAGAGCTTGG 1131
DB 903 ACTTCATTACCTGAACTGAAACGATTAATCACTTACGGGTCAATTCACACAGAGCTTGG 962
QY 1132 GAAGCTTACGACTGTTGTTGATCGAATGAGGCCCAACATGATGTGGAGAACCTATACC 1191
DB 963 AAGGCTACAGAGGCTTGTGTTGACTGAACTTGGCAATACCACTGGAAAGAACCAATTC 1022
QY 1192 TGATCATCTGAGCTCTTGCACAAATCTTAAACAGCTTAATGTTTCATGGGAACAATTAG 1251
DB 1023 TGACAACTTAAGTTCAATGTGTAATCTCAATAGCTTCAATGCTTATGGCAACAAGTTAAA 1082
QY 1252 TGGCACTATACCCCGAGCAATTTCAAAAGCTAGAAAGTATGACTTAACTTCTGTCAG 1311
DB 1083 TGGGACCATTCCTCGTTCGTTGCGGAAACTTGAAAGCATGACCTATTAAATCTGTATC 1142
QY 1312 CAACAATATCAAGAGTCCAAATCCCGTTGAGCTATCGTATGGGTAACTTAGATCATT 1371
DB 1143 AAACCTCATATAGTGTCTCTATTTCTATTGAGTTATCAAGGATCAACAATTTGGACAGCT 1202
QY 1372 GGAATCTTCCAAACAAGATAAATGGAATCATTCCTTCTTCCCTGGTGAATTTGAGCA 1431
DB 1203 GGAATTTATCCGTAAACATGATGACTGGTCCAAATTCATCATTAATGGACGCTAGAGCA 1262
QY 1432 TCTTCTCAAGATGAACCTTGAAGATAAATCATATTAACGTGGTGAATTCAGAGCACTTGG 1491
DB 1263 TCTATTGAGACTTAACCTTGAAGCAAGAAATGGCTAGTGGATTCATCCCGGGAGTTTGG 1322
QY 1492 AAATCTAAGAAGCATCTGGAATATAGATCTTCAATATATGATATCTCGGCCCAATTC 1551
DB 1323 TAATTTGAGAGATGTCTAGAGATTTGATTTATCTTAATATCACTTGTGGCTGATTC 1382
QY 1552 AGAAGACTTAACCAATTAACAGAAATATTTTGTGAGACTGGAAAAATAAATACCTGAC 1611
DB 1383 TCAGAAACTTGAAATGCTGCAAAACGTATGTTGC----- 1417
QY 1612 TGGTAATGTTGGTTCAATTAAGCCAACTGTCTACGTCTATGATATGATCTCA 1671
DB 1418 -----TAAATGTGCTGTCAA 1433
QY 1672 CAACCTGTAGGTATATCCCTAAGAACAAATTAATCTTCAAGATTTTACACAGACGCT 1731
DB 1434 TAATTTGGCTGGTGTGTTCTCTGCTGCAACAACTTACACAGGTTTTCACCTGACAGCTT 1493
QY 1732 CATTTGCAATCTGTGCTTGTGCGGTAGTGGCTAACTCACCGTGTGATGATTTCTGTCG 1791
DB 1494 TTTAGGTAAATCTGTGGAATCTGTGGAATCTGGCTTGTTGCTGCTGCTCACTGGCCA 1553
QY 1792 AACTGTACAGTGTCAATCTCTAGAGCACTATTTCTGGAAATAGCTATTTGGGGGACTTGT 1851
DB 1554 CCAAGAGAAACCGGCTATCTCAAAAGGCTGCATTAATGTGGTGTGCTGTGGGTGACTTGT 1613
QY 1852 GATCCTTCTGATGGTCTTAAATAGACGCTTGCACCGCATATCTCTCTCTTTCTTGA 1911
DB 1614 TATCTCTTATATATCTTAAAGTCTTTTGCAGGCCACATGCTCACTGCTTTTAAAGA 1673
QY 1912 TGGATCACTTGAACAACAGTAATTTATGACACCGAAGCTGTCAATCTTCATATGAA 1971
DB 1674 TGTCACTGTAAAGCAAGGACAGTAAGAAATGCTCCCCCAAGCTGTGATCTCTCATATGAA 1733
QY 1972 CATGGCACTGACGCTTACAGAGATATCAAGAAATGACAGAAATCTAAGTGAAGTA 2031
DB 1734 CATGGCCCTTCACTATACATGATGATTAATGAGATACATGAGAACTTGTGATGAATA 1793
QY 2032 TATCATTTGGGACGAGACATCAACGACTGTATACAAATGTGTTTGAAGATTTAAACC 2091
DB 1794 CATCATTTGATGATCGGGGCTGCAAGTACAGTTTAAATGTGTCTTAAAGATTTGCAACC 1853
QY 2092 GGTTCGATTAAAGCGGCTTAACTCTCAACCAACGATCAATGAACAATTTGAAACAGA 2151

DB 1854 GGTGGCAATTAATAAACTGTATGCCACTTACCCACAGAGCCTTAAGGAATTTGAAACTGA 1913
QY 2152 ACTCGAGATGCTAAGATGATCAAGACAGAAATCTTTGAGGCTTCAAGCTTATTCCTC 2211
DB 1914 GCTTGAAGACTTGTGTGATCAAGACCGGAATCTATGTCAGCTTCAAGGATCACTAT 1973
QY 2212 CTCTCACTTGGGGAGTCTTCTGTCTATGACTATTTTGAATAATGTAGCTCTGGGATCT 2271
DB 1974 ATCACTGTGGGAACTCTCTTTATATATTAATGAAATGTGGCAGGCTTATGGGATGT 2033
QY 2272 TCTTCAT--GGCCCTACGAAGAAAAAGCTTTGATTTGGGACACAGGCTTAAATAGC 2328
DB 2034 TTTACATGAAGGTTCATCCAAAGAAAAAATTTGACTGGGAACTCTGCTACGGAATGG 2093
QY 2329 ATATNGTCAGCAAGAGTTTACTATATCAACCAATGACTGTAGTCCAAAGATCATTTCA 2388
DB 2094 TCTTGTGACGCTCAAGGCTTGTCTTACCTTCAACATGACTGCAATCCGATTAATTC 2153
QY 2389 CAGAGAGTGAAGTCTCCAACTTCTTTGACAAAGACTTGAAGGCTGTTTGAACAG 2448
DB 2154 TCGGAGTGTAAATCAAGAATATACTCTTGACAAAGATTAAGAGCCATCTTACAG 2213
QY 2449 TTTTGAATGCGAAAAAGCTTGTGTGTCAAAATGACATATCTTCAACTTACGTATGG 2508
DB 2214 CTTTGAATGCTAAGAGCTTATGTGTCTCAAAAACCTCACACATCAACCTATGTCAATGG 2273
QY 2509 CAGATATGTTATATGACCCCGAGTATGCTGCACTTCAAGGCTCACTGAGAAATCCGA 2568
DB 2274 AACTATTTGGCTAATGATGATCTGATGACCGCCGACCTTCCGCTCTCAAGAAAGCTGA 2333
QY 2569 TGTCTACA--GTATGGAATATGCTTCTTGAATTTTAAACCGAGAAAAACCGTTGATG 2627
DB 2334 TGTCTACAGCTATGAGATTTGTTCTGTGAGCTGTGCTGACATGGCAAGAACCTAGTGACA 2393
QY 2628 ACGAATCCAAATCTCCACCATCTATATGTCAAAAGACGGGAAACATGAAGTATGAAA 2687
DB 2394 ACGAATCC-----TATCGAAGACGCGACACAAACGAGTATGATTA 2434
QY 2688 TGGCAGATCCAGACATCAATCGACATGAGTAAAGATCTCGGTGTGTAAGAAATTTTCC 2747
DB 2435 CCGTGAACCTTGACATCGGGGACACCTGCAAGACCTCGGAGGTGAAAGACTGTTC 2494
QY 2748 AACTGGCACTCTATGACCAAAAGACAGCGAATGATGACCAACATGACACAGGTGA 2807
DB 2495 AGCTGGGCTCTTTTGACCAAGGGAACCTCGGACCGACGAGATGACAGAGTGG 2554
QY 2808 CTGTGTTCTGGCAAGTTTATATCTATCGGAACAACCACTGCTGGACTG----- 2858
DB 2555 TGGCGCTCTGGAATGCTGTGTGAACCCGGAACCGCGCCMAAGCGTGGCGCACAGC 2614
QY 2859 ACAAGTCAAGGACGCTGGGCTGTGCTGTGATGATGATGATGAAATCTCAAGACTC 2918
DB 2615 TGGCGGACCGGTGCGACAGCCGTGCAAGCTTACATCAACGATGATGATGATGATG 2674
QY 2919 CTCATTCTGTCAATTTGCTC--TTCCATGATGCTTCTGATGCTCAATGTTTCTTCG 2975
DB 2675 CCGGCGCTCTCTCTGGGCAACCTGACAGCACTCTGGAAGCGCGAGCTGTCTCAAGT 2734
QY 2976 TTGACAAAGTTATTTCTCAGAAACGTGAGTAG 3007
DB 2735 TCGGCGAGGCACTCGACAAACATGAGATAG 2766

RESULT 12
ADA71018 standard; DNA; 2796 BP.
XX ADA71018;
AC
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 4341.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
KM gene; ds.
XX
XX Oryza sativa.
OS
XX MO2003000898-A1.
PN
XX
PD 03-JUN-2003.
XX
XX 22-JUN-2001; 2001MO-IB001105.
PF
XX 22-JUN-2001; 2001MO-IB001105.
PR
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX MPI; 2003-175290/17.
DR
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 6; SEQ ID NO 4341; 899pp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
SQ Sequence 2796 BP; 729 A; 659 C; 635 G; 773 T; 0 U; 0 Other;
Query Match 32.9%; Score 1044.4; DB 8; Length 2796;
Best Local Similarity 62.9%; Pred. No. 1.8e-295;
Matches 1832; Conservative 0; Mismatches 911; Indels 171; Gaps 7;
QY 112 TCTCTTCTGCTTGAAGTTAGTACTGACTTCAAGAGAGGCAAGTGTCTGA 171
DB 36 TCTCGTCGCGCTCTGCTGCTCGCCGCGCGTTCGATGATGGGTGACGCTGCGA 95
QY 172 GATTAGAAGTCTTCAAGATGTGAACATGTTCTTTATGATGACGACAACTTACCTTC 231
DB 96 GATCAAGAAAGTCTCTCCGCAATGTGACAAAGTACTGATGATGGCCGCGGC----- 150
QY 232 TTCGATTAATTGCTCGAGAGAGTGTGTTGTGAATAATGTCACCTTCAATGTTGTC 291
DB 151 ----GACTACTGCTCGTGGGGGCGTCTCTCGACAAAGTCACTTGGCCGCTCGCGC 206
QY 292 TCTTAATTGTCAGATTGAATCTTATGAGAAATCTCACTGCTATTGAGATCTCA 351
DB 207 GCTCAACCTATCCGGGCTCAACTCGAGGCGAGATCTCCGGCGTGGAGGTTGAA 266
QY 352 GAGTCTCTTGTCAAT---TGATCTGAGAGTATCGCTTGTCTGACAAATCCCTATGA 408
DB 267 GGGCATATGCTCGATGATGAGAAAGCGTGTGTATCTTGTGTTTGGAAAAATGTG 326
QY 409 GATTGTGACTGTCTTCTTTGCAAAACTAGACTTATCTTCAATGAAATTAAGTGATGA 468
DB 327 GCTTGCTGCTGCTTGAAGTCTGCAAGTAACTTTGACTTGAAGTCAAAATGGGCTGTGCGCA 386
QY 469 CATACCGTTTTCGATTTCGAAGTTGAAGCAACTTGAAGCAAGTATTCTGAAGATAACCA 528
DB 387 GATCCCTGATGATGATGGCGATTTGTTATCATCAATAAAACTGTATTTGAAAGAACCA 446

QY 529 ATTGATAGACGCGATCCCTTCAACACTTTCAGAGATTCCAAACCTGAAATTCGACCTT 588
DB 447 ACTGATCGAGGTATATCCATCAACGCTCTCACAGCTCCCAAATTTTGAAGATTTTGACCTT 506
QY 589 GGCACAGAAATPAACTGAGTGTGAGATACCAAGACTTATTTACTGAAATGAAGTCTTCA 648
DB 507 GGCACAGAAATPAACTGAGTGTGAGATACCAAGACTTATTTACTGAAATGAAGTCTTCA 566
QY 649 GTATCTTGGTTCGAGGAAACAACTAGTGGTAACTTCTCCAGATTTGTGTCACT 708
DB 567 ATACTGGGATTTACGGGATATATTATTAAGAGGACAGATCTCCCGAGATTAATGCGCAGTT 626
QY 709 GACTGCTTGTGATTTTGAAGTAAAGAAACAAAGTTGACTGATGATTAACCTGAGAC 768
DB 627 GACTGGGCTTTGTA----- 641
QY 769 GATAGAAATTTGACACTGCTTCCAGGTTTGGACTTGTCTTCAATCACTAAGTAACTGTGA 828
DB 642 -----CTTGATTTGTCTTCAATPAACTTTCTGGATC 674
QY 829 GATCCCTTTTGAATGAGTGGCTTCTCTGCAAGTGTGCAACATTATCTTGAAGGCAATCACT 888
DB 675 AATTCCTTTTCAATGATGTTTCTTACAGATTTGCTACACTATCTTTCGAAGGGAACATGTT 724
QY 889 CTCTGGAAGATTCATCACTGATGATGTTGCTCATGCAAGCCCTTGACAGTCTTAGATCTAAG 948
DB 735 TACTGCTCTATTTCATCACTGATTTTGAATTTGATGAGGCTCTGCTGTACTGATCTGAG 794
QY 949 TGGCAACTGTTGAGTGTGATCTATTCCTCGATTCGGAATCTTACTTTCACCGAGAA 1008
DB 795 TTACAAACCAATTTGCTGTGCTATTCATCGATGATAGGCAATTTAACTATACCTGAGAA 854
QY 1009 ATTGATTTTGCACAGTAAACAGTGTGTTAATTCACCTGAGCTTGGAAACATGTC 1068
DB 855 GCTGTATATGCAAGGCAATTAAGTTAAAGGTCCAAATACCACTGAACTTGGAAATATGTC 914
QY 1069 AAATCCCAATTAACCTGAATCAATGATATATCATCTCAGGGGCTATATCCACAGAGCT 1128
DB 915 AACCTTCAATTAATTAAGTAACTTAAGATATATCACTTAGGGGTTATCTTCAAGAGTT 974
QY 1129 TGGGAAGCTTACTGACTTGTGTTGATCTGAATGTGGCCAAATATGATCTGGAAGACTTAT 1188
DB 975 CGGAAAGCTTAACAGGGTTATTTGACTTAACCTTGAAACAAACACTTGAAGTCCAAT 1034
QY 1189 AACTGATCACTGAGCTCTTTCGCAAAATCTPAAACAGCTTAATGTTTCATGGAACAAATT 1248
DB 1035 CCTGATTAACATPAGCTCATGTGTGATCTCAATAGCTTCAATGCTTAATGGCAACAGATT 1094
QY 1249 TGTGGCACTATPACCCGAGCAATTTCAAAAGCTAAGAAAGTATGACTTAATCTGTG 1308
DB 1095 AAATGGAGCCATTCCTCTTCAATGATTAACCTTGAGAGATGACTTATTTGAATTTGTC 1154
QY 1309 CAGCAACATATCAAAAGTCAATCCCGTGTGACTATCTGATTCGTAACCTTAAGATAC 1368
DB 1155 ATCAAAATTTTCAAGGTGTTTATCTTATGAGCATATGAGAAATPACAAATTTTGGACAC 1214
QY 1369 ATTGATCTTTTCCACACAAAGATAAATGAATCATTTCTTCCCTTGTGTGATTTGCA 1428
DB 1215 CTTT----- 1218
QY 1429 GCATCTTTCAGATGATGATGATGATGATATATPACTGATGATGATGATGATGATGATGAT 1488
DB 1219 -----AAGCTTGGCAACAAATGTTCTAGTAGATTTATTTCTTGGCAAAAT 1262
QY 1489 TGGAAATCTAAGAGCATATGAAATAGATCTTTTCAAAATATGATATCTTGGCCCAAT 1548
DB 1263 TGGCAACTTGAAGAGATATGAGAGATGATATGATGATGATGATGATGATGATGATGATGAT 1322
QY 1549 TCCAGAAAGCTTAACCAATPACAGAACTPAAATTTTGTGAGATGAGAAATATATACCT 1608
DB 1323 TCTCAAGAACTCGAATCTGCAAAATCTGATGTTGTTAAATCTTCMAAAACAAACAT 1382
QY 1609 GACTGTAAATGTTGTTTCAATTTAGCCAACTGTCTCAGTCTCAGTATGATGATGATGATGAT 1668

Db 1383 AACGGGGAGTGTCTTCTCAGCATGATGACTGCTCAGCCTCAATCTTAATGATATCTTA 1442
 Qy 1669 TAACAACCTGTGAGTGTATATCCCTAAGAACATATCTTCTCAAGATTTTCCACAGCAG 1728
 Db 1443 TAAATAATTTGGCTGGTGTGTGTAACCTACTGTATACACATCTTCTCAGGTTTTGCGTCAG 1502
 Qy 1729 CTTCATTTGGCAATCTGGTCTTTTCCGGTAGTGGCTTAACTCACCGTGTCAATGATTTCTCG 1788
 Db 1503 CTTTGGGTAATCCAGGACTTTGTGTGATATGAGCTTGGTTCTTCTGCGCTTATCTGG 1562
 Qy 1789 TCGAATCTGACGAGTGTCAATCTCTAGACAGCTATTCTTGAATATGCTATTGGGGACT 1848
 Db 1563 CCATCAACAGAAAACCACTAATCTCAAGGCTGCAATCTTGGAAATTCGCGGTGGGCT 1622
 Qy 1849 TGTGATCTCTTCTAATGCTCTTAATAGACGCTTGGCCGACCGGATATATCTCTCTTTCT 1908
 Db 1623 TGTATCTCTCTGTGATCTTATAGAGGCTGTGAGGCTCTATAGTCCACTGTTCAT 1682
 Qy 1909 TGAATGATCACTTGACAAACAGTAATCTTATTCGACACCGAAGCTCGTCAATCTTCAAT 1968
 Db 1683 AGATGTCTCTGTAGCAAAACAGTACGATGTTCCCCCAAGCTGGTTATCTTCAAT 1742
 Qy 1969 GAAATGGAACCTCCAGCTTTTACGAGATATCATGAGATGACAGAAATCTTAAGTGAA 2028
 Db 1743 GAACCTTCCCTTCTGTATACGAGATATATAGCATGACTGAAAACTGATGAGAA 1802
 Qy 2029 GTATATATTTGGGACGAGGACATCAACATCTGTATACAAATGTCTTTGAAAGATTGTA 2088
 Db 1803 GTATATATTTGGGATCGAGACATCCACACGGTTTATTAATGTCTTGAAGAACCCCAA 1862
 Qy 2089 ACCGTTGCGATTTAAGGGCTTTTACTCTCAACCCACAGTCAATGAAACAGTTTGAAC 2148
 Db 1863 ACCAGTGGCAGTAAAAAGCTATATGCCCATATCCACAGGCTTCAAGAAATTTGAAC 1922
 Qy 2149 AGAATCTGAGATGCTAAGTATGATCAACACAGAAATCTTGTGAGCTTACAGCTTATTC 2208
 Db 1923 TGAGCTTGAGATGTTGTGATGATCAAAACCGGAATCTAGTCACTTCAAGATATTC 1982
 Qy 2209 CCTCTCTCACTGGGAGTCTTCTGTCTATGATATTTGGAAAAATGTTAGCCCTGAGGA 2268
 Db 1983 CCTATCTCTGTGGAAATCTTCTTCTTACGATTAATGAAAAATGAAAGCCCTTGGGA 2042
 Qy 2269 TCTTCTTCAT---GGCCCTACGAGAAAAAGACTTTGATTTGGGACACAGGCTTAAAT 2325
 Db 2043 TGTTTTGCATGAAAGTCCAACTAAGAAAGAAACCTTGATTTGGGAAATCTGCTACGAAT 2102
 Qy 2326 AGCATATGTCAGACACAGGTTAGCTTATCTACACCATGATCTGTAAGTCCAGGATCAT 2385
 Db 2103 TGCCTGTAGGTGGCCGACCAAGGCTTGTCTTATCTTATCATATGATGATGACCACGATAT 2162
 Qy 2386 TCAAGAGAGTGAAGTGTCCAACTTCTTGTGACAAAGCTTAAAGGCTGTTGAC 2445
 Db 2163 ACACAGGAGTGAATCAAAAAATATATCTTGTATTAAGATTAAGAGGACATCTTAC 2222
 Qy 2446 AGATTTTGAATAGCGAAAAAGCTTGTGTGTCAAACTCAATCTTCAATCTTACGTGAT 2505
 Db 2223 AGACTTTGGCATTTGCTAAGAGTTGTGTGTTCAAAAACTCACAGTCCACTATGTCAT 2282
 Qy 2506 GGGCAGATAGTTTACATGACCCCGAGTATGCTGCACTTTCACGCGCTCACTGAAATC 2565
 Db 2283 GGGAACTATTGGCTATTCGATCTGTAGTATGCTGCACTCCCGTCTCAATGAAAAATC 2342
 Qy 2566 CGATGTCTAAGTATAGGAATAGTCTTGTGATTTGTAAACCGGAGGAAAGCCGTGA 2625
 Db 2343 TGTATGTCTAAGCATGTGCAATGTGTGCTTGAAGCTGTGACCGGAAAAAGCCAGTGA 2402
 Qy 2626 TGAAGATTCATCTCCACCATCTGATATGTAAGAGCGGGGAAACATGAGTATGATGA 2685
 Db 2403 CAAGGATGCAATCTCATCTGATCTTGTCAAAGCGGCTAAATGTGTGATGAGA 2462
 Qy 2686 AATGCGATTCACACATCACTGACGTGTAAAGATCTCGTGTGTGAAGAAATTTT 2745

Db 2463 GACAGTCCAGCCGAGACATTGACAGACATTGCAAGATCTTGTGAGTCAAGAGTGT 2522
 Qy 2746 CCAACTGGGCACTCTTATGACCAAAAAAGACGCGGAATGATCGACCCCAATGACAGGT 2805
 Db 2523 CAGCTGGCGCTCTTCTTGGACCAAGAGACACCATGGAATCGGCGCAATGACAGGT 2582
 Qy 2806 GACTCGTGTCTCGGCAAGTTTATGTATGGAACAACCACTGTGCTC-----GAC 2856
 Db 2583 TGTGCGGCTCTCGAGACTGCTAGTTGCTGCCGACCCGCAAGATCCGACAGCAGCT 2642
 Qy 2857 TGACAGTCAAGCAGCTGCTGCTGTGCTGTCTACGTGATGATGATGCAATCTCAAGAC 2916
 Db 2643 GGGCATGCCCCAGCGGCTGCTGTCCGACCTACATCAAGAGATGTGAGTTAAGG 2702
 Qy 2917 TCTCATTTGTGCAATGTCTC---TTCCATGAGTGTCTGATGCTCAATCTGTTCTCG 2973
 Db 2703 CACCAAGGCTCTCTCTGCGCCCACTGTGTGTACTTCCGATGTGAGCTGTTTCTCA 2762
 Qy 2974 GTTTGACAAATTAATTTCTCAGAAACAGTGAAG 3007
 Db 2763 GTTTGGGAGTCAATTTCTCAGAAACAGAGTAG 2796

RESULT 13
 ADI32615
 ID ADI32615 standard; DNA; 3000 BP.
 XX
 AC ADI32615;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Rice transpiration efficiency-related ERECTA DNA.
 XX
 KW plant; transpiration efficiency; ERECTA; breeding; genetic engineering;
 KW rice; ds; gene; chromosome 6.
 XX
 OS Oryza sativa.
 XX
 FH Key Location/Qualifiers
 FT 1..3000
 FT /product= "Rice transpiration efficiency-related ERECTA
 FT protein"
 XX
 PN WO2004005555-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 02-JUL-2003; 2003WO-AU000854.
 XX
 PR 02-JUL-2002; 2002AU-00003339.
 XX
 PA (AUSU) UNIV AUSTRALIAN NAT.
 XX
 PI Maele J, Farquhar GD, Gilmore SR;
 XX
 DR WPI: 2004-091390/09.
 DR P-PSDB: ADI32616.
 XX
 PS Claim 3; SEQ ID NO 3; 209pp; English.
 XX
 CC The invention relates to a novel method for selecting a plant having
 CC enhanced transpiration efficiency comprising detecting a genetic marker
 CC for transpiration efficiency, where the marker comprises a nucleotide
 CC sequence linked genetically to an ERECTA locus in the genome of the plant
 CC and selecting a plant that comprises or expresses the genetic marker. The
 CC method of the invention may be useful for selecting a plant having
 CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic

CC variant or protein-encoding region may be useful in the preparation of a
CC genetic construct for modulating the transcription efficiency of a plant.
CC Furthermore, the ERBCTA genes may be useful for producing plants having
CC enhanced transcription efficiency by both traditional plant breeding and
CC genetic engineering approaches. The current sequence is that of the rice
CC ERBCTA DNA of the invention which is located on chromosome 6.

XX Sequence 3000 BP; 796 A; 749 C; 724 G; 731 T; 0 U; 0 Other;

Query Match 32.6%; Score 1035.2; DB 12; Length 3000;
Best Local Similarity 63.8%; Pred. No. 9.5e-293;
Matches 1687; Conservative 0; Mismatches 888; Indels 69; Gaps 5;

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QY 234 CGGATTTGTTGTTGAGAGGTGTTGTTGAAAATGTCACCTTCATTTGTTGTC 293
DB 179 CCGACCACTGCGGTGGCGGGCTCACCTGCGCAACGCTCTTGGCCCTCCGCC 238
QY 294 TTAATTTGTCAGATTGTAATCTTGATGAGAAATCTGACCTGCTATTGAGATCTCA 353
DB 239 TGAATCTTCAAACTTAACCTAGAGGTGATCTGCGCGGCATCGAGAGCTCAAGA 298
QY 354 GTCTCTTGTCAATGTATCTGCGAGTATGCTTGTCTGCACAATCCCTGATGATTG 413
DB 299 ATCTACAGTTCGTTGATCTCAAGGGGAAACAAGCTCAGCTGCAAAATCCAGATGAGATTG 358
QY 414 GTGACGTCTCTCTTGCAAAACCTTAGACTTATCTTCAATGAATTAAGTGTGACATAC 473
DB 359 GGGACCTGCATCTCTTAAATATTGATGATTTGTGGCAACTGCTTATGAGAACATCC 418
QY 474 CGTTTTCGATTTCGAAAGTTGAAGCACTTGAGAGCTGATTTGGAAGATTAACCAATTGA 533
DB 419 CCTTCCTCATCTCAAGCTCAAGAGCTTAGAGAGCTGATTTGGAAGAACACAGCTCA 478
QY 534 TAGAGCCGATCCCTTCAACCTTTACAGATTCCTCAAACTGAAATTTGGAATTGGAC 593
DB 479 CGGAGCCCACTCCCTTCCACATTTGCCAAATTCMAATTCMAAGACATTTGACCTGGCAC 538
QY 594 AGAATAAAGTCAAGTGTGATGATACCAAGACTTATTTATCTGGAATGAAGTTCTTCAGATAC 653
DB 539 AGAACCAAGCTTACAGGCGATATCCCAAGGCTCATATATGGAATGAAGTTCTTCATATCC 598
QY 654 TTGGGTTGCGAGGAAACAACTTAGTCGTAACAATTTCTCCAGATTGTTGTTCAACTGACTG 713
DB 599 TAGGTTTGAAGGGGTAATCTGACTGCTGAGAACTTTGTCACTGACATGTGCAACTGACTG 658
QY 714 GTCTTTGTTATTTTGAAGTAAACAACGTTTGAAGTGTGATATACCTGAGACATAG 773
DB 659 GCGTGTGTATCTTTGATGTAAAGGGGAAACAATCTCAAGGGACCATTCAGAGAGCATAG 718
QY 774 GAAATTGCACTGCTCCCAAGTTTGGACCTTGTCTTCAATCAAGCTTAACTGGTGAAGTCC 833
DB 719 GGAATCTGCACAGCTTGAATTTCTGACATTTCTGTATTAACAAATCTCTGGGAAATAC 778
QY 834 CTTTTCACATCGGCTTCTGCAAGTTGCAACATTTATCATTTGCAAGGCAATCACTCTG 893
DB 779 CTTAACAACTAGGCTTCTTCAAGTAGCACAAGTGTACTTCAAGGAAATAGACTGACTG 838
QY 894 GGAAGATTCCATCATGATTTGTCTCATGCAAGCCCTTGCAGTCTTAGATCTAATGAGCA 953
DB 839 GGAATAATTCAGATGTGATTTGGCTGTATGCAAGCTCTGTCTTCAAGACTGAGTAGA 898
QY 954 ACTTGTGAGTGAATCATTTCCCTCCGATTTCTCGGAAATCTTACTTTTCAACCGAATAATGT 1013
DB 899 ACAGCTGTGAGGGCCCATTTCTTATATCTGAGCAATCTATCTATCTGGAATAATCTAT 958
QY 1014 ATTTCGACAGTAAACAAGTGAAGTGTTCATTTCCACTGAGCTTGGAAACATGTCAAAAC 1073
DB 959 ATTATCATGGGAACAACCTACTGAGTCAATACCGCGGAGCTTTGGGAATATAGTAAC 1018
QY 1074 TCCATTACTGGAACCTCATGATATCATTTCAAGGCTCATATACCAACAGAGCTTGGGA 1133
DB 1019 TTAGTACCTCAACAAGTAATGATGAATTTGGTGGCACAATTTCCAGAGAGCTTGGCA 1078
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QY 1134 AGCTTACTGCTTGTGATCTGATGATGCGCAACAATGATCTGAGAGACTATACCTG 1193
DB 1079 AACTTGAAGAGCTTTTGAACCTAATTTTCCAAACAACATCTTCAAGGCTCTATTCTG 1138
QY 1194 ATCATCTAGCTCTTGCACAAACTTAAACAGCTTAAATGTTCAATGGGAACAAGTTTAGT 1253
DB 1139 CAAACATCACTTCTTGACATGCTCTTAAACAATTCATATGTTTATGGCAATATAGCTAATG 1198
QY 1254 GCACATATCCCGAGACTTTTCAAAAGCTAGAAAGTATGATCTTATCTTATCTGCCACA 1313
DB 1199 GTTCTATCTCTGTGTGTTTCCAAAGTTGAGAGTCTGATCTTGAACCTTATCTTCA 1258
QY 1314 ACAATATCAAGGCGCAATCCCGTGTAGCTATCTGATCCGTAATCTTATGATATCAATTTG 1373
DB 1259 ACAATTTCAAGGCAATATCTTCTGAGCTTGTGATCATATCACTTGTGACATATGG 1318
QY 1374 ATCTTTTCAACCAACAAGATTAATGAAATCTTCTTCTTCTGATTTGAGAGATC 1433
DB 1319 ATCTTCTCTCAATGAAATCTGAGACAGATTCCTGCTACATTTGGTATCTAGAGACCC 1378
QY 1434 TTCTCAAGATGAATCTGAGTGAATCATATTAATCTGTGTATTTCCAGGCGACTTTGGA 1493
DB 1379 TTCTTGAACCTGAATTTGAGTGAAGAACCATCTGTATGGCCAGTCTCTGAGATTTGGA 1438
QY 1494 ATCTGAAGACATCATGGAATGATCTTCAATATATGATCTCTGCGCCCAATTCGAG 1553
DB 1439 ACTTGAAGAGCTGCAAGTATGATATGTTCACAAACAACCTTATCTGAGTGTGCGCG 1498
QY 1554 AAGAGCTTAAACAATTAACAACATTAATTTGCTGAGACTGGAATAATTAACCTGACTG 1613
DB 1499 AGGAACCTGGAACAACCTTCAAAACCTTGATAGCTGATTTCTTAACAACAATTTGGTTG 1558
QY 1614 GTATATGTTTGTATTAAGCAACTGTCTCACTCA-----CTGATTTGAAT 1660
DB 1559 GGGAGATCTCCCTGTCAATTTGGCCCACTGCTTCACTTAATTAACCTTGCAGATTTCA 1618
QY 1661 GTATCTCATPACAAACCTCGAGTGAATCCCTTAAGAACAAATTAATCTTCAAGATTTTCA 1720
DB 1619 TTGTCTATPACAAATTTATTTGAGACATGTCCTGATGCAAGAACATTTCTGAAATTTCCA 1678
QY 1721 CCAGA-----CAGCTTCA 1733
DB 1679 ATGGAAGACATCTTCAATTTCTGATTGCAACCAAGTACATTAATCAATAATGACAGCTTC 1738
QY 1734 TTGGCAATCTCTGCTTTTGGCGTATGTTGGCTAACTCACCGTGTCAATGATTTCTGCGAA 1793
DB 1739 TTGGTATCTCATTAATGATGATTTTACTGCGCAAGATTCAGAGTGTGACACTCTCATGGA- 1797
QY 1794 CTGTAGAGGTGAATCTCTAGAGCAGCTATTCTTGAATATGCTATTGGGGGACTGTGA 1853
DB 1798 --CAAGAGTTAATATTTCAAAGACAGCAATGCTTGCATTAATCTTAAGCTTTATCATAT 1855
QY 1854 TCCCTTCAATGCTTAAATAGCAGTGTGCGGACCGCATATCTCTCTCTTTCTTGATG 1913
DB 1856 TGGCTGCGGTGTGCTGTGTTGGCTATATTAATAACAATCAACACAGCAGCTTGTCAAG 1915
QY 1914 GATCACTTAACAACAAGTAATCTTATGCAACCGAAGCTCTGATCTTCAATGAACA 1973
DB 1916 GATCCGATTAAGCCAGTGAAGGAC-----CTCAAGAGCTAGTGTCTTCCAGATGAGCA 1969
QY 1974 TGGCACTCAACGTTTACGAGGATATCATGAGAAATGACAGAAATCTTAATGGAATATAT 2033
DB 1970 TGGCTATCAATCTTACGAGGACATATAGGCTGACAGAAATTTGACGAGAAATATCA 2029
QY 2034 TCATTTGGGACCGAGGATCAAGACTGTATACAAATGTTTGTGAAGATTTGTAACCGG 2093
DB 2030 TCATTTGGCTATGCGGCTCAAGACGTGTACAAATGATTAATCTCAAGAGCGGCAAGGCCA 2089
QY 2094 TTGCGATTAAGGCGCTTACTCTTCAACAACCAAGTCAATGAAACAGTTTGAACGAAAC 2153
DB 2090 TTGCTGTCAAGGCGCTTTTACAGTCAATATTAACCATATGCTCCGAGAGTTTGAACGAAAC 2149
QY 2154 TCGAGATGTAAATGATCATCAAGACAGAAATCTTGTGAGCGCTAACAAGTTATTCCTCT 2213
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Db 2150 TAGAGCAATTGGAGATACGGCAGAGATCTGTTAGCTTCATGGCTTCGCTAT 2209
QY 2214 CTACTTGGGAGCTTCTGTTCTATATCTATTTGGAAAAATGGAGCTTCGGATTTTC 2273
Db 2210 CTCACATGGAAACTTGCTCTTCTATATTAACATGAAAAATGGTTCTTGTGGATCTTC 2269
QY 2274 TTGATGGCCCTACGAGAAAAAGACTCTTGATTTGGGACACAGCGCTTAAGATGATATG 2333
Db 2270 TCCACGGTCCATCAAGAAAAAGTAGAGTCAACTGGGACACAAAGACTAGATCGGGTCG 2329
QY 2334 GTSCAGACAGAGTTTATGCTTATCTACACCATGACTGTAGTCCAAAGATCATTCACAGAG 2393
Db 2330 GAGCTGCAAGAGGCTGGCTATCTCCACCATGACTGCCAACCTCGCATATATCACAGAG 2389
QY 2394 ACGTGAAGTGTCCACATTTCTTTGACAAAGACTTAGAGGCTGTTTACAGATTTTG 2453
Db 2390 ATGTCAAGTCTCCACATCTGCTCGACGAGAACTTCGAAGCGCACCTTCAGATTTG 2449
QY 2454 GAATAGGAGAAAGCTTGTGTGTCAAAAGTCACATACCTTCAACTAGATGGGACAGA 2513
Db 2450 GCATTAGCAAAATGTCTCCCTCTGCAAGTCCATGCTCTCACTTATGTCTAGAAACA 2509
QY 2514 TAGGTTACATAGACCCGAGATAGCTGCACTTCACGGCTCCTAGAGAAATCCGATGCT 2573
Db 2510 TCGGCTCATTTGATCCGAGATATGCGAGACTTCGAGGCTCAATGAGAAATCTGATGTG 2569
QY 2574 ACAGTTATGGAATGCTCTTCTTGAAGTTTAAACCCGAGAAAGCCGTGATGACGAAT 2633
Db 2570 ACAGCTTCGGCATCTGCTCTTCTGAAATTTGTCACAGGAAAGGCGGTGACAAACGAAT 2629
QY 2634 CCATCTCCACCATCTGATATATGTCAAAGACGGGGAACAATGAATGATGAAATGGCAG 2693
Db 2630 CGAAGTTGCAATTAATTAATCTCTCCAAAGTGATGACAAACAGTATGAGGCAATGG 2689
QY 2694 ATCCAGACATCAGATCGACGCTGTAAGATCTCGGTGTGTGAAGAAATTTTCAACTGG 2753
Db 2690 ACTCGAGGTGTGAGTACGCGACGAGACATGGAGACTGTGACGAGAGCCCTTCAGCTCG 2749
QY 2754 CACTCTTATGACCAAAAGACAGCCGAATGATGACCCCAACATCAGTACAGTCTGTG 2813
Db 2750 CCCTTCTGTGCACCAAGAGCACCTTTCAGACCGGCCGACCATGACAGAGTTGCAAGGG 2809
QY 2814 TTCT 2817
Db 2810 TGCT 2813
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RESULT 14
AD59740
ID AD59740 standard; cDNA; 2533 BP.

AC ADX59740;
DT 21-APR-2005 (first entry)
XX plant full length insert polynucleotide seqid 30583.
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.

Unidentified.

US2004034888-A1.

19-FEB-2004.

XX

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PF 28-APR-2003; 2003US-00425114.  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAO/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
DR  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
PS Claim 1; SEQ ID NO 30583; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carboxylate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 2533 BP; 656 A; 630 C; 589 G; 658 T; 0 U; 0 Other;  
XX  
Query Match 32.0%; Score 1015.4; DB 13; Length 2533;  
Best Local Similarity 68.7%; Pred. No. 5,7e-287;  
Matches 1413; Conservative 0; Mismatches 641; Indels 3; Gaps 1;  
QY 794 GTTTGGACTGTCTCAATCAATCAGTAACTGTGAGATCCCTTTGACATGGCTTCCTG 853  
Db 48 GTAGGATTTGTCTTACACCGCTTTATGAGACCAATCCCATTTCAACATTTGGTTCTTA 107  
QY 854 CAAGTTGCAACATTTATATTTGCAAGGCAATCACTCTTGGGAAAGTTTCATGAGTAT 913  
Db 108 CAAGTGTCACTACTATCTCTTGGCAAGGAAACAGTTCACTGGCCCAATCTTTAGTAT 167  
QY 914 GGTCATGCAAGCCCTTGGAGTCTTAGATCTAAGTGGCACTGTGTTAGTGTGATATT 973  
Db 168 GGCTTATGAGAGCTCTCGCTGTCTAGATCTAGTATCAACCAATTAATGTGTCATATA 227  
QY 974 CTTCGATTTGCGAAATCTTACTTTCACCGAGAAATGTATTTGACAGCTAACAGCTG 1033  
Db 228 CCATCTTATTAAGCAACTGACATACAGAAAGCTGTACATGCAAGCAACAGGTTA 287  
QY 1034 ACTGTTCAATTTCACTGAGCTTGGAAATATGTCAAATCCATTAACCTGGAAGTCAAT 1093  
Db 288 ACTGATGATACACACGAGCTAGGAAATATGTCAACACTTCACTTACGAACTGAAT 347  
QY 1094 GATATCATCTCAAGGCTCATATATACACAGAGCTTGGGAAAGTCTGACTTTGAT 1153  
Db 348 GATATCACTTATGAGGTCAATTTCCACGAGCTTGGAAAGGCTTACAGAGCTTTTGAC 407  
QY 1154 CTGAATGTGGCAACAAATGATCTGGAAGGACCTTATACCTGATCATCTGAGCTTTGACA 1213
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Db      408 CTGAACCTTGGAAATACCACTTGAAGACCAATTCCTGCAACCTTAAGTTCATGTCGTG 467
Qy      1214 AATCTAAACAGCTTAAATGTTTCATGGGAACAAGTTTAGTGCCACTATACCCCGAGCATTT 1273
Db      468 AATCTCAATAGCTTCAATGCTTATGSCAACAAAGTTAAATGGAAACCATTCCTCGTTCGCTG 527
Qy      1274 CAAAAGTAAAGATAGACTTACTTAACTGATCCAGCAACAATATCAAAAGGTCATC 1333
Db      528 CGGAACCTTGAAGCATGACCTATTTAAATCTTTCATCAAAATTTTCATPAAGTGCGCTTAAT 587
Qy      1334 CCGGTGAGCTATCTCGTATCGGTAGTACTAGATACATTTGATCTTTCACAAACAAGATA 1393
Db      588 CTAATTAGCTATCAAGAGATCAACAATTTGGACACGTTTGACCTTATCTCTGAATGATG 647
Qy      1394 AATGGAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1453
Db      648 ACGGATCAATTTCCATCATCATCTGCGAACCTAGAGCATCTATTGAGGCTTAACTTGAGC 707
Qy      1454 AGAATCATATTAATCTGCTGATGTTCCAGGCGACCTTGGAAATCTAAGAAGCATCATGGA 1513
Db      708 AAGAATGATCTAGTTGATTCATCTCCGCGAGTTGTAATTTGAGAAGTGCATGAG 767
Qy      1514 ATAGATCTTTCAAATATATGATATCTGCGCCAAATCCAGAGAGCTTAAACAATTACAG 1573
Db      768 ATTGATTTATCTATATATCATCTTGCTGCTGATTCCTCAAGAACTTGGAAATGCTGCA 827
Qy      1574 AACATAATTTTCTGAGACTGGAAAATATPACTGACTGTAATGTTGTTGTTCAATGACC 1633
Db      828 AACCTGATGTTGCTAAACCTGSAACACAAATATTAATGCGATGCTCTCTCTGATG 887
Qy      1634 AACTGTCATGCTCACTGATTTGAATGATATCTCATAAACAACCTCGTAAGTGAATCCCT 1693
Db      888 AACTGCTTCAAGCTCAAAATCTTAAATGTCATATACATTAATTTGGCTGCTGCTCTCT 947
Qy      1694 AAGAACAATATCTTCTCAAGATTTTTCACAGACAGCTTCAATGGCAATCCCTGCTTTCG 1753
Db      948 ACTGACAAACAATCTCAACAGCTTTTTCACATGACAGCTTTTAGTATCTCTGACCTCTG 1007
Qy      1754 GGTAGTGGCTTAAACCTGACGCTGATGATCTCTGTCGAACCTGTAAGAGTGCATCTCT 1813
Db      1008 GGATATTTGCTGCTGCTTCTCATGTCGTTCACATGCGCACGAGCAAAACCGCCAACTCA 1067
Qy      1814 AGAGAGCTATTTCTGGAATAGCTATGAGGAGACTTGTGATCTTCTCATAGGCTTTAATA 1873
Db      1068 AAGGCTGCCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
Qy      1874 GCAGCTTCCGACCGCATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1933
Db      1128 GCTGTATGACGGCCACACCATCCACCTCTTTTAAAGATGCCATGTAAGCAGCCAGTGTG 1187
Qy      1934 ACTTAATTCGACACCGAAGCTGCTGATCTTTCATATGAACTAGGACATCCACGTTTACGAG 1993
Db      1188 AGCAATGCTCACCCAAAGCTGCTGATCTTTCATATGAACATGGCTTTCATGCTTTGAT 1247
Qy      1994 GATATCATGAGATGACAGAGATCTTAAGTGAAGAGATATCAATTTGGGACCGAGCATCA 2053
Db      1248 GATATTAATGAGATGAGTGAAGACTTGAAGTGAAGAAATCAATGATGATCGGGGACATCA 1307
Qy      2054 AGCACTGTATACAAATGCTTTTGAAGAAATGTAAACCGGTTGCGATTAAGCGGCTTAC 2113
Db      1308 AGTACAGTTTATTAATGCTTCTTAAGAAATTTGCAAACTGAGCAATTAAGAAAGCTGTAT 1367
Qy      2114 TCTGACAAACCCACAGTCATGAAGAACTGTGAACAGAACTCGAATGCTAAGTGCATC 2173
Db      1368 GCCCACTACCTCTCAGAGCTTAAAGAAATTTGAACCTGAGCTCGAGCTGTTGATGATC 1427
Qy      2174 AAGCAAGAAATCTGAGAGCTTAAAGCTTATTCCTCTCACTGGGAGTCTTCTG 2233
Db      1428 AAGCAACCGGAATCTAGACGCTTCAAGGGTACTCGTTCACCTGTTGGAACTCTCTC 1487
Qy      2234 TTCTATGACTATTTGGAAAAATGAGCTCTGGAGTCTTCTGAT--GGCCCTACGAG 2290
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Db      1488 TTTTATGATTTATGAGAGTGGACGCTTATGGGATTTTATACATGAAGCTCATCCAG 1547
Qy      2291 AAAAAGCTTTGATTTGGACACACGGCTTAAAGATAGCATATGCTGACACAAAGTTTA 2350
Db      1548 AAGAACAACCTTGTACGTGGTACCTCGCTACGATCTCTTGTGTGACGCTCAAGGCTC 1607
Qy      2351 GCTTATGACACATGACCTGATGCTCCAGAGATCAATTCACAGACGGAAGTGTCTCAAC 2410
Db      1608 GCTTACCTTCAACATGACCTGACGCGCAAGATTAATTAATTAACCGGAGCTTAAGAAAT 1667
Qy      2411 ATTCTCTTGGACAAAGACTTAGAGGCTGTTTGAACAGATTTTGAATAGCAAAAGCTTG 2470
Db      1668 ATATCTCTGACAAAGATTAATGAGGCCATCTTAAGACTCTTGGCATCGCTAAGAGCTTA 1727
Qy      2471 TGTGTGTAAGTCACTACTTCACTTAACTGATGAGGACAGATAGTTACATAGACCC 2530
Db      1728 TGTGTCTGAAAGACTCACAGTCAACCTTACGTATGGGCACTATTGGTTACATTTGATCCC 1787
Qy      2531 GAGTATGCTGCACTTACAGGCTCAGTGAAGATCCGATGCTTACAGTTATGGAATGTC 2590
Db      1788 GAGTACGCGCGACCTCCGCTTACAGAGAGTGTGATCTTACAGCTACGGGATGTT 1847
Qy      2591 CTTCCTGAGTTGTTAAACCGAAGGAAAGCCGTTGATGACGAATCCAATCTCAACATCTG 2650
Db      1848 CTGCTGAGCTGCTGACCGGCAAGAGCCAGTGAACAAGAGCATCTTCAATCACTTG 1907
Qy      2651 ATATATGTAAGACGGGGAACAATGAATGATGAAATGGCAATCCAGATCAATCATCG 2710
Db      1908 ATCTTATCGAAGACGGGAGCAACGAGTATGAGACGCTGACCCCGACGTTGGGAGAC 1967
Qy      2711 ACGGTAAAGATCTCGGTGTGTAAGAAAGTTTCCAACTGACATCCATAGCACAAA 2770
Db      1968 AACTGCAAGACCTGCGCGAGGTGAAGAACTGTTCAGCTGAGCGCTCTCTGACCAAG 2027
Qy      2771 AGACAGCCGATGATGACCCACCAATGACACAGTGAATCTGCTGCGACAGTTTATG 2830
Db      2028 CGGCAAGCTTCCGAGACGGGCGAGATGACAGATGAGTGGCTGCTTGAATCTGCTG 2087
Qy      2831 CTATCGGAACACCAACC 2847
Db      2088 AACCCGAGCGCGCGCC 2104

RESULT 15
ADX27817
ID ADX27817 standard; cDNA; 1872 BP.
XX
AC ADX27817;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 10637.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; lignin production; plant growth regulator;
KW galactomanan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; se.
XX
OS Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
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PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
PS Claim 1; SEQ ID NO 10637; 15bp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.bseqdata.uspo.gov/sequence.html?docID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX
SQ Sequence 1872 BP; 556 A; 401 C; 374 G; 541 T; 0 U; 0 Other;
Query Match 31.4%; Score 995.8; DB 13; Length 1872;
Best Local Similarity 73.9%; Pred. No. 2.8e-281;
Matches 1283; Conservative 0; Mismatches 437; Indels 15; Gaps 1;
QY 1286 AGTATGACTTAACCTTAATCTGTCCGCAACAATATCAAAAGGTCACATCCCGTTGAGCTA 1345
DB 2 AGCATGACCTCTTGAATCTTCTTCCACACATCTTCAGGGCGCAATTCGAATGAAGT 61
QY 1346 TCTCGTATCGGTAACTTAGATACATTTGGATCTTTCACAACAAGATTAATGAATCAAT 1405
DB 62 TCGGGAATTGGCAATTGGATACATTTGATTTCAACAATTAATTAAGTTGGTTCATC 121
QY 1406 CTTTCTCCCTGGTGATTTGGAGACATCTTCTCAAGATGAACCTTGAGTAATCATATA 1465
DB 122 CTTTCTCCCTGGTGATTTGGAGACATCTTCTCAAGATGAACCTTGAGTAATCATATA 181
QY 1466 ACTGATGATGTTCCAGGCGAATTGGAATCTTAAGAGCATGAGAAATGATCTTCA 1525
DB 182 ACAGGATTTATTCAGAGAAATTTGGAATCTTAAGAGTGTTAAGAAATGATCTTCA 241
QY 1526 AATTAATGATATCTTGCGCCCAATTCAGAGAGCTTAAACAATTAAGAGCAATATTTTG 1565
DB 242 AATTAATCAACTCTGCTGCTGATCTGATGAACTTGAAGCTTCAAAAATGATATCC 301
QY 1586 CTGAGAGTGAATAATTAACCTGATGCTAATGTTGTTATAGCAATGCTGCTAGT 1645
DB 302 TTGAGACTTGAATAATTAACCTGATGCTAATGTTGTTATAGCAATGCTGCTAGT 361
QY 1646 CTCACGTATTTGATGATCTCATTAACAACCTGATGCTGATCTTCAAGAAACAATTAAC 1705
DB 362 CTCTCTACTTAATGCTGCTCATTAACAACCTGATGCTGATCTTCAAGAAACAATTAAC 421
QY 1706 TTCTCAAGATTTTCAACAGAGAGCTTCAATTTGGCAATCTGCTTTTGGCGTAGTTGGCTA 1765

DB 422 TTACACAGTTTCCCTCCGACAGTTTCATTTGAAACCCTGCTGTTGGTAAATGGCTG 481
QY 1766 AACTCACGGTGTATGATTTCTGTCGCAACTGTACGAGTGCATCTCTAGACAGCTATT 1825
DB 482 AATTTCGGTGTATGATTTCTGTCGCAACTGTACGAGTGCATCTCTAGACAGCTATT 541
QY 1826 CTTGGAATGATCTATTGGGGGACCTTGTGATCTTCTCAATGATCTTTAATAGACGCTTGGCA 1885
DB 542 CTTGGAATGATCTATTGGGGGACCTTGTGATCTTCTCAATGATCTTTAATAGACGCTTGGCA 601
QY 1886 CCGCATATCTCTCTCTCTTTTCTTGTATGATACCTTACAAACCAATTAATTTGACA 1945
DB 602 CCAATATGCTCTCTCTCTTTTCTTGTATGATACCTTACAAACCAATTAATTTGACA 661
QY 1946 CCGAAGCTGCTCATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2005
DB 662 CCAAGCTGATGATCTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 721
QY 2006 ATGACAGAGATCTTAAGTGAAGATATATGATGATGATGATGATGATGATGATGATGAT 2065
DB 722 ATGACAGAGATCTTAAGTGAAGATATATGATGATGATGATGATGATGATGATGATGAT 781
QY 2066 AATGCTGTTTGAAGATTTGTAACCGGTCGATTTAAGCGCTTTACTCTACACCA 2125
DB 782 AATGCTGTTTGAAGATTTGTAACCGGTCGATTTAAGCGCTTTACTCTACATCC 841
QY 2126 CAGTCAATGAAACAGTTTGAACAGAACTGAGATGATGATGATGATGATGATGATGATGAT 2185
DB 842 CAATGATTTAAGATTTGTAACCGGTCGATTTAAGCGCTTTACTCTACACCA 901
QY 2186 CTTGTGAGCTTCAAGCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2245
DB 902 CTGTGATGCTTCAAGCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 961
QY 2246 TTGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2305
DB 962 ATGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021
QY 2306 TGGACACACGCGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2365
DB 1022 TGGACACACGCGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1081
QY 2366 GACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2425
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DB 1262 TCAAGGCTCACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
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DB 1322 ACTGGAAGAAAGCGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1381
QY 2666 GGGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2725
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QY 2726 GGTGTGTGAAGAAAGTTTCAACTGCACTGCTATGACCAAAAGACAGCGGAATGAT 2785
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QY 2786 GAGAGCTTAAGAAAGTTTCAACTGCACTGCTATGACCAAAAGAGGACAGCTGAT 2835
DB 1502 AGGCGCAATGACGAAAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1561

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2006, 18:07:16 ; Search time 14319 Seconds
(without alignments)
12403.087 Million cell updates/sec

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Perfect score: 3176
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hlc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	915.4	28.8	2895	13	CL963372 OaIRCC009
2	638	20.1	639	7	AV827602 AV827602
3	621.2	19.6	626	1	AV523662 AV523662
4	604.4	19.0	974	9	CX675276 UCRCS08_6
5	548.6	17.3	948	10	DR929080
6	535	16.8	535	1	AV528628
7	532.2	16.8	535	1	AV529393 AV529393
8	530.8	16.7	1273	6	CX043849 CX043849
9	530.8	16.4	889	10	AY106598 Zea maye
10	519.8	16.4	889	10	DR938199 EST112973
11	519.6	16.4	841	9	DR069682
12	517.6	16.3	815	10	DV137758
13	506.2	15.9	511	1	AI992763
14	505.6	15.9	823	10	DV129724
15	501	15.8	501	1	AV529789
16	495.4	15.6	868	10	DT756599
17	486.2	15.3	859	10	DT730942
18	482.8	15.2	805	11	BZ508185
19	482.4	15.2	907	10	DT763952

20	473.4	14.9	857	11	BZ508175	BZ508175 BOOAN82TR
21	470.6	14.8	791	8	CO104679	CO104679 GR_EB003
22	452.8	14.3	705	8	CV705151	CV705151 UCRPT01_0
23	451.8	14.2	816	10	DT599409	DT599409 she01-1tm
24	448	14.1	990	10	DR929079	DR929079 EST112061
25	447.8	14.1	816	5	CF438419	CF438419 EST674764
26	441.8	13.9	870	10	DT728959	DT728959 EST116280
27	441.2	13.9	446	10	DR363249	DR363249 6626397 C
28	437.4	13.8	939	10	DT763951	DT763951 EST119780
29	433.2	13.6	710	3	BQ869038	BQ869038 QSD4H05_Y
30	427.4	13.5	429	7	AV798760	AV798760 AV798760
31	424	13.4	679	1	AI937984	AI937984 sc06607_Y
32	419.4	13.2	769	8	CV566963	CV566963 Mdlv40085
33	416	13.1	416	3	BP612895	BP612895 BP612895
34	415	13.1	720	2	BG125328	BG125328 EST470974
35	415	13.1	687	10	DT751244	DT751244 EST118509
36	410.4	12.9	799	10	DM130381	DM130381 CLSK7069_Y
37	410.4	12.9	881	8	CV292292	CV292292 aoF01-7ms
38	409.6	12.9	745	8	CV567734	CV567734 Mdlv40060
39	408.8	12.9	873	10	DR938198	DR938198 EST112973
40	408.6	12.9	751	8	CO531771	CO531771 3530_1_20
41	408.6	12.9	854	9	CX675277	CX675277 UCRCS08_6
42	408	12.8	641	8	CV003016	CV003016 pam01-21m
43	406.4	12.8	871	10	DR805250	DR805250 ZM_BFB003
44	404.8	12.7	740	8	CO092850	CO092850 GR_Ea14C
45	402.2	12.7	407	3	BP831239	BP831239 BP831239

ALIGNMENTS

RESULT 1
CL963372 2895 bp DNA linear GSS 21-SEP-2004
DEFINITION OaIRCC009320 Oryza sativa Expressed Library Oryza sativa (indica
CL963372
CL963372.1 GI:52381472
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
clade; Euharoidae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 2895)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.

ANALYSIS OF TRANSCRIPTIONAL REGULATION OF THE RICE GENOME AND
ITS COMPARISON TO ARABIDOPSIS
Unpublished (2004)
JOURNAL
COMMENT
Contact: Chen Chen
Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80486876
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
location/Qualifiers
1..2895
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/mol_type="genomic DNA"
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/clone_lib="Oryza sativa Expressed Library"
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FEATURES

source
ORIGIN
Query Match 28.8%; Score 915.4; DB 13; Length 2895;
Best Local Similarity 62.9%; Pred. No. 3.3e-247;
Matches 1529; Conservative 0; Mismatches 816; Indels 84; Gaps 4;

QY	392	GGA	CAAAATCCCTGATGAGATTGGATGCTGTTCTTCTTTGGCAAACTTAAGCTTAATCTTC	451
Db	349	GGT	AGATCTCGCGCGGCATCGAGAGCTCAAGATCTACAGTTCTGTGATTTGTCTGGC	408
QY	452	AAT	GAATTAAGTGGGATGACATACCGTTTTCGATTTCCAAAGTTGAAGCAACTGACAGCTG	511
Db	409	AAC	TCTGTATGGAGACATCCCTTCTTCATCTTCCAGCTCCAAAGCTTGAAGACTG	468
QY	512	ATT	CGAAGAAATTAACCAATGTATAGAGCCGATCCCTTCACACTTTCACAGATTTCAAA	571
Db	469	ATT	TGAAGAACACACAGCTACCGGGACCCATCCCTTCCATGTGTCCAAAATTCAAAT	528
QY	572	CTG	AAATTTCTGGACTTGGACATGGCACAGATAAATCTCACTGCTGTGATATCCAAAGCTATTAC	631
Db	529	CTC	AGACATTTGGACCTGTGGCACAGAACCAAGCTTACAGCGCATATCCAAAGGCTCATATAC	588
QY	632	TGG	ATGAATGAAGTCTTCACTATCTTGGGTGGAGAGAAACAATTAGTCGTATATTCCT	691
Db	589	TGG	ATGAATGAAGTCTGCAATTAATCTAGTTTGAAGGGTAACTCACTGACTGGAACTTTGTCA	648
QY	692	CCAG	ATTTGTGTCAACTGACTGCTGTCTTGGTATTTTGAAGTAAGAAACAACAGTTTACT	751
Db	649	CCT	GACATGTGCCAACTGACTGCGCTGTGTGATCTTTGATGTAAAGGGAAACAATCTCA	708
QY	752	GGT	ATATACCTGAGACGATAGAAATTGCACTGCTTCACAGTTTGGACTTGCTCTAC	811
Db	709	GGG	ACATTTCCAGAGAGCATAGGGAACTGCACAGCTTTGAGATTTGAGATTCATATTCGAT	768
QY	812	AAT	CAGCTAACTGTGTGATCCCTTTTACAATCGGCTCCGCAAGTTGCAACATTAATCA	871
Db	769	AAC	CAAAATCTCTGGAGAAATACCTTACAACTAAGGCTTTCTTCAAGTAGCCACTGTCA	828
QY	872	TTG	CAGGCAATCAACTCTCTGGAGAAATTCATCACTGATTTGTCTCATGCAAGCCCTT	931
Db	829	CTT	CAGAGAAATAGACTGACTGGGAAATTCACAGTGTGATTTGGCTGTGATGCAAGCTCTT	888
QY	932	GCA	GCTTATGATCTAATGTGGCACTTGTGATGTGATTAATTCCTCCGATTTCTGGAAAT	991
Db	889	GCT	GTTTCTA-----	897
QY	992	CTT	ACTTTCACCGAAATTTGATTTGACAGATTAACAGCTGACTGTTCAATTCACCT	1051
Db	898	-----	TTATTACATGGGAAACAATTTACTGTGAGTATACCGCG	936
QY	1052	GAG	CTTGGAAACATGTCAAAATCCCATTAATCCGGAACCTAATGATATCATCTCACGGT	1111
Db	937	GAG	CTTGGGAACATGATTAATCTTACCTAATCTAACAATGAAATGATATGATTTGGTGGC	996
QY	1112	CAT	ATACACACAGACTTGGGAGCTTAATCTGCTTTGATCTGAATGTGGCCAAAT	1171
Db	997	ACA	ATTTCCAGACGAGCTTGGCAAACTTAAGAGCTTTTGAATTAATCTTGGCCAAAC	1056
QY	1172	GAT	CTGGAAGACCTAATCTGATATCTGAGCTTCTTGCACAAATCTTAACAGCTTAAT	1231
Db	1057	AAT	CTTCAAGGCTCAATCTCTGCAAAACATGCTTTTGCATGCTCTTAACAAATTCAT	1116
QY	1232	GTT	CATGGGAACAATTTAGTGGCACTATACCCGAGCATTTCAAAAGCTAGAAAGTATG	1291
Db	1117	GTT	ATGCAATTAAGCTTAATGTTCTATCTCTGTGTTTCCAGAAATGGAGAGCTG	1176
QY	1292	ACT	TACCTTAATCTGTCCAGCAACAATATCAAAGTCAATCCGGTGTAGCTATCTCGT	1351
Db	1177	ACT	TACTTGAACCTTAATCTTCAAAACAATTTCAAAGCAATATTTCTTCTGACCTTGTGAC	1236
QY	1352	ATC	GGAATTAATGATATCATTTGATCTTTTCCAAACAAGATTAATGGAATCATTCCTCT	1411
Db	1237	ATC	ATCAATCAACTGGACACATTTGATCTTTCTCAATGAATTCCTGTGACAGTTCTCGCT	1296
QY	1412	TCC	CTTGGATTTGGAGCATCTTCTCAAGATGAACCTTGAAGAAATCATATAACTGCT	1471
Db	1297	ACC	ATTTGGATCTGAGACACTTCTTGAATCGAATTTGAATGAAGAACATCTTGTATGGG	1356
QY	1472	GTA	GTTCCAGCGCACTTGGAAATCTAAGAGCATATGAATATGATCTTTCAATAT	1531

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OY	1532	GATATCTCTGGCCCAATTCGAGAAAGCTTAAACAAATTACAGAACATAATTTTGCTGAGA	1591
Db	1417	AACCTATCTGTAGTCTGCCCGGAGAACTTGGACAACTTCAAAACTTGATAGCTCGATTT	1476
OY	1592	CTGGAAAAATAAAGCTGACGTGTATGCT--TGCTCAATTAGCCCACTGCTCAAGTCTC	1648
Db	1477	CTTAAACAACAATTTGGTTGGGGAGATCCCTGCTCAATGGCCCACTGCTTCAGCTTA	1536
OY	1649	ACTGATTTGAATGATATCTCATACAAACCTCGTAGTGATATCCCTAAGAACATAATTC	1708
Db	1537	AATAAAGCTGAATTTGTTCATAACAATTTATCTGGACATGCTCCGATGGCAAAAGAACTTC	1596
OY	1709	TCAAAGTTTTCACCAAGACAGCTTCATTGGCAATCTGAGTCTTTGGGGTAGTTGGCTAAAC	1768
Db	1597	TCGAAATTTCCCAATGGAAAGCTTCCTGGGTAAATCCATTACTGCAATGTTATCTGCCAAAT	1656
OY	1769	TCAACGGTATGATATTCGTGCGAACTGACAGAGTGCATATCTAGACAGACTATTCCTT	1828
Db	1657	TCCAGCTGTGAGACACTCTCAATGGA--CAAAAGTTAAATTTCAAAGACAGCAATTCCT	1713
OY	1829	GGAATAGCTATTTGGGGGACCTGTGATCTCTTCATAGTCTTAAATAGCAGCTTCCGACCG	1888
Db	1714	TGCATTATCTTAGGCTTTATCATATATGCTCTGCGTCTCTGTTGGCTATATATATAAACA	1773
OY	1889	CATATATCTCTCTCTTTCTCTGATGGATCACTTGACAAACCGATAACTTATTCGACACCG	1948
Db	1774	AATCAACCAAGCAGCTCTGCAAAAGGATCGAATAGCCGTGCAG-----GACCTTCA	1827
OY	1949	AAGCTCTCATTCCTTCATATGAAACATGAGCACTCCAGTTTACAGAGATATCATGAAATG	2008
Db	1828	AAGTATGTTCTCTCCAGATGACATGGCTATTCATTAATTCAGAGACATCATGAGCGTG	1887
OY	2009	ACAGAGATTAAGTGAAGAGTATATCATATTGGGACAGAGCATCAAACCTGTATATACAA	2068
Db	1888	ACAGAGAAATTTGACGAGAAATATCATCATTTGGCTATAGGGCTCAAGCACTGTCTAACAA	1947
OY	2069	TGATTTTGAAGATTTGAACCGGTTGGCATTTAAGCGGCTTTACTCTCAACCCACAG	2128
Db	1948	TGTGAATCAAGACGGGCAAGGCAATGCTGTCTCAAGCGGCTTTACAGTCAGTAATACAT	2007
OY	2129	TCAATGAACAAGTTTGAACAGAACTCGAGATGCTAATGATCATCAAGCAGAAATCTT	2188
Db	2008	AGCTCCGAGAAAGTTTGAACAGAACTAGAGACAATGGGACGATACGGGACAGGAATCTT	2067
OY	2189	GTAGGCTTAACAACCTATATCCCTCTCTCACTTGGGGAGTCTCTGTCTATATACATTTTG	2248
Db	2068	GTTAGCTTCATAGGCTTCTGCTATCTCCACATGAAACTTGTCTTCTATATTAATCATG	2127
OY	2249	GAAAAATGTAAGCTCTGGGATCTTCTTCAATGCGCCCTACGAGAAAAAAGACTTTGATTGG	2308
Db	2128	GAAAAATGTTCTTGTGGGATCTTCTCCACGGTCCATCAAAAGAAAGTGAAGCTCAACTGG	2187
OY	2309	GACACAGGCTTAAAGATAGATATGTGTGACAGCAAGGTTTAGTATTATTAACCATGAC	2368
Db	2188	GACCAAGATGTGAGATCGCGGTGGAGCTGCACAAAGGCGTGGCTATCTCCACATGAC	2247
OY	2369	TGTGTGTCAGAGATTCATTCACAGACGTAAGTCTGCCAACATTCCTTTGGACAAAGAC	2428
Db	2248	TGCAACCTCGCATATCCACAGATGTCAAGTCTCCAAATCTGCTGTGACAGAAAC	2307
OY	2429	TTAGAGGCTCTGTTGACAGATTTTGGAAATAGCGAAAAAGCTGTGTGTCTCAAAATGCAT	2488
Db	2308	TTTCGAAACGCACTCTCAGATTTTCGGCATAGCCAAATGTGTCTCCCTCTGCCAAATGCCAT	2367
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Db	2368	GCTTCCATTATGTGCTAGGAACCATTCGGCTACATTATCCGAGATATCCAGAACTTCC	2427
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Db 2488 GGGAGGAAGCCGCTGCAACGAACTGCACTTGATTAATGTAATCTTCAAGCTGAT 2547
QY 2669 AACATGAACTGATGGAATATGAGATCCAGATCATCATGACGTGTAAAGATCTCGT 2728
Db 2548 GACACACATCATGAGGAGGAGTGGACTCGAGGTGTCACTGACGTGACGACGACATGGGA 2607
QY 2729 GTGGTGAAGAAAGTTTCCAACTGGCAGCTCCATGACCAAAAGACAGCCGAATGATCGA 2788
Db 2608 CTGGTGAAGAAAGCTTCCAGCTCGCCCTTCTGTGACCAAGAGGACCCCTTCAGACCGG 2667
QY 2789 CCACATGAGCAGCAGGAGTCTGTTCT 2817
Db 2668 CCGACCATGACGAGGTTGCAAGGGTCT 2696

RESULT 2
AV827602 639 bp mRNA linear EST 01-APR-2002
LOCUS AV827602 RAF19 Arabidopsis thaliana cDNA clone RAF109-17-H05 5'
DEFINITION mRNA sequence.
ACCESSION AV827602
VERSION AV827602.1 GI:19869662
KEYWORDS EST
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 639)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda PUC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified plasmid vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/Plant/index_e.html) for further
details.

FEATURES
source
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.9e-169;
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QY 121 CTGAGCTTAGTACTGACTGACTTCAAGAGAGGAGCAAGCTTCTGAGATTAAGAA 180
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QY 181 GTCATTCAAGATGTGAACATGTTCTTATGATGATGACCACTTCACTTCTTGAATTA 240
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QY 361 GTCGAATTGATCTGCGAGATATGCTTGTCTGACAAATCCCTGATGAGATTGGTACTG 420
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QY 541 GATCCCTTCAACACTTTCACAGATTCGAACCTGAATTTCTGAGCTTGGACAGAAATTA 600
Db 542 GATCCCTTCAACACTTTCACAGATTCGAACCTGAATTTCTGAGCTTGGACAGAAATTA 601
QY 601 ACTCAGTGTGAGATTCGAAGCTTATTTAATGGAATG 638
Db 602 ACTCAGTGTGAGATTCGAAGCTTATTTAATGGAATG 639

RESULT 3
AV523662/c 626 bp mRNA linear EST 18-FEB-2004
LOCUS AV523662 Arabidopsis thaliana aboveground organs two to six-week
DEFINITION old Arabidopsis thaliana cDNA clone APZL35f03F 3', mRNA sequence.
ACCESSION AV523662
VERSION AV523662.1 GI:8683190
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 626)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
JOURNAL PUBLISHED
10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 626
/organism="Arabidopsis thaliana"
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/ecotype="Columbia"
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XhoI"

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ORIGIN

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Matches 623; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2512 GATAGGTATACATGACCCCGAGTATGCTCCGACATTCACGGCTCATGAAATCCGATGT 2571
DB 626 GATAGGTATACATGACCCCGAGTATGCTCCGACATTCACGGCTCATGAAATCCGATGT 567
QY 2572 CTACAGTTATGAAATAGTCCCTTTGAGTTGTTAAACCGAAGAAAGCCGTTGATGACGA 2631
DB 566 CTACAGTTATGAAATAGTCCCTTTGAGTTGTTAAACCGAAGAAAGCCGTTGATGACGA 507
QY 2632 ATCCATCTCCACCATCTGATATGTCAAAGACGGGAACAATGAGTATGAAATGGC 2691
DB 506 ATCCATCTCCACCATCTGATATGTCAAAGACGGGAACAATGAGTATGAAATGGC 447
QY 2692 AGATCCAGATCATCATGACGCTGTAAGATCTCGTGTGAGTGAAGAAATGTTCCACT 2751
DB 446 AGATCCAGATCATCATGACGCTGTAAGATCTCGTGTGAGTGAAGAAATGTTCCACT 387
QY 2752 GGCACCTCTATGACCAAAAGACAGCCGAATGATGACCAACAATGACAGCAGTACTG 2811
DB 386 GGCACCTCTATGACCAAAAGACAGCCGAATGATGACCAACAATGACAGCAGTACTG 327
QY 2812 TGTTCCTCGCAAGTTTATGCTATGCGAACAACAACCTGCTGCGATGACACGTCAGCGAC 2871
DB 326 TGTTCCTCGCAAGTTTATGCTATGCGAACAACAACCTGCTGCGATGACACGTCAGCGAC 267
QY 2872 GCTGGCGGTGTTGCGTCACGTCGATGATGCAAAATCTCAAGCTCCTCATTCCTGCA 2931
DB 266 GCTGGCGGTGTTGCGTCACGTCGATGATGCAAAATCTCAAGCTCCTCATTCCTGCA 207
QY 2932 TTGCTCTTCATGAGTCTCTGATGCTCAACTGTTCTTCGAGTTGAGACAAGTTATTC 2991
DB 206 TTGCTCTTCATGAGTCTCTGATGCTCAACTGTTCTTCGAGTTGAGACAAGTTATTC 147
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QY 3052 CGTTAACCTGTTGAAATAATATGTCATGTAAGATTAATGACAGCCTTATTTA 3111
DB 86 CGTTAACCTGTTGAAATAATATGTCATGTAAGATTAATGACAGCCTTATTTA 27
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DB 26 TTAGACAAGTGTGTGTGTAATG 1

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RESULT 4
LOCUS CX675276
DEFINITION UCRCS08_61B07_b Parent Washington Navel Orange Callus cDNA library
sequence.
ACCESSION CX675276
VERSION CX675276.1
KEYWORDS EST.
SOURCE Citrus sinensis
ORGANISM Citrus sinensis
Bukariyote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

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REFERENCE
1 (bases 1 to 974)
Close,T.J., Roose,M.L., Ye,X.R., Fenton,R.D., Manamaker,S.,
Landry,B., Hubert,N., Laforest,M., Landry,J. and Ligonde,A.
Development of EST Resources and New Genetic Markers for California
Citrus - Parent Washington Navel Orange Callus cDNA Library -
UCRCS08-3
Unpublished (2005)
Contact: Timothy J. Close
Department of Botany & Plant Sciences
University of California
Riverside, CA 92521-0124, USA
Tel: 909-787-3318
Fax: 909-787-4437
Email: timothy.close@ucr.edu

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JOURNAL
COMMENT

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FEATURES
Source
Seq primer: T7
Location/Qualifiers
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/lab_host="E. coli TJC121"
/clone_lib="Parent Washington Navel Orange Callus cDNA
Library UCRCS08-3"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Parent Washington navel
orange embryogenic callus was established from undeveloped
ovules of ca. 10 mm diameter young fruits under open
pollination on Murashige-Skoog medium at 25°C with 16 h
light in a tissue culture room. Embryogenic callus,
globular and heart stage embryos were pooled in
approximately equal portions in RNAlater (Ambion), then
RNA was extracted using TRIzol Reagent (Invitrogen).
Poly(A) RNA was purified from 500 microgram of total RNA
using Qiagen Oligotex. A primary cDNA library was produced
using a lambda ZAP XR cDNA Synthesis Kit (Stratagene).
These steps were performed by Xinrong Ye (Roose lab, UC
Riverside). One million pfu from the primary library were
maas excised to produce a phagemid population by Raymond
Fenton (Close lab, UC Riverside). Phagemids were plated,
plasmid DNA purified, cDNA clones archived, and DNA
sequences determined bi-directionally using an ABI3730 at
DNA Landmarks (Landry, Hubert, Laforest, Landry, Ligonde).
Chromatogram files were downloaded by FRP to UC Riverside
(bby Close), then processed at UC Riverside (by Manamaker,
Close lab) using the HarveST pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a phred 17
region of at least 100 bases were assembled, then chimeras
were removed following manual inspection of assemblies
(Close, Roose, Manamaker). Sequences that survived all
removal steps were submitted to GenBank."

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ORIGIN

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Query Match      19.0%; Score 604.4; DB 9; Length 974;
Best Local Similarity 76.3%; Pred. No. 3.4e-159;
Matches 743; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

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DB 1 GAATTTATTTCTCGAGAGTTTGTTGTAATCTAAGAAAGTTTATGAAATAGTCTTTACAT 60
QY 1529 AATGATATCTCTGCGCCCAATTCAGAAAGACTTACCAATTAAGAAACATATTTTCTG 1588
DB 61 AATCATCTCAGTGGCGGATTCCTGAGAACTTAGTCAGTTCAGAAACATGTTCTCTTG 120
QY 1589 AGACTGAAATATTAACCTGACTGATGTTGTTCAATTAACCAACTGTCAGTCTC 1648

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 Db 181 TCTGTCTTAACCTATCTTATTAACACCTGTGGTATATCTCTCAAGCAATTAATCTTC 240
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 Db 241 TCAAGATTTTACACGAGAGTTTATTTGAATCTGCTTTTGGGTATTTGGCTCAT 300
 Qy 1769 TCACCGTGTATGATTTCTGCTGCACTGTAAGATGTCAATCTCTAGACAGCTATTCTT 1828
 Db 301 TCTGACATGCGGTGATCTCAATCCAAAGCAAGTTCATTAATTTTAAAGCAGTATTCTC 360
 Qy 1829 GGAATGACTATTTGGGGGAGCTTGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1888
 Db 361 GGAATGCTCTCGGTGACCTTGTATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 Qy 1889 CATTAATCT 1948
 Db 421 CACATCT 480
 Qy 1949 AAGCTGTCTATCT 2008
 Db 481 AAGTTAGTATCT 540
 Qy 2009 ACAGAGATCTTAAGTGAAGTATATCTTTGGGACCGAGCATTAACACTGTATTAATAA 2068
 Db 541 ACCGAGATTTGGTGAAGTACATTAATTTGGGCTATCGAGTATACAGTGTATACAG 600
 Qy 2069 TGTGTTTGAAGATTTGTAACCGTGGTGGATTAAGCGGCTTTACTCTCAACACCCAG 2128
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 Qy 2129 TCAATGAACAGTTTGAACAGAACTCGAATGCTTAAGTATGATCAACAGCAAGAACTCTT 2188
 Db 661 TGTGTTGAAGATTTGTAAGACAGAGCTTGAAGCGGTTGGGAGCATCAAGCCAGAACTCTG 720
 Qy 2189 GTAGAGCTTAAGCTTATCT 2248
 Db 721 GTAGAGCTTAAGCTTATCT 780
 Qy 2249 GAAATGCTAGCTCTGAGATCT 2308
 Db 781 GAAATGCTAGCTCTTGGATATCT 840
 Qy 2309 GACACAGCGCTTAAGATAGATATGTGACAGCAAGAGTTTACTTATCTCAACCATGAC 2368
 Db 841 GACACTGCTGAATAATAGACTAGAGCTGACAAAGGCTAGGCTATTATACCATGAT 900
 Qy 2369 TGTAGTTCAGAGATCTATTCACAGAGAGTGAAGTCTGCAACATCTCTTGGACAAAGAC 2428
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 Qy 2429 TTAGAGGCTCGTTT 2442
 Db 961 TTGGAAGCCATCT 974

RESULT 5
 DR929080
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 ORGANISM

DR929080 948 bp mRNA linear EST 02-AUG-2005
 EST1120619 Aquilegia cDNA library Aquilegia formosa x Aquilegia
 pubescens cDNA clone COINU40, mRNA sequence.
 DR929080.1 GI:71698443
 EST.
 Aquilegia formosa x Aquilegia pubescens
 Aquilegia formosa x Aquilegia pubescens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 Ranunculaceae; Aquilegia.

REFERENCE
 1 (bases 1 to 948)

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Hodges, S.A., Rensink, W., Buehl, C.R., Borevitz, J., Kramer, E.,
 Nordborg, M., and Tomkins, J.
 Generation of ESTs from Aquilegia
 Unpublished (2005)
 Other ESTs: EST1120618
 Contact: Scott Hodges
 Department of Ecology, Evolution and Marine Biology
 University of California, Santa Barbara
 Santa Barbara, CA 93106, USA
 Tel: 805 893 7813
 Fax: 805 893 4724
 Email: hodges@lifesci.ucsb.edu
 Seq primer: M13 Reverse.

FEATURES
 source

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 flower buds, leaves and roots"
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 F2, F3, and F4 lines of Aquilegia formosa x A. pubescens
 were grown from seed in greenhouses at UC Santa Barbara.
 From these plants three sets of tissue were collected: 1)
 Small flower buds (<10 mm) and very young inflorescences
 (71 & 29% by weight respectively), 2) Medium (7-20 mm) and
 large (at or near anthesis) flower buds (65 & 35% by
 weight respectively) and 3) Shoot apical meristems. A
 fourth set of tissue was collected from plants of A.
 formosa. These plants were grown from seed in sand and at
 approximately 1 month root tissue and leaf tissue of
 various developmental stages were collected (84 & 16% by
 weight respectively). Total RNA was extracted from each
 set of tissue and pooled in the following proportions:
 1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled
 total RNA, mRNA was extracted and enriched for full-length
 messages and then normalized with proprietary methods by
 Invitrogen."

ORIGIN

Query Match 17.3%; Score 548.6; DB 10; Length 948;
 Best Local Similarity 74.5%; Pred. No. 2.2e-143;
 Matches 704; Conservative 0; Mismatches 239; Indels 2; Gaps 1;

Qy 1759 TTGGCTAAATCTCACCGTGCATGATTTCTCGTCAAGCTGACAGTGTCAATCTCTAGAGC 1818
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 Qy 1819 AGCTAATCTTGAATAGCTATTGGGAGCTTGTGATCTCTTCATGCTTAAATAGCAGC 1878
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 Qy 1879 TTGGCAGCGCAATATCT 1938
 Db 121 ATGCAAGCGCAATATCT 180
 Qy 1939 TTGCAACCGAAGCTGTCATCT 1998
 Db 181 TATCTCACCAAGCTGTATCT 240
 Qy 1999 CATGAGATGACAGAGATCTAAGTGAAGTATATCTTTGGGACAGGAGCATCAAGCAC 2058
 Db 241 CATGAGATGACAGAGATTTTGAAGTGAAGTATATATTTTGAAGGACATCTGACAC 300
 Qy 2059 TGTATCAATGTGTTTGAAGATTTGAACCGGCTTGAAGGAGGCTTAACTCTCA 2118
 Db 301 TGTCTTAATGTGCTCTGAAGACTGCAAGCAGTAAAGCATTAATCTCTCA 360
 Qy 2119 CAACCAAGTCAATGAACAGTTTGAACAGAACTCGAAGTCTAAGTACATCAAGCA 2178

Db 361 TTACCTCAGAGCCCTGAGAGGATTGTGACAGAGCTGAGACTGTGGAGTATCAACA 420
QY 2179 CAAAAATCTGTGAGCCTACAGGCTTATTCCTCTCAGCTGGGAGATCTTCTGTCTA 2238
Db 421 TCGGAATCTTGTGTTTCTCCAGGGATCTCTTCTCTCTTCTGGAAAACCTTCTTTTA 480
QY 2239 TGACTATTTGGAAAATGGTACCCTTGGGATCTTCTTCATGGCCCTACGAGAAAAAGAC 2298
Db 481 TGACTACATGAGATGTAGCTTGGGATCTCTCATGGCCCTCAAAAAACAGAA 540
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Db 781 TCGACCTCTGCGCTTACTGAGAGCTGTGATGTTAGCTATGGAGATTTGCTTCTTGA 840
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Db 899 CTGACTGCCAACATGCCGTCAATGAGACTGTTGATCTGCACAT 943

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DEFINITION AV528628 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone APZL1410R 5', mRNA sequence.
ACCESSION AV528628
VERSION AV528628.1 GI:8688911
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS 1 (bases 1 to 535)
TITLES Aaamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/planc/.
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XhoI"

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QY 3017 AGGAGGAAATCTTTAAACGATATCTTTTCTTGGCTTAAGCTGTAGAAAAATTAATG 3076
Db 115 AGGAGGAAATCTTTAAACGATATCTTTTCTTGGCTTAAGCTGTAGAAAAATTAATG 56
QY 3077 TCTCATGTTAAAGTATTAATGACATGCTTATTTATTTAGCAAGTGTGTGTG 3131
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RESULT 7
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VERSION AV529393.1 GI:86889676
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS 1 (bases 1 to 535)
TITLES Aaamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7 (3), 175-180 (2000)
PUBMED 10907847
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/planc/.
Location/Qualifiers

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-139;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTAAGATATCTAAAAACGACGCTTTTAAAGCTGTGTGAAGAAAGCTCTGTTT 60

QY 90 GAGATATGTTCTTCTTGGGTTTCTCTTCTGCTTGAAGCTTAGTACTGTGACTT 149
Db 61 GAGATATGTTCTTCTTGGGTTTCTCTTCTGCTTGAAGCTTAGTACTGTGACTT 120

QY 150 AGAGAGGAGCAAGCTTCTGAGATTAAAGAGTCATTCAAGATGTGAACAATGTTCTT 209
Db 121 AGAGAGGAGCAAGCTTCTGAGATTAAAGAGTCATTCAAGATGTGAACAATGTTCTT 180

QY 210 ATGACTGACACACTTCACTTCTTGGATTAATGTGCTGAGAGAGGTGCTTGTGAAA 269
Db 181 ATGACTGACACACTTCACTTCTTGGATTAATGTGCTGAGAGAGGTGCTTGTGAAA 240

QY 270 ATGTCACTTCAATGTTGTGCTCTTAAATTTGTGACATTTGAATCTTGATGAGAAATCT 329
Db 241 ATGTCACTTCAATGTTGTGCTCTTAAATTTGTGACATTTGAATCTTGATGAGAAATCT 300

QY 330 CACCTGCTATGAGATCTTCAAGAGTCTCTTGTCAATTTGTCGAGGTAATCGCTTGT 389
Db 301 CACCTGCTATGAGATCTTCAAGAGTCTCTTGTCAATTTGTCGAGGTAATCGCTTGT 360

QY 390 CTGGAACAATCCCTGATGAGATTGTGATGCTTCTTGTGCAAAACTTGAAGCTTATCT 449
Db 361 CTGGAACAATCCCTGATGAGATTGTGATGCTTCTTGTGCAAAACTTGAAGCTTATCT 420

QY 450 TCAATGAATTAAGTGTGACATACCGTTTTCATTTGCAATTTGAAGTGAACAATTGAGCAGC 509
Db 421 TCAATGAATTAAGTGTGACATACCGTTTTCATTTGCAATTTGAAGTGAACAATTGAGCAGC 480

QY 510 TGATTTCTGAAGATTAACAATTGATGAGACCGATCCCTTAAACATTTTCAAGAT 564
Db 481 TGATTTCTGAAGATTAACAATTGATGAGACCGATCCCTTAAACATTTTCAAGAT 535

RESULT 8
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DEFINITION UCRCS07.13G10.g Parent Washington Navel Orange Thrip-Challenged
Plavado CDNA Library UCRCS07 Citrus sinensis cDNA clone
ACCESSION UCRCS07.13G10-N19-1-7.g, mRNA sequence.
VERSION CX043849
KEYWORDS CX043849.1 GI:56528140
SOURCE EST.
ORGANISM Citrus sinensis
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eustosids II; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 810)
Close,T.J., Roose,M.L., Federici,C.F., Fenton,R.D., Watkins,P.,
Morse,J., Wamamaker,S., Lyon,M., Ye,X.R., Jang,C., Quintilio,C.,
Ikeda,J., Collin,M., Kacar,Y., Landry,B., Hubert,N., Laforest,M.,

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TITLE

Landry,J. and Ligonde,A.
Development of EST Resources and New Genetic Markers for California
Citrus - Parent Washington Navel Orange Thrip-Challenged Plavado
CDNA Library UCRCS07
Unpublished (2004)
Contact: Timothy J. Close
Department of Botany & Plant Sciences
University of California
Riverside, CA 92521-0124, USA
Tel: 909-787-3318
Fax: 909-787-4437
Email: timothy.close@ucr.edu

FEATURES

source

Seq primer: T3.

Location/Qualifiers

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1. 810
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Thrip-Challenged Plavado CDNA Library UCRCS07"
/note="Vector: lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Trees were grown in the field
at University of California, Riverside using standard
horticultural practices. Young fruits were placed in a
cage with thrips (Scirtothrips citri). Infestations were
conducted by Watkins (Morse lab) and flavado collected by
Federici (Roose lab) from May-June 2003. The thrips were
collected from naturally infested Rus plants by sucking
into a tube. A flexible hose was attached to a tube that
extended into a covered vial, and another tube stuck out
of the vial at a right angle. The bent tube was held above
the thrips, sucking on the flexible tube created a vacuum,
pulling the thrips into the vial. Thrips were knocked off
the Rus plant onto a manila folder, then only second
instars were captured. This was done repeatedly until
enough were obtained. Approximately 7-10 thrips were caged
on each fruit within a plastic vial made of a 8 cm long by
5 cm diameter tube that had a very fine mesh organdy
fabric glued to the bottom. The plastic cap was slit from
the edge to the center so it could be slipped over the
stem of the fruit. It was put in place, the thrips were
knocked into the vial and it was fastened onto the cap
then all gaps were closed with masking tape. The thrips
naturally move up to the fruit. The cages were left in
place for two days, then removed. The fruit were checked
to be sure the thrips had stayed on, and then brought to
the lab to cut off the flavado using a razor blade. Only
the flavado from the stem 1/3 to 1/2 of the fruit was
used. For controls an equal number of comparable sized
fruit were caged without thrips, and the peel collected
from them in the same manner. Tissues were frozen in
liquid nitrogen, then stored at -80C until further
processing. Fenton (Close lab) purified RNA by the phenol
method described in J. Japanese Soc. Hort. Sci. 1996. 64
(4): 809-814, purified poly(A) mRNA using an Oligotex mRNA
Kit (Qiagen), produced a primary cDNA library using a
lambda ZAP XR cDNA Synthesis Kit (Stratagene), then
mass-excised 0.77 million plu from the primary library to
produce a phagemid population. The library was made from
equal portions of RNA from each of the two treatments.
Phagemids were plated, plasmid DNA purified, cDNA clones
archived, and DNA sequences determined bi-directionally
using an ABI3730 at DNA landmarks (Landry, Hubert,
Laforest, Landry, Ligonde). Chromatogram files were
downloaded by FTP by Close, then processed by Wamamaker
(Close lab) using the Harvest pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a

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high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Close, Roose, Federici, Wamaker, Lyon, Ye, Yang, Collin, Kacar, Ikeda, Quintilio). Sequences that survived all removal steps were submitted to Genbank."

Query Match	16.8%; Score 532.2; DB 8; Length 810;
Best Local Similarity	78.6%; Pred. No. 9.5e-139;
Matches 636; Conservative 0; Mismatches 173; Indels 0; Gaps 0;	
Db	464 GGAGACATACCGTTTGCATTCGAGTGAAGCACTTGAGCAGTATTCGAAGAT 523
1	GGAGACATACCGTTTGCATTCGAGTGAAGCACTTGAGTATTCGAATTTGAAAAC 60
QY	524 AACCAATTGATAGACCGATCCCTTCAACATTTGACAGATTCGAAACCTGAAATTCG 583
61	AATCAGTTGATGGACCAATTCCTTCACTTGTCTCAGCTTCTTAATTTAAAGTTTGA 120
QY	584 GACTGGCAGAAATAAATCAAGTGGAGATACCAAGACTATTTCTGGAATGAAGT 643
121	GACCTGGCTAAATTAACCTCAGTGGAAATACCAAGCTTTATACCTGAATGAAGTC 180
QY	644 CTTCAGATCTTGGGTTGCGAGAAACAATTAAGTTCGATTCGAGATTTGT 703
181	TTTCAATATCTTGGTTTCCAGGGAACAATCGTGGTACACTTCTCCAGATATGT 240
QY	704 CAATGATCGTCTTTGGTATTTTGAAGTAAACAACAGTTGACTGTATATCTT 763
241	CAGCTTCTGGGTTGTGTATCTTGAATGTAATTAACAGTTGACAGGAGCATTCCT 300
QY	764 GAGACGATAGAAATTCAGCTGCTTCAGGTTTGAAGTTCCTCAATCAGCTACT 823
301	CAGAAATATGGCAATTCAGCTTCTTCAGGCTTGAATCTTCAACCAAGCTAAGT 360
QY	824 GGTGAGATCCCTTTGACATCGGCTTCGCAAGTTCCAATATGATTCAGAGCAAT 883
361	GGAGAGATTCATTCACATTTGGGTTTGGAAATGATCTATATCTTGGCAAGAAAT 420
QY	884 CAATCTCTGGGAAGATTCATCAGTATGTTGTTCAATGCAAGCCCTTGCAGTTTAT 943
421	CAGCTGACAGGGAAGATTCATCAGTATGTTGTTCAATGCAAGCCCTTGCAGTTTAT 480
QY	944 CTAGTGGCAACTGTTGAGTGGATCTATTCCTCGAATTCGGAATCTTACTTACC 1003
481	TTTGCTGCAACATGTAAGTGAAGCCATTCCTCCATTTAGSAAATTTGAGTTACACA 540
QY	1004 GAGAAATTTGATTTGACAGTAAACAGTGAAGTTCATTCACCTGAGCTTGAAC 1063
541	GAGAAATTTGATTTTACAGATTAACAAGTGAAGTTCATTCACCTGAGCTTGAAC 600
QY	1064 ATGTCAAAATCCCTTACCTTGAACCTCAATGATATATCTCAGGGCTATATACCA 1123
601	ATGCAAAAGCTTCACTCTGGAATTAATGATATATCAGCTCAAGGAGCATATTCCTCA 660
QY	1124 GAGCTTGGGAAGCTTCACTGATTTGATCTGAATGAGGCAATGATCTGGAAGA 1183
661	GCGCTTGGGAAGCTTCACTGATTTTATGATCTGAATGAGGCAATGATCTGGAAGA 720
QY	1184 CTTATACCTGATCTGAGCTCTTGGCAAAATTAACAGCTTAAATGTTTCATGGAAC 1243
721	CTATATCTGCAATCTTAAATGTTTCATGCAAAATCTCAACAGCTGGAATGTCATGAAT 780
QY	1244 AAGTTTATGTCAGTATATCCCGAGCATT 1272
781	AAGTTTAAACGAAACATTCGCGCAGCATT 809
RESULT 9	
LOCUS	AY106598 1273 bp mRNA linear HTC 22-FEB-2005
DEFINITION	Zea mays PC0069596 mRNA sequence.

ACCESSION	AY106598
VERSION	AY106598.1
KEYWORDS	HTC; GI:21209676
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 1273)
AUTHORS	Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villada,H., Fang,Z., Morgante,M., Landewe,T., Fenger,K., Uesche,F., Hanafey,M., Tingey,S., Chou,H., Wang,R., Soderlund,C. and Coe,E.H.
TITLE	Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization
JOURNAL	Plant Physiol. 134 (4), 1317-1326 (2004)
REFERENCE	2 (bases 1 to 1273)
AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL	Unpublished (2002)
REFERENCE	3 (bases 1 to 1273)
AUTHORS	Coe,E.H.
TITLE	Direct Submission
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZMDB and may be found by BLAST searching at MSL, maizegap.org; ZMDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZMDB: www.zmdb.iastate.edu.
FEATURES	
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	/mol_type="mRNA"
	/db_xref="maizegdb:633781"
	/db_xref="taxon:4577"
	/clone_lib="Maize Mapping Project/DuPont Consensus Library"
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
ORIGIN	
Query Match	16.7%; Score 530.8; DB 6; Length 1273;
Best Local Similarity	69.2%; Pred. No. 2.7e-138;
Matches 769; Conservative 0; Mismatches 337; Indels 6; Gaps 3;	
Db	1742 CTTGCTTTGCGGTAGTGGTAACTCAACGCTGATGATTCGTCGAACTGTACGA 1801
1	CTTGCACTCTGTGATATTTGGCTTGTCTTCAATGCTGCTCCACTGGCACCAGCAAA 60
QY	1802 GTGTCAATCTCTAGACGATATTTTGAAATGATTTGGGGAAGTGTGATCTTCTC 1861
61	CCGCCAATCTCAAGGCTGCATTAATTTGGTGTGTGGTGGAGACTGTATATCTCTCTG 120
QY	1862 ATGTCTTATACAGCTTGGCCGACCGCAATATCTCTCTCTTCTGATGATGACTT 1921
121	ATGATCTTATACAGCTGTATGCAAGCCACACATTCACCTGCTTTTAAAGTGCACATGTA 180
QY	1922 GACAAACAGTAACTTATTCGACCGAAGCTGTCATCTTTCATATGAACATGCACTC 1981
181	AGCAAGCAGTATGCAATGTCTCACCACCAAGCTGTATCTTTCATATGAACAGGCTCTT 240
QY	1982 CAGCTTACGAGATATCATGAGAAATGACAGAAATCTTAAGTAAAGATATATTCGGG 2041


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Db      241 CATGCTTTGATGATATATGAGGATGACAGAGAACTTGAGTGAATAATCATATTGA 300
QY      2042 CAGGAGCATCAAGACACTGTATACAAATGCTTTGAAGAAATGTAAACCGGTGCATT 2101
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QY      2102 AAGCGGCTTACCTCTCAACACCC-ACAGTCAATGAACAGTTTGAACACAGAACTCGGAT 2160
Db      361 AAAAAGCTGTATGCCACTACCTCGAGAGCTTTAAGAAATTGAACCTAGCTCGAGAC 420
QY      2161 GCTAAGTACATCAAGACAGAAATCTTGTAGCCT--ACAAGCTTATTCCTCTCAC 2218
Db      421 TGTGTGATGATCAAAACCGGAATCTAGTACGCTTGCCAAAGGATCTGTTGTACCT 480
QY      2219 TTGGGAGTCTTCTGTTCTATGACTATTGGAAAATGTAAGCTCTGGGATCTTTCAT 2278
Db      481 GTTGGGAACCTCTCTTTTATGATATATGAGAGTGGAGCTTATGGATGTTTATCAT 540
QY      2279 ---GGCCCTACGAAGAAAAGACTTGATTGGGACACAGGCTTATAGATAGATAGT 2335
Db      541 GAAGGCTCATCAAGAAAGAACTTGACTGGGTGACTGCTACGAGATCGCTTGTGT 600
QY      2336 GCAGCAAGGTTTATGCTTATCTACACCATGACTGTAGTCCAAAGATCATTCACAGAC 2395
Db      601 GCAGCTCAAGGCTCGCTTACCTTACCATGACTGCGACGCCCAAGAAATTCACCGGAC 660
QY      2396 GTGAAGTCTGTCACATCTCTTGGACAAAGACTTGAAGGCTCGTTGACAGATTTTGA 2455
Db      661 GTTAAATCAAAAGATATATCTCTCGACAAAGATATAGGCCCATCTTACAGACTTGGC 720
QY      2456 ATAGCGAAAAGCTGTGTGTGTCAAGTCAATCTTCACTTACCTTACGATGGGACAGATA 2515
Db      721 ATGCTTAAAGCTTATGTGTCTCGAAGATCAACGTCACCTACGTCATGGGACTATT 780
QY      2516 GGTTCATAGACCCCGAGATAGTCTCGCACTTCAACGCTCACTGAATCCGATGTCTAC 2575
Db      781 GGTTCATAGTATCCGAGTACGCGGACCTCCGCTCAACGAAAGTGTGATGTCTAC 840
QY      2576 AGTTATGAAATAGTCTCTTCTTGAAGTGTAAACCGAAGAAACCGTTGATGACGAATCC 2635
Db      841 AGCTACGGGATCTTCTGCTGAGCTGCTGACCGGCAAGGACAGTGAACAACGAGTGC 900
QY      2636 AATCTCCACATCGATGATATGTCAAAGACGGGGAACAAATGATGAAATGCGCAT 2695
Db      901 AATCTCCATCATCTGATCTTATGAAAGACGCGAGCAACAGGTCATGAGACGTTGAC 960
QY      2696 CCAGACATCATCGACGTTAAAGATCTCGTGTGTGAAGAAAGTTTCCAACTGGCA 2755
Db      961 CCCGACGTGGGACACACTGCAAGACCTGGGAGGTGAAGAACTGTTCCAGCTGGCG 1020
QY      2756 CTCCTATGACCAAAAAGACGCGAATATGACCCCAATGACCAAGGACTCGTGT 2815
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QY      2816 CTCGAGGTTTATGCTATGCGAACAACCAAC 2847
Db      1081 CTGACTGCTGTGTGAACCGGAGCGCGCC 1112

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RESULT 10
DR938199      889 bp      mRNA      linear      EST 02-AUG-2005
LOCUS        DR938199
DEFINITION   EST1129738 Aquilegia cDNA library Aquilegia formosa x Aquilegia
ACCESSION   DR938199
VERSION     DR938199.1 GI:71707562
KEYWORDS    EST.
SOURCE      Aquilegia formosa x Aquilegia pubescens
ORGANISM    Aquilegia formosa x Aquilegia pubescens
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
            Ranunculaceae; Aquilegia.

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REFERENCE    1 (bases 1 to 889)
AUTHORS      Hodges,S.A., Rensink,W., Buell,C.R., Borevitz,J., Kramer,E.,
              Nordborg,M. and Tomkins,J.
TITLE        Generation of ESTs from Aquilegia
JOURNAL      Unpublished (2005)
COMMENT      Other ESTs: EST1129737
              Contact: Scott Hodges
              Department of Ecology, Evolution and Marine Biology
              University of California, Santa Barbara
              Santa Barbara, CA 93106, USA
              Tel: 805 893 7813
              Fax: 805 893 4724
              Email: hodges@lifesci.ucsb.edu
              Seq primer: M13 Reverse.
FEATURES
  source
    1..889
    /organism="Aquilegia formosa x Aquilegia pubescens"
    /mol_type="mRNA"
    /db_xref="taxon:338618"
    /clone="COLPM01"
    /tissue_type="mixed shoot and floral apical meristems,
    flower buds, leaves and roots"
    /lab_host="DH10B T1 (T1 and T5 phage resistance)"
    /clone_lib="Aquilegia cDNA library"
    /note="Vector: pCMV SPORT6.1; Site 1: EcoRI; Site 2: NotI;
    F2, F3, and F4 lines of Aquilegia formosa x A. pubescens
    were grown from seed in greenhouses at UC Santa Barbara.
    From these plants three sets of tissue were collected: 1)
    Small flower buds (<10 mm) and very young inflorescences
    (T1 & T9 by weight respectively), 2) Medium (7-20 mm) and
    large (at or near anthesis) flower buds (65 & 35% by
    weight respectively) and 3) Shoot apical meristems. A
    fourth set of tissue was collected from plants of A.
    formosa. These plants were grown from seed in sand and at
    approximately 1 month root tissue and leaf tissue of
    various developmental stages were collected (84 & 16% by
    weight respectively). Total RNA was extracted from each
    set of tissue and pooled in the following proportions:
    1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled
    total RNA, mRNA was extracted and enriched for full-length
    messages and then normalized with proprietary methods by
    Invitrogen."

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ORIGIN

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Query Match      16.4%; Score 519.8; DB 10; Length 889;
Best Local Similarity 75.4%; Pred. No. 3.2e-135;
Matches 672; Conservative 0; Mismatches 217; Indels 2; Gaps 2;

QY      1726 CAGCTTCATTGGCAATCCGTGTTGGCGTATGGCTAAACTCACCGTGCATGTTG 1785
Db      1 CAGCTTCATTGGGAACCTTATCTGTGTGTAATGATGATTCACATGTGTACAGTTG 60
QY      1786 TCGTCGACGTGTACGATGTCATCTTAGAGCAGCTATCTTGAATAGCTTATGGGGG 1845
Db      61 CCACCTCAACGAACGAGCTCCAAATATCTAAAGCGCTATTTTGAAGAAATGTTGGGGG 120
QY      1846 ACTTGATGCTCTTCTCATGCTTAAATAGACGTTGCCGACCGCATTAATCTCTCTT 1905
Db      121 ACTTGTATCTCTTCTTATGATCTTAGTGACAGATACAGACCGCAATATCCACTCTCT 180
QY      1906 TCTTGATGATCACTTGACAAACCAAGTAACTTATGACACCGGACCTGTCATCTTCA 1965
Db      181 TTCAGAAAGTACTCTTGACAAACCAATAGTCTATATCTCAACAAAGCTGTGATCTTCCA 240
QY      1966 TATGAACATGCACTTCACGTTTACGAGATATCATGAGAAATGACAGAAATCTAAATGA 2025
Db      241 TATGAACATGCGCTTTCATGTAATAGCAAAATCATGAGAAATGACGAGAAATTTGATGA 300
QY      2026 GAAGTATATCATTTGGGACAGACATCAAGCACTGTATCAAAATGTGTTTGAAGAAATG 2085
Db      301 GAAATATATATATTTGTTTAAAGCACTGTCTTAAATGTGTCTTGAAGAAATG 360
QY      2086 TAAACGGTTGGATTAAGCGGCTTACTCTCAACCAACGATCAATGAACAGTTTGA 2145

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Db      361  CAGACCGAGTACCAATAAGAGGCTATCTCTCATTTACCTTCAGAGCCTGAAGAGTTGA 420
Qy      2146 AACAGAACTGAGATGTAGTAGCATCAAGACACAGAAATCTGTGAGCTTACAGCTTA 2205
Db      421  GACAGAGCTGAGACTGTGGAGATATCAAGACATCGAAATCTGTGCTCCAGGATA 480
Qy      2206 TTCCCTCTCTCACTTGGGAGCTTCTGTCTATAGTATTTGGAAATGGTAGCCTCTG 2265
Db      481  CTCTTGTCTCTCTTCTGGAACCTCTCTTTATAGTACATGAGATGGTAGCCTTGT 540
Qy      2266 GGATCTTCTTCATGCGCCCTTACGAAAGAAAGACTCTTGATTGGGACACAGGCTTAAAT 2335
Db      541  GGATCTCTCTCATGCGCCCTGCAAAAAACAGAACTGGAGGATCTCGCCCTCAAAAT 600
Qy      2326 AGCATATGCGACGACAAAGTTAGCTTATCTACACATGACCTGTGTCCAGAGATCAT 2385
Db      601  AGCTTTGGAGCTGCGAGAGGGGCTTATCTTTCATCATGATGTAGTCCGCTATAGT 660
Qy      2386 TCACAGAGACGTGAAGTCTGTCACATTTCTTGGACAAAGACTTAGAGGCTGTTGAC 2445
Db      661  CCACAGAGAGTGAATTCATCCAACTACTCTGACAAAGATTTTGAAGCCATCTCAC 720
Qy      2446 AGATTTGGAATGCGAAAGCTTGTGTGTCTCAAGTCACTACTTCACTTACGTGAT 2505
Db      721  AGATTTGGAATGCGAAAGCTTGTGTGTCTCAAGTGTACACTGACCTATGTTAT 780
Qy      2506 GGGACAGATAGGTATACATGAGCCCGAGTATGCTGACCTCAGGCTCAGTGAATC 2565
Db      781  GGGACAGATGCTGATACATGAGCCCGAGTATGCTGACCTCAGGCTCAGTGAATC 839
Qy      2566 CGATGCTACAGTATGGAATGATCTTCTTGAATTTGAATCCGAGGAA 2616
Db      840  TGATGT-TACAGCTATGGAGTTGTCCTCTGAGCTGTGACGGGAGGAA 889

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RESULT 11
LOCUS   DR066962                      841 bp    mRNA    linear    EST 07-JUN-2005
DEFINITION she01-10ms1-a04 She01 Saruma henryi cDNA clone she01-10ms1-a04 5',
            mRNA sequence.
ACCESSION DR066962
VERSION   DR066962.1 GI:67006033
SOURCE    EST.
ORGANISM  Saruma henryi
            Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; magnolids; Piperales;
            Aristolochiaceae; Saruma.
REFERENCE 1 (bases 1 to 841)
            dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
            Openheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
            Leebens-Mack, J., Landherr, L., Junt, D. and Mall, K.
            Generation of ESTs from early flower buds of Saruma henryi
            Unpublished (2004)
COMMENT   Contact: Claude dePamphilis or James Leebens-Mack
            Mueller Laboratory
            Penn State University
            208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
            State University, University Park, PA 16802, USA
            Tel: 814 863 6413
            Fax: 814 865 9131
            Email: cwd3@psu.edu or jh110@psu.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Plant
            Genome Network website (http://psn.cornell.edu)
            Plate: she01-10ms1 row: a column: 04
            Seq primer: M13F
            Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="Pn:She01-10ms1-a04"

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/dep_stage="2.5mm buds"
/lab_host="SOLR"
/clone_lib="She01"
/note="Vector: pBluescript SK (+/-); Site.1: EcoRI;
Site.2: XhoI. This is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at http://Fgp.bio.psu.edu"

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Query Match      16.4%; Score 519.6; DB 9; Length 841;
Best Local Similarity 76.3%; Pred. No. 3.6e-135;
Matches 639; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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Qy      278  TTCAATGTTGCTCTCTTAATTTGTGAGATTGAACTTGAGTGAAGAAATCTGACCTGCT 337
Db      4      TTGATGTTGTTGGCTTAATCTGTGAGGCTCAATCTAGATGAAGAAATATCCCTGCA 63
Qy      338  ATTGAGATCTCAAGAGTCTTGTCAATGATCTGGAGATAATGCTTGTCTGACAA 397
Db      64  ATTGAGGCTTAAAGGCTTGTCTCTCATGATCTAAGGGGAATCATCTGTCGGGAG 123
Qy      398  ATCCCTGATGAGATTGGTGAATGCTGCTTCTTTCGAAACTTAGACTTATCTTCAATGAA 457
Db      124  ATTCTGATGATGATGTTGATGCTGCTTCTTTCGAAAGCTTGAATCTGCTGCACTAC 183
Qy      458  TTAAGTGTGACATACCGTTTTCGATTTGCAATGTAAGCACTTGAAGAGCTGATTTCTG 517
Db      184  ATTACGGGAGCAATTCATCTCAATTTCAAAATGGAAGCACTAGAAACCTTGTGTTG 243
Qy      518  AAGATTAACCAATTTGATAGACCGATCCCTTCAACCTTTCACAGATTTCCAAACCTGAAA 577
Db      244  AAGAACCAACAGTATACAGACCAATCCCTTCAACCTTTCAGATTTCTTAACTTGA 303
Qy      578  ATTCTGAGCTTGGACAGATTAATCACTGATGATGATGATGATGATGATGATGATGAT 637
Db      304  ATTTTGAACCTGCTCAAAATTAATCACTGATGATGATGATGATGATGATGATGATGAT 363
Qy      638  GAAATCTTCAATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 697
Db      364  GAAATCTTCAATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
Qy      698  TTGTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 757
Db      424  ATGTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
Qy      758  ATACCTGAGAGATGAGAAATGCACTGCTTCAGATTTTGAATCTGCTCAATCAG 817
Db      484  ATTCTCAAAATTTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 543
Qy      818  CTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877
Db      544  CTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
Qy      878  GGCAATCACTGCTTGGGAAGATTCATGATGATGATGATGATGATGATGATGATGATGAT 937
Db      604  GGAATATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
Qy      938  TTGATATTAAGTGAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 997
Db      664  CTGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
Qy      998  TTACCGAGAAATTTGATTTTGAACAGTAAAGCTGCTGCTTCAATTTCACTGATGAT 1057
Db      724  TACATGAGAAATTTGATTTTGAACAGTAAAGTGAACAGGAGGATTTCTCTGATGAT 783
Qy      1058  GGAACATGTCAAATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1115

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DB	784	GGCAACATGACAAAGCTTCACCTACTATCTTAATGATGATATATACCTTACCGGGGATA	841
RESULT 12	DV137758	815 bp	linear
LOCUS	DV137758		EST 03-OCT-2005
DEFINITION	DV137758		815 bp mRNA linear
ACCESSION	CV03118A1E10.f1		CV03-normalized library
VERSION	CV03118A1E10.f1 5,		mRNA sequence.
KEYWORDS	DV137758		
SOURCE	DV137758.1	GI:76846764	EST.
ORGANISM	Euphorbia esula (leafy spurge)		
REFERENCE	Euphorbia esula		
AUTHORS	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucosids I; Malpighiales; Euphorbiaceae; Euphorbioideae; Euphorbiaceae; Euphorbia.		
TITLE	1 (bases 1 to 815)		
JOURNAL	Anderson, J.V., Horvath, D.P., Thimmapuram, J., Liu, L., Hernandez, A., Kim, W.R. and Mikel, M.		
COMMENT	Direct submission, Anderson, J.V. 2005		
	Unpublished (2005)		
	Contact: James V. Anderson		

1605 Albrecht Blvd, Biosciences Research Laboratory, Fargo, ND
58105, USA
Tel: 701 239 1263
Fax: 701 239 1252
Email: andersjv@fargo.ars.usda.gov
Adaptors and tags in 5'-end sequenced clones:
(Vector) . . . TACCTGATATCG (End Vector) (Start
EcoRI adaptor) AATTCGATGCTGGG (End EcoRI adaptor) (Start
Insert) . . . AAAAAAAAAAAAAAAAAA (End Insert) (Start
Tag) (Start NotI site/Vector) GCGCGCCGCCCGG . . . Base
Calling/Quality Scores: PHRED from Washington University Genome
Center/Quality Trimming: Cross match from Washington University
Genome Center PHRAP suite. Low quality bases (Phred score < 20)
were trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATAGCACTCACTATAGG (T7)
BACKWARD: ATTAACCTCACTAAAG (T3)
Insert Length: 815 Std Error: 0.00
Plate: CV031181 row: E column: 10
Seq primer: TAATAGCACTCACTATAGG (T7)
High quality sequence stop: 815.

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FEATURES
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tissue (leaf, stem, flowers, seeds, shoots, galls, root
and crown buds) from outdoor plants, cold acclimated
tissues (leaf, stem, and crown buds), crown and root buds
from decapitated greenhouse p ants, and seedlings. The
library was constructed and normalized as described by
Ronald, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. An identifying tag was added at the
3' during cDNA synthesis: insertAAAAAAAAAAAAAAAAATTCGT."

```

Query	Match	Best Local Similarity	Matches	Conservative	Score	Pred.	No. Mismatches	DB	Length	Indels	Gaps
QY	1742	CTGTGCTTTTCGGTAGTTGCTGAACCAACCGTGTCTGATTCCTGCTGCAACTGTACGA	16.3%	77.1%	517.6	1.3e-134	187	10	815	0	0

Db	1	CGTGGTCTTTGGCTATTTGGCTAAATTTCTCAATGACGCAAACTCGTCCAGACAGACA	60
Qy	1802	GTGTCAATCTCTYAGAGACGATTTCTTGGAAATAGCTATTGGGGGACTTGTGATCTCTC	1861
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Qy	1862	ATGGTCTTAADAGAGCTTGGCCGACCGCATATCTCTCTCTTTCTTGATNGATCACTT	1921
Db	121	CTGATCTTGTAGTGGAGCTTTGGCCGACATATTCAAACCCCTTTTCCAGATGATCTT	180
Qy	1922	GACAAACCAAGTAATCTTATTTGACACCCGACCTGTCATCTTCAATATGAACATGGCACTC	1981
Db	181	GACAAACCACTCACTTACTCAACACAAAGTTGGTGTATCTTCAATGAACATGGCACTC	240
Qy	1982	CAGCTTTACGAGATATCATAGAGATGACAGAAATCTAAAGTGAAGTATATCATTTGGG	2041
Db	241	CATGTGTACAGAGATATCATAGAGATGACCGAGAAATTTAAGCGGAATATGTAAATGGC	300
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VERSION	AI992763		
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REFERENCE	Arabidopsis thaliana		
AUTHORS	Bokarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 511)		
	Chen, J., Montiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Georgene, G., Burns, D., Grifflin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C.,		

ORGANISM
Euphorbia esula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Euphorbiales; Euphorbiaceae; Euphorbioidae; Euphorbiae; Euphorbia.

REFERENCE
AUTHORS
Kim, W.R. and Mikel, M.
TITLE
JOURNAL
COMMENT
Contact: James V. Anderson
USDA/ARS
1605 Albrecht Blvd, Biosciences Research Laboratory, Fargo, ND 58105, USA
Tel: 701 239 1263
Fax: 701 239 1252
Email: andersjv@fargo.ars.usda.gov

FEATURES
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Matches 508; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1948 GAAGCTCGTATCTTCTATATGAACATGGACCTCCAGTTTACGAGATATCATGAAAT 2007
61 GAAGCTCGTATCTTCTATATGAACATGGACCTCCAGTTTACGAGATATCATGAAAT 120
2008 GACAGAGAACTTAAGTGAAGTATATCATTTGGGACAGGACATCAAGCACTGTATCA 2067
121 GACAGAGAACTTAAGTGAAGTATATCATTTGGGACAGGACATCAAGCACTGTATCA 180
2068 ATGATGTTTGAAGAAATGTAAACCGGTTGGGATTAACGGCTTACTCTCAACACCCACA 2127
181 ATGATGTTTGAAGAAATGTAAACCGGTTGGGATTAACGGCTTACTCTCAACACCCACA 240
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2188 TGTGAGCTTCAAGCTTATTCCTCTCTCACTTGGGAGTCTTGTTCATATGACTATTT 2247
301 TGTGAGCTTCAAGCTTATTCCTCTCTCACTTGGGAGTCTTGTTCATATGACTATTT 360
2248 GGAATAATGTAAGCTTGGGATCTTTCATAGGCGCTACGAGAAAGAAAGACTTTGATG 2307
361 GGAATAATGTAAGCTTGGGATCTTTCATAGGCGCTACGAGAAAGAAAGACTTTGATG 420
2308 GGAACACACGGCTTAAGATAGCATATGTGACAGCAAGGTTTATGCTTATCATCCATGA 2367
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481 CTGTAGTCCAAAGATCTTACACAGACGTG 511

RESULT 14
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LOCUS
DEFINITION
CV03054B2E05.f1 CV03-normalized library Euphorbia esula cDNA clone
ACCESSION
DVI29724
VERSION
DVI29724.1 GI:76838726
KEYWORDS
Euphorbia esula (leafy spurge)
SOURCE

ORGANISM
Euphorbia esula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Euphorbiales; Euphorbiaceae; Euphorbioidae; Euphorbiae; Euphorbia.

REFERENCE
AUTHORS
Anderson, J.V., Horvath, D.P., Thimmappuram, J., Liu, L., Hernandez, A., Kim, W.R. and Mikel, M.
TITLE
JOURNAL
COMMENT
Contact: James V. Anderson
USDA/ARS
1605 Albrecht Blvd, Biosciences Research Laboratory, Fargo, ND 58105, USA
Tel: 701 239 1263
Fax: 701 239 1252
Email: andersjv@fargo.ars.usda.gov

Adaptors and tags in 5'-end sequenced clones:
Vector). . . TAGCTTCAATCG(End Vector)(Start
EcoRI adaptor).AATTCATTTGGTGG (End EcoRI adaptor)(Start
Insert). . . AAAAAAAAAAAAAAAAAA(End Insert)(Start Tag)TGGCT(End
Tag)(Start NotI site/Vector)GCGGCCGCCACCGCG. . . Base
Calling/Quality Scores: PHRED from Washington University Genome
Center. Vector Trimming: Cross-match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20)
were trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length.
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REVERSE: ATTACCTCACTAAG (T3)
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tissue (leaf, stem, flowers, seeds, shoots, galls, root
and crown buds) from outdoor plants, cold acclimated
tissues (leaf, stem, and crown buds), crown and root buds
from decapitated greenhouse p angs, and seedlings. The
library was constructed and normalized as described by
Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. An identifying tag was added at the
3' during cDNA synthesis: insertAAAAAAAAAAAAAAAAAATGCGT."

ORIGIN

Query Match 15.9%; Score 505.6; DB 10; Length 823;
Best Local Similarity 76.1%; Pred. No. 3.3e-131;
Matches 627; Conservative 0; Mismatches 196; Indels 1; Gaps 1;

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61 AACATGGCACTCCAGCTTACGAGATATCATGATGATGACAGAGATCTAAGTGAAG 120
2030 TATATCACTTGGGACGAGATCAAGCACTGTATACAAATGTGTTGAAGAAATTTGA 2089
121 TATGTAATGTGCTATGAGATCAAGCAAGTATACAAATGTGTTGAAGAAATTTGA 180
2090 CCGGTTGCGATTAAGCGCTTACTCTCAACACCAAGTCAATGAACAGTTTGAACA 2149

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VERSION	AV529789.1			
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SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
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AUTHORS	Asamizu E., Nakamura Y., Sato S. and Tabata S.			
TITLE	1. (bases 1 to 501) A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries			
JOURNAL	DNA Res. 7 (3), 175-180 (2000)			
PUBMED	10907847			
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizue@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/. Location/Qualifiers 1..501 /organism="Arabidopsis thaliana" /mol_type="mRNA" /ecotype="Columbia"			
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Job time : 14326 secs

JOURNAL DNA Res. 7 (3), 175-180 (2000)
 PubMed 10907847
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yama 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/kazusa/>.
 FEATURES
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GenCore version 5.1.9
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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:*
1: gb env:*
2: gb pat:*
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4: gb pl:*
5: gb pr:*
6: gb ro:*
7: gb sts:*
8: gb sy:*
9: gb un:*
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12: gb hcg:*
13: gb in:*
14: gb om:*
15: gb ba:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3136.2	98.7	3176	2	E12705 Arabidops
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4	2930	92.3	2930	2	AX651657 Sequence
5	1495.4	47.1	1508	4	AK221886 Arabidops
6	1343.8	42.3	3673	4	AK073793 Oryza sat
7	1161.8	35.0	3089	4	AY244746 Arabidops
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11	1102	34.7	82212	4	AC004484 Arabidops
12	1044.4	32.9	2796	4	AX654471 Sequence
13	1035.4	32.6	3184	4	AY332474 Oryza sat
14	915.4	28.8	2895	2	AX654770 Sequence
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16	552.4	17.4	1888	4	AK060260 Oryza sat
17	533.8	16.8	4356	2	BD267395 Compositi
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21	284.2	8.9	549	4	AY069973 Camelina
22	275	8.7	11000	4	AP008212_016 Continuation (17 o
23	275	8.7	14313	4	AP000559 Oryza sat
24	275	8.7	155643	4	AP000391 Oryza sat
25	269.4	8.5	81736	4	AB019235 Arabidops
26	267.4	8.4	4686	2	AX654735 Sequence
27	263.4	8.3	104607	4	AT172814 Arabidops
28	248.4	7.8	3375	2	AX505972 Sequence
29	241.6	7.6	3330	2	AX654255 Sequence
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32	234.4	7.4	143582	4	OSJN00271 Arabidops
33	232	7.3	83232	4	AP004503 Lotus cor
34	225.4	7.1	3222	2	BD267346 Compositi
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36	224.8	7.1	4017	2	BD267387 Compositi
37	224.8	7.1	4017	2	ARS66908 Sequence
38	224.8	7.1	4056	2	BD267340 Compositi
39	224.8	7.1	4056	2	ARS66861 Sequence
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ALIGNMENTS

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DEFINITION	(At2g26330) mRNA, complete cds.				
ACCESSION	AY035110				
VERSION	AY035110.1	GI:14334873			
KEYWORDS	FLI_CDNA.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
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AUTHORS	Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shim,P., Southwick,A., Shinzaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.				
TITLE	Arabidopsis Full Length cDNA Clones				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3192)				
AUTHORS	Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koeseema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shim,P., Southwick,A., Shinzaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-MAY-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA				
COMMENT	Riken Genomic Sciences Center (GSC) members carried out the collection and clustering of RFLP cDNAs (RFLP cDNA : RIKEN Arabidopsis Full-Length cDNA) : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinzaki,K.				

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S. X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K., Goldsmith, A. D., Lee, J. M., Quach, H. L., Tang, C. C., Tortum, M., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Kallin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyer, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shim, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES

source

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers

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Matches 3175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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SOURCE unidentifed
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 3176)
AUTHORS Mitsuoka,N. and Robaato,E.U.

TITLE GENE CODING FOR PROTEIN CONTROLLING MORPHOGENESIS OF PLANT
JOURNAL Patent: JP 1997056382-A 1 04-MAR-1997;
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BIO KENKYUSHO:KK
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 1997056382-A/1
PD 04-MAR-1997
PF 24-AUG-1995 JP 1995216187
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Qy	3087	AGATATTATGACATGCCCTTATTTATTTATTAAGCAAGATGTGTGTGTAATATGCTTCAGAC	3146
Dp	3061	AGATATTATGACATGCCCTTATTTATTTATTAAGCAAGATGTGTGTGTAATATGCTTCAGAC	3120
Qy	3147	TGGCACTTAGACTTCATATA	3167
Dp	3121	TGGCACTTAGACTTCATATA	3141

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	AUTHORS	REFERENCE	JOURNAL	PUBMED	FEATURES
ATTU47029	3176 bp	Arabidopsis thaliana ERBCTA mRNA, complete cds.	U47029	U47029.1	GI:1345131	Arabidopsis thaliana (thale cress)	Brassicaceae	Arabidopsis ERBCTA gene encodes a putative kinase with extracellular leucine-rich repeats	Torii, K.U., Mitsuoka, N., Oosumi, T., Matsura, Y., Yokoyama, R., Whittier, R.F. and Komeda, Y.	Submitted (23-JAN-1996)	Journal of Molecular Biology	2682444	1. 3176 2. (bases 1 to 3176) 3. (bases 1 to 3176) 4. (bases 1 to 3176) 5. (bases 1 to 3176) 6. (bases 1 to 3176) 7. (bases 1 to 3176) 8. (bases 1 to 3176) 9. (bases 1 to 3176) 10. (bases 1 to 3176) 11. (bases 1 to 3176) 12. (bases 1 to 3176) 13. (bases 1 to 3176) 14. (bases 1 to 3176) 15. (bases 1 to 3176) 16. (bases 1 to 3176) 17. (bases 1 to 3176) 18. (bases 1 to 3176) 19. (bases 1 to 3176) 20. (bases 1 to 3176) 21. (bases 1 to 3176) 22. (bases 1 to 3176) 23. (bases 1 to 3176) 24. (bases 1 to 3176) 25. (bases 1 to 3176) 26. (bases 1 to 3176) 27. (bases 1 to 3176) 28. (bases 1 to 3176) 29. (bases 1 to 3176) 30. (bases 1 to 3176) 31. (bases 1 to 3176) 32. (bases 1 to 3176) 33. (bases 1 to 3176) 34. (bases 1 to 3176) 35. (bases 1 to 3176) 36. (bases 1 to 3176) 37. (bases 1 to 3176) 38. (bases 1 to 3176) 39. (bases 1 to 3176) 40. (bases 1 to 3176) 41. (bases 1 to 3176) 42. (bases 1 to 3176) 43. (bases 1 to 3176) 44. (bases 1 to 3176) 45. (bases 1 to 3176) 46. (bases 1 to 3176) 47. (bases 1 to 3176) 48. (bases 1 to 3176) 49. (bases 1 to 3176) 50. (bases 1 to 3176) 51. (bases 1 to 3176) 52. (bases 1 to 3176) 53. (bases 1 to 3176) 54. (bases 1 to 3176) 55. (bases 1 to 3176) 56. (bases 1 to 3176) 57. (bases 1 to 3176) 58. (bases 1 to 3176) 59. (bases 1 to 3176) 60. (bases 1 to 3176) 61. (bases 1 to 3176) 62. (bases 1 to 3176) 63. (bases 1 to 3176) 64. (bases 1 to 3176) 65. (bases 1 to 3176) 66. (bases 1 to 3176) 67. (bases 1 to 3176) 68. (bases 1 to 3176) 69. (bases 1 to 3176) 70. (bases 1 to 3176) 71. (bases 1 to 3176) 72. (bases 1 to 3176) 73. (bases 1 to 3176) 74. (bases 1 to 3176) 75. (bases 1 to 3176) 76. (bases 1 to 3176) 77. (bases 1 to 3176) 78. (bases 1 to 3176) 79. (bases 1 to 3176) 80. (bases 1 to 3176) 81. (bases 1 to 3176) 82. (bases 1 to 3176) 83. (bases 1 to 3176) 84. (bases 1 to 3176) 85. (bases 1 to 3176) 86. (bases 1 to 3176) 87. (bases 1 to 3176) 88. (bases 1 to 3176) 89. (bases 1 to 3176) 90. (bases 1 to 3176) 91. (bases 1 to 3176) 92. (bases 1 to 3176) 93. (bases 1 to 3176) 94. (bases 1 to 3176) 95. (bases 1 to 3176) 96. (bases 1 to 3176) 97. (bases 1 to 3176) 98. (bases 1 to 3176) 99. (bases 1 to 3176) 100. (bases 1 to 3176)

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ORIGIN

Query Match 98.7%; Score 3136.2; DB 4; Length 3176;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 147 CAGAGAGGAGAGCAAGCTTGAGAGATTAGAAGCTTCAAGAGTGTGAACATGTTT 206
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Db 301 TCTCACTGCTATTGAGAGATCTCAAGAGTCTTGTCAATTGATCTGAGAGTATGCT 360

QY 387 TGTCTGAGCAAAATCCCTGATGAGATGAGTGTGACTGTTCTTCTTGCAAAACTTGAATTAT 446
Db 361 TGTCTGAGCAAAATCCCTGATGAGATGAGTGTGACTGTTCTTCTTGCAAAACTTGAATTAT 420

QY 447 CCTTCATGAAATTAAAGGTGACATACCCTTTTGATTTGCAAGTTGAAGCACTTGAGC 506
Db 421 CCTTCATGAAATTAAAGGTGACATACCCTTTTGATTTGCAAGTTGAAGCACTTGAGC 480

QY 507 AGCTGATTTCTGAAGATTAACCAATTGATAGGACCGATCCCTTCAACACTTTCACAGATTTC 566
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QY 567 CAAACCTGAAAAATCTGGACTTGGCAAGAAATAAATCTCAGTGTGAGATACCAAGACTTA 626
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QY 627 TTTTCTGGAATGAAAGTTCTTCAAGTATCTTGGGTTGCCAGGAAACAATCTTATCGGTAA 686
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 LOCUS AX651657
 DEFINITION Sequence 480 from Patent WO03000898.
 ACCESSION AX651657
 VERSION AX651657.1 GI:29154475
 KEYWORDS
 SOURCE
 ORGANISM *Arabidopsis thaliana* (thale cress)
Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE
 AUTHORS Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M.,
 Katagiri, F., Quan, S., Tao, Y., Whitcham, S., Xie, Z., Zhu, T. and Zou, G.
 TITLE Plant genes involved in defense against pathogens
 JOURNAL Patent: WO 03000898-A 480 03-JAN-2003;
 Syngenta Participations AG (CH)
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 /db_xref="taxon:3702"
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 Matches 2930; Conservative 0;

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QY	617	CCAAGACTTATTTACTGGAATGGAAGTTCTTCAGTATCTTGGGTGGCAGGAACCACTTA	676
Db	541	CCAGACTTATTTACTGGAATGGAAGTTCTTCAGTATCTTGGGTGGCAGGAACCACTTA	600
QY	677	GTCGGTAACAATTCCTCAAGATTTGTGTCACTGACTGGTCTTTGGTATTTTGAACGTAA	736
Db	601	GTCGGTAACAATTCCTCAAGATTTGTGTCACTGACTGGTCTTTGGTATTTTGAACGTAA	660
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Db	661	AACAACTATTTGACCTGGTATGATACCTGAGACGATAGGAATATTCACCTGCCCTTCAGATT	720
QY	797	TTGGACTTGCTCTTACCAATCAGCTAACCTGGTAGATCCCTTTTGAACATCGGCTTCCTCAA	856
Db	721	TTGGACTTGCTCTTACCAATCAGCTAACCTGGTAGATCCCTTTTGAACATCGGCTTCCTCAA	780
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QY	917	CTCATGCAAGCCCTTGAGCTCTTAATCTTAAGTGGCAACTGTTGAGTGGATCTATTCCT	976
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Db	1681	AGTTGGCTAACTCAACCCGTGTATATTTCTGTGCAATGTATGAGAGTGTAAATCTTGA	1740
Qy	1817	GCAGCTATTTCTGGAATTAAGCTTTGGGGGACTTGGATCTCTTCATGATGCTTAAATAGA	1876
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Db	1861	TATTTGCAACCCGAAGCTCTCATCTCTTCAATAGAACATGGCACTCCAGTTTAGAGAT	1920
Qy	1997	ATCATGAGATGACACAGAAATCTAAGTGAAGATATCATTTGGGACGAGCATCAAGC	2056
Db	1921	ATCATGAGATGACACAGAAATCTAAGTGAAGATATCATTTGGGACGAGCATCAAGC	1980
Qy	2057	ACTGTATACAAATGTGTTTGAAGATGTATAACCGGTTGCGATTTAAGCGGCTTTACTCT	2116
Db	1981	ACTGTATACAAATGTGTTTGAAGATGTATAACCGGTTGCGATTTAAGCGGCTTTACTCT	2040
Qy	2117	CACACCCACAGTCATTAAGAAAGATTTGAAACAGAACTCGAGATGCTAAGTACATCAAG	2176
Db	2041	CACACCCACAGTCATTAAGAAAGATTTGAAACAGAACTCGAGATGCTAAGTACATCAAG	2100
Qy	2177	CACAGAAATCTTGTGAGCCTACACAGCTTATCCCTCTCTCACTTGGGGAGCTTCTGTTC	2236
Db	2101	CACAGAAATCTTGTGAGCCTACACAGCTTATCCCTCTCTCACTTGGGGAGCTTCTGTTC	2160
Qy	2237	TATGACTATTTGGAAAAATGTAAGCCTCTGEGATCTTCTTCAATGCGCCTAACGAAAAAG	2296
Db	2161	TATGACTATTTGGAAAAATGTAAGCCTCTGEGATCTTCTTCAATGCGCCTAACGAAAAAG	2220
Qy	2297	ACTCTGATTTGGGACACACGCGCTTAAGATAGCATATGTCACGACCAAGGTTTAGCTTAT	2356
Db	2221	ACTCTGATTTGGGACACACGCGCTTAAGATAGCATATGTCACGACCAAGGTTTAGCTTAT	2280
Qy	2357	CTACACCATGACGTGATCCAGAGATCAATTCACAGACAGTGAAGTCTCTCCACATCTC	2416
Db	2281	CTACACCATGACGTGATCCAGAGATCAATTCACAGACAGTGAAGTCTCTCCACATCTC	2340
Qy	2417	TTGGACAAAGAATTTAGAGCTCGTTTGCACAGATTTTGGAAATAGCGAAAAAGTTGTGTG	2476
Db	2341	TTGGACAAAGAATTTAGAGCTCGTTTGCACAGATTTTGGAAATAGCGAAAAAGTTGTGTG	2400
Qy	2477	TCAAAGTCACATCTTCAACTTAACGTGATGGGACAGATAGGTTACATAGACCCCGAGAT	2536
Db	2401	TCAAAGTCACATCTTCAACTTAACGTGATGGGACAGATAGGTTACATAGACCCCGAGAT	2460
Qy	2537	GCTGCACTTCAAGGCTCACTGAGAAATCCGATGTCTACAGTTATAGAAATAGTCTCTT	2596
Db	2461	GCTGCACTTCAAGGCTCACTGAGAAATCCGATGTCTACAGTTATAGAAATAGTCTCTT	2520
Qy	2597	GAGTTGTTAAACCCGAGAGAAAGCCGTTGATGACGATCCAACTTCCACCATCTGATATAG	2656
Db	2521	GAGTTGTTAAACCCGAGAGAAAGCCGTTGATGACGATCCAACTTCCACCATCTGATATAG	2580
Qy	2657	TCAAAGACGGGGAACAATGAGTATGAGAAATGCGAATCCAGACATCAATCGACGTGT	2716
Db	2581	TCAAAGACGGGGAACAATGAGTATGAGAAATGCGAATCCAGACATCAATCGACGTGT	2640
Qy	2717	AAAGATCTCGGTGTGTGAAAGATTTTCCAATGCGACTCTCTATGACCAAAAAAGAG	2776

Db	2641	AAAGATCTCGGATGTGTGTAAGAAAATTTTCCAACTGGACACTCTATGACCAAAAAGAC	2700
Oy	2777	CCGAATGATCCAACTCCAAATGACACAGTGACTCGTGTCTTCGGAGATTATGCTATCG	2833
Db	2701	CCGAATGATGACACCAACAAATGACACAGGTGACTCGTGTCTTCGGAGATTATGCTATCG	2760
Oy	2837	GACACACCACTGCTGGACACTGACACGTCAGGACGCTGGGCTGGTTCGAGTACGTCAT	2896
Db	2761	GACACACCACTGCTGGACACTGACACGTCAGGACGCTGGGCTGGTTCGAGTACGTCAT	2820
Oy	2897	GAGTATGCAAAATCTCAGACTCTCTCATTTCTGTCAATTCCTCTTCATGAGTCTTCGAT	2956
Db	2821	GAGTATGCAAAATCTCAGACTCTCTCATTTCTGTCAATTCCTCTTCATGAGTCTTCGAT	2886
Oy	2957	GCTCACTGTTTCTTCTGGTTTGGACAGTATTTCTCAACAGTACGATGA	3006
Db	2881	GCTCACTGTTTCTTCTGGTTTGGACAGTATTTCTCAACAGTACGATGA	2930
RESULT 5			
LOCUS	AK221886		
DEFINITION	Arabidopsis thaliana mRNA for putative receptor-like protein kinase, partial cds, clone: RAFL2-23-M12.		
ACCESSION	AK221886		
VERSION	AK221886.1		
KEYWORDS	GI:62321113		
SOURCE	FLI CDNA.		
ORGANISM	Arabidopsis thaliana (thale cress)		
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REFERENCE			
AUTHORS	1. Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sekurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
TITLE	Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) CDNAs		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1508)		
AUTHORS	Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sekurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-MAR-2005) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-2 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: msek@gs.riken.jp, URL: http://range.gsc.riken.jp/, Tel:81-45-503-9625, Fax:81-45-503-9586)		
COMMENT	An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). This clone is in a modified Bluescript vector. Please visit our web site (http://range.gsc.riken.jp/) for further details.		
FEATURES			
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CDS			

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Query Match	47.1%	Score 1495.4	DB 4	Length 1508
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1496	Conservative	0	Mismatches 1	Indels 0
			Gaps	0

QY	1680	TAGGTGATATCCCTAAGAAACAATACTTCTCAAGATTTTCAACAGACAGCTTCAATGGCA	1739
Db	1	TAGGGGATATCCCTAAGAAACAATACTTCTCAAGATTTTCAACAGACAGCTTCAATGGCA	60
QY	1740	ATCTGTGCTTTTCCGGTAGTGTGGCTAAACTCACCGTGCATGATTTCTGTGGAATCTGTAC	1799
Db	61	ATCTGTGCTTTTCCGGTAGTGTGGCTAAACTCACCGTGCATGATTTCTGTGGAATCTGTAC	120
QY	1800	GAGTGTCAATCTCTAGAGCAGCATTTCTGGAAATAGTATTTGGGGGACTGTGATCTCTTC	1859
Db	121	GAGTGTCAATCTCTAGAGCAGCATTTCTGGAAATAGTATTTGGGGGACTGTGATCTCTTC	180
QY	1860	TCATGCTTTAATAGCAGCTTGCACACCGCATATATCTCTCTCTTTTCTTGTATGATGATCAC	1919
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QY	1920	TTBACAAACAGTAATCTTATTTGACACCGGAGGCTGTCATCTTCATATGAAATAGGAC	1979
Db	241	TTBACAAACAGTAATCTTATTTGACACCGGAGGCTGTCATCTTCATATGAAATAGGAC	300
QY	1980	TCCACGTTTACGAGGATATCATAGATGACACAGAAATCTTAAGTGAAGATATATCATTTG	2039
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QY	2040	GGACGCGAGCATATAGCAGTGTATACAAATGTGTTTTGAAGATTTGTAAACCGGTTGCCA	2099
Db	361	GGACGCGAGCATATAGCAGTGTATACAAATGTGTTTTGAAGATTTGTAAACCGGTTGCCA	420
QY	2100	TTTAAAGGGCTTTTACTCTGCACAAACCCACAGTCAATGAAACAGTTTGAACACGAATCTGAGA	2159
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QY	2160	TGCTAAGTAGCATCAAGCACAAGAAATCTTGTGTGAGCTTACACAGTTATTCCTCTCTCACT	2219
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QY	2220	TGGGGAGTCTTCTGTTCTATAGATATTTTGGAAAAATGGTGGCTCTGGGATCTTCTTCATG	2279
Db	541	TGGGGAGTCTTCTGTTCTATAGATATTTTGGAAAAATGGTGGCTCTGGGATCTTCTTCATG	600
QY	2280	GGCCTTACGAAAGAAAAGACTCTTGATTGGGACACACGGCTTAAAGATAGCATATGTGTGACG	2339
Db	601	GGCCTTACGAAAGAAAAGACTCTTGATTGGGACACACGGCTTAAAGATAGCATATGTGTGACG	660
QY	2340	CACAAAGTTAAGTTATCTACACATAGCATGTGTGTCACAAAGATCATTCACACAGACGTGA	2399
Db	661	CACAAAGTTAAGTTATCTACACATAGCATGTGTGTCACAAAGATCATTCACACAGACGTGA	720
QY	2400	AGTGTGTCAACATTTCTTGTGACAAAGACTTAGAGGCTGTTTGAAGATTTTGAATAG	2459
Db	721	AGTGTGTCAACATTTCTTGTGACAAAGACTTAGAGGCTGTTTGAAGATTTTGAATAG	780
QY	2460	CGAAAAGCTTGTGTGTGTCAAAGTCAATATTTCAACTTAACGTGATGGGACAGATAGGTT	2519
Db	781	CGAAAAGCTTGTGTGTGTCAAAGTCAATATTTCAACTTAACGTGATGGGACAGATAGGTT	840

Oy		2520	ACATAGACC	CCGAGTATCTCGACCTTGACGGCTCACTGAGAATTCGAATGTCTACAGTT	2579
Db		841	ACATTGACCCC	GAGTATCTCGACTTCACGGCTCCTAGGAATTCGATGTCTACAGTT	900
Oy		2580	ATGGAATAGT	CTCTCTTAGTTGTTTAACCCGAAAGAACCGCTTGATGACGAATCCCATC	2639
Db		901	ATGGAAATAGT	CCTTCTTAGTTGTTTAACCCGAAAGAACCGCTTGATGACGAATCCCATC	960
Oy		2640	TCCACCATCT	TATAATGTCOAAAAGACGGGGAAACAATGAAGTAGAATGGCACATCCAG	2699
Db		961	TCCACCATCT	TATAATGTCOAAAAGACGGGGAAACAATGAAGTAGAATGGCACATCCAG	1020
Oy		2700	ACATCACA	TGCACCGTGTAAGATCTCGGTGGTGGAAGAAGTTTCCAATCGGACATCC	2759
Db		1021	ACATCACA	TGCACCGTGTAAGATCTCGGTGGTGGAAGAAGTTTCCAATCGGACATCC	1080
Oy		2760	TATGACACCAA	AAGACGCCGAATGTCAGACCCACCAATGACACCGAGTGACTCGTGTCTCG	2819
Db		1081	TATGACACCAA	AAGACGCCGAATGTCAGACCCACCAATGACACCGAGTGACTCGTGTCTCG	1140
Oy		2820	GCAAGTTTTAT	GCTATCGGAACAACCACTGCTGCAGTGCAGACGTCGCTG	2879
Db		1141	GCAAGTTTTAT	GCTATCGGAACAACCACTGCTGCAGTGCAGACGTCGCTG	1200
Oy		2880	GTTCTGCTAG	CGTAGATAGTAATGCAAAATCTCAACCTCTCATCTGTCATTCGCTT	2939
Db		1201	GTTCTGCTAG	CGTAGATAGTAATGCAAAATCTCAACCTCTCATCTGTCATTCGCTT	1260
Oy		2940	CCATGAGTGC	CTTCTGATGCTCAACTGTTTCTCGTTTGAGCAAGTATTTCTCGAGACA	2999
Db		1261	CCATGAGTGC	CTTCTGATGCTCAACTGTTTCTCGTTTGAGCAAGTATTTCTCGAGACA	1320
Oy		3000	GTGAGTAGTTT	TGCTTGAAGAGAGAAATCTTTAAACGGTATCTTTGCTGCTTAAGC	3055
Db		1321	GTGAGTAGTTT	TGCTTGAAGAGAGAAATCTTTAAACGGTATCTTTGCTGCTTAAGC	1380
Oy		3060	TGTTAGAAAA	ATTATATGTCCTCATCTGTAAGTATATATGACACTGCTTATATATAGACAA	3119
Db		1381	TGTTAGAAAA	ATTATATGTCCTCATCTGTAAGTATATATGACACTGCTTATATATAGACAA	1440
Oy		3120	GTCGTCGTG	TGGAATATGTCCTTCAACACGAGGCACTTAGACTTCCTTAAGTCTTGTSCC	3176
Db		1441	GTCGTCGTG	TGGAATATGTCCTTCAACACGAGGCACTTAGACTTCCTTAAGTCTTGTSCC	1497
RESULT 6					
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LOCUS					PLN 24-JUL-2003
DEFINITION			Oryza sativa (japonica cultivar-group) cDNA clone:J033070P05, full insert sequence.		
ACCESSION			AK073793		
VERSION			AK073793.1		GI:32983816
KEYWORDS			FLI CDNA; CAP trapper.		
SOURCE			Oryza sativa (japonica cultivar-group)		
ORGANISM			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoidae; Oryzaceae; Oryza.		
REFERENCE			1		
AUTHORS			The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team;		
			Kihuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Dol,K.,		
			Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,		
			Kojima,K., Nami,T., Ohneda,E., Yahagi,M., Suzuki,K., Li,C.,		
			Ohseuki,K., Shisiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Okono,Y., Murakami,K.,		
			Tida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,		
			Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,		
			Naitaka,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nishizawa,J.,		
			Iweda,R., Ishibiki,U., Kawamata,M., Yoshimura,A., Miura,J.,		
			Kusunegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;		
			Kawai,J., Carrinini,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,		
			Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Iton,M.,		

[illegible]

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Db	2557	TTTTCATGTAAGAGTCCAACTGAAGAAAGAAAAAACTGATTGGGAAACTCGCTACGAAATTGC		2616
Qy	2329	ATATGGCTACACACAAGGTTTAAAGTATATCTACACCATGACGTGTAGTCCAAAGATCATTTCA		2388
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Qy	2389	CAGAGACGTGAAGTGTGTCMACTTCTCTTGGACAAAGACTTAGAGGCTCGTTTGACAGA		2448
Db	2677	CAGGAGTATGAAATCAAAAAAATATACCTCTTGATTAAGATTATAGGACATCTTACAGA		2736
Qy	2449	TTTGGAAATAGCGAAAGACTGTGTGTCTCAAAGTCATATCTTCACTTACGTGATGGG		2508
Db	2737	CTTTGGCACTTCTAAGAGTTTGTGTGTTCAAAAACCTCACAGTCCACTTGTGATAGGG		2796
Qy	2509	CACAGTATGTTATACATAGACCCCGAGTATGCTGCGACTTCACGGGCTCACTGAGAAATCCGA		2568
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Qy	2689	GGCAGATCCACACATCAATGAGAGTGTAAGATCTCGGTGGTGGAAGAAAGTTTCCCA		2748
Db	2977	AGTCGACCCGACATTCGACACACTTGAAGAGATTTGTGTAAGGTCAAGAAAGGTTTCCA		3036
Qy	2749	ACTGGCACTCTCTATGACCAAAAGACAGCCGAATATGACGCCAATATGACCAAGTGAC		2808
Db	3037	GCTGGCGCTCTTTTGACCAAGAGACAAACATCGATGCGCCGACAAATGACAGAGTTGT		3096
Qy	2809	TCGTGTCTCGGCACTTTATGCTATCGGAAACAAACACCTGCTGC-----GACTGA		2859
Db	3097	GCGGCTCTGGAACGTGCTAGTTGTCGCCGACCCGACCGGAAGTCCGACAGCAGCTGGC		3156
Qy	2860	CACGTACACGACGCTGGGTGTGTCGTGCTAGCTGCATAGATATGAATCTCAAGACTCC		2919
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Qy	2920	TCATCTCTGTCATTTGCTC---TTCATAGAGCTCTGTATGCTCAACGTGTTCTTCGGTT		2976
Db	3217	CAGCGTGTCTTCCTGCGCCCACTCGTCTGTATCTTCGATGCTGAGCTGTTTTCAGATT		3276
Qy	2977	TGACCAAGTATTTCTCAGAAACAGTAGATTAG		3007
Db	3277	TGGCAGAGTCAATTTCTCAGAAACACAGATAG		3307
RESULT 7				
LOCUS	AY244746	3089 bp	mRNA	linear
DEFINITION	Arabidopsis thaliana ERECTA-like kinase 2 (ERL2) mRNA, ERL2-er12			
ACCESSION	AY244746			
VERSION	AY244746.1	GI:37954361		
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE				
AUTHORS	Shpak, E.D., Berthiaume, C.T., Hill, E.J., and Torii, K.U.			
TITLE	Synergistic interaction of three ERECTA-family receptor-like kinases controls Arabidopsis organ growth and flower development by promoting cell proliferation			
JOURNAL	Development	131 (7),	1491-1501	(2004)

PIRMBD	14985254
REFERENCE	2 (bases 1 to 3089)
AUTHORS	Snpak,E.D., Berthiaume,C.T. and Torti,K.U.
TITLE	Direct Submission
JOURNAL	Submitted (27-FEB-2003) Biology, University of Washington, 1521 NE Pacific, Seattle, WA 98195-1800, USA
FEATURES	
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CDS	
ORIGIN	
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QY	330 CACCTGCTATTGGAGATCTCAAGAGCTCTTGTCATTTGATCTTGCGAGATATCGCTTGT 389
DB	454 CATCTGCCCTTTGGAGATTGATGAATGTGCAATTAATAGACTTGCGAAGAAATTAATTTGG 513
QY	390 CTGGAACAAATCCTGATGAGATTTGGTACTGTCTTCTTTGCAAACTTAGACTTAATCT 449
DB	514 GTGTGCAAAATCCAGATGAGATTGGAACATGTGTTTCTTGTGCTTAATGTGATTTCTTCA 573
QY	450 TCATGAAATTAAGTGTGACATTAACCTTTTCGATTTGGAAGTTGAAACCTTAGAGACAGC 509
DB	574 CCAATTTGTTGTTTGGAGACATACCGTTTTCATCTCTTAAACTCAACACAGCTGAGATTTC 633

QY 510 TGAATCTGAAGAAATTAACCAATTGATAGGACGATCCCTTCAACATTTCACAGATTCCAA 569
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DB 754 ACTGGAATGAAGTCTTCAGATCTTCGTTTACGTGGAAATGTTAACTGGGACATTT 813
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DB 1294 ACAATCTTGAAGGCTGATTCATCTAACTAGTGTCTGTGCTGCTGAAATCAATTC 1353
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QY 1290 TGAATTAACCTTAATCTGTCCAGCAACAATATCAAAAGTCCGATGAGCTATCTC 1349
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QY 2127 AGTCAATGAACAGTTTGAACAGAACTCGAAGATGCTAATGATGATCAAGACAGAAATC 2186
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Db	2845	GACACATCAAGAAACATTTGACGTAGTCTCTTGTGTGACCAACGAAATCTTTGGAGA	2904
Qy	2787	GACCCACAAATGACACAGGTGATGCTGTCTCGGACAGTTTATTCGAAACAAACA	2845
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DEFINITION	AY244745	allele, complete cds.	
ACCESSION	AY244745	GI:37954359	
VERSION	AY244745.1	GI:37954359	
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ORGANISM		Arabidopsis thaliana	
REFERENCE		Bukatyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
AUTHORS	Shpak, E.D., Berchianume, C.T., Hill, E.J. and Torii, K.U.		
TITLE	Synergistic interaction of three ERECTA-family receptor-like kinases controls Arabidopsis organ growth and flower development by promoting cell proliferation		
JOURNAL	Development 131 (7), 1491-1501 (2004)		
PUBMED	14985254		
REFERENCE	2 (bases 1 to 3100)		
AUTHORS	Shpak, E.D., Berchianume, C.T. and Torii, K.U.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-FEB-2003) Biology, University of Washington, 1521 NE Pacific, Seattle, WA 98195-1800, USA		
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Qy	131	GTAGCTACTGTGACTTCAGAGAGAGGAGCAACCTTGCTGAGATTAAAGTCATTCAA	190
Db	263	GTTGCTTCGGCTATGAAACAAAGAGGAAAGCTCTGATGCGCATTAAGGCTCTTCACG	322
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Db	323	AACCTTAGTAATATGCTTTTGGATTGGAGCATGTTCAACAAGTACTGTGTTCTGG	382
Qy	251	AGAGGTGTCTTGTGAAAATGTCACCTTCAATGTTGTTCTTTAATTTGTCAAGATTG	310
Db	383	CGAGGTGTTTTCGCAACAAGTTAGCTACCTCGTGTCTCTGAAATTTGTCCAGCTCG	442
Qy	311	AATCTTGATGAGAAATCTCACCTGCTATGAGATCTCAAGAGTCTCTGTCAATTGAT	370
Db	443	AATCTTGAGAGGAGATATCTCAGCTATTGAGACTTACGAAATTTGCAATCAATGAC	502
Qy	371	CTGCGAGTAATGCTTGTCTGCAACAATCCTGATGAGATTGTACTGTTCTTCTTG	430
Db	503	TTGCAAGGTAAATTAACATGACAGGTCAAAATCCAGATGAGATTGGAATCTGCTTCTT	562
Qy	431	CAAACTTAACCTTATTCCTTCAATGAATTAAGTGTGACATACCGTTTTCGATTGGAG	490
Db	563	GTTATCTGGAATTTGTCGAGAAATCTGTTATATGAGACATACCTTCTCAATCTCAA	622
Qy	491	TTGAGCAACTTGAGAGCTGATTTCTGAAGATTAACAATTTGATAGCCGATCCCTTCA	550
Db	623	CTCAAGAGCTTGAATATCTGATCTGAGAACATCACTCAGAGTCTGTACACGCA	682
Qy	551	ACACTTTCACAGATTCCAAACCTGAAAATTTCTGACTTGGACAGAAATTAATCACTAGT	610
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Qy	671	AACCTTAGCTGTAACATTTCTCCAGATTGTGCAACTGACTGATCTTGGTATTTTGAAC	730
Db	803	ATGTTGACTGGAACGTTATCTTCTGATATGTGTCAGCTAACCGGTTTGTGTACTTTGAT	862
Qy	731	GTAAGAAACAAGTTTGAATGATGATTAACCTGAGACATAGAAATTTGACTGCTTC	790
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Qy	791	CAGGTTTGAATTTGCTTCAATCAATCACTAATCTGAGAGATCCCTTTTGAATCGGCTTC	850
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Qy	851	CTGCAAGTTGCAACATTAATCATGCAAGCAATCAACTCTCTGGAGAAATTTCCATCAGTG	910
Db	983	CTCCAAGTTCTACTCTGTACTTCAAGAAACAGATTAACGGGTGAAATTTCCAGAAAGTT	1042
Qy	911	ATTGCTCATGCAAGCCCTTGAGCTTTAGATCTAAGTGGCAACTTTGTAAGTGATCT	970
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Qy 1808 ATCTTAGAGCAGCTATTTCTGGAATAGCTATTGGGGAGCTTGTGATCTTTCATGATC 1867
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Qy 1868 TTAATAGCAGCTTGGCCAGCGCATATCTCTCTCTCTTCTTGTATGATCATCTTGACAA 1927
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Qy 2048 GCATCAAGCCTGTATTCAAATGTGTTTGAAGAATGTAAACCGGTTGCGATTAAGCGG 2107
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RESULT 9
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LOCUS 9295 bp DNA linear PAT 27-APR-1998
DEFINITION Arabidopsis thaliana gene involved in morphogenesis.
ACCESSION E12706
VERSION E12706.1 GI:3251538
KEYWORDS JP 1997056382-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1. (bases 1 to 9295)
AUTHORS Mitsuoka,N. and Robaato,E.U.
TITLE GENE CODING FOR PROTEIN CONTROLLING MORPHOGENESIS OF PLANT
JOURNAL Patent: JP 1997056382-A 2 04-MAR-1997;
CHIKYU KANRYO SANJO GIUTSU KENKYU KIKO, MITSURU GYOSAI SHOKUBUTSU
BIO KENKYUSHO:KK
OS Arabidopsis thaliana (chale cress)
PN JP 1997056382-A/2
PD 04-MAR-1997
PF 24-AUG-1995 JP 1995216187
PT MITSUKAWA NORIHIRO, ROBAATO EFU UTSUTSURA
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Qy	1921	TGACAAAC-----
Db	6001	TGACAAACAGGCTTACTCTCAAAACATTTACGAATGTTCTTCACTTCAATGATATC
Qy	1929	-----CAGTAACTTATTCGACACCGAAGCTCGT
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DEFINITION	Arabidopsis thaliana DNA for receptor protein kinase, complete cds.
ACCESSION	D83257
VERSION	D83257.1 GI:1389565
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SOURCE	Arabidopsis thaliana (hale creese)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 Torii,K.U., Mitsuoka,N., Oosumi,T., Matsuura,Y., Yokoyama,R., Whittier,R.F. and Komeda,Y.
TITLE	The Arabidopsis ERRECTA gene encodes a putative receptor protein kinase with extracellular leucine-rich repeats
JOURNAL	Plant Cell 8 (4), 735-746 (1996)
PUBMED	862444
REFERENCE	2 (bases 1 to 9295)
AUTHORS	Mitsuoka,N.
TITLE	Direct Submission
JOURNAL	Submitted (29-JAN-1996) Norihiro Mitsuoka, Mitsui Plant Biotech.Kes.Inst., Research Division, FCI-D21, Seigen 2-1-6, Tekkuba, Ibaraki 305, JAPAN (E-mail:tsun01129@koryu.statci.go.jp, Tel:0298-58-6252, Fax:0298-58-6234)

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ACCESSION AC004484
VERSION AC004484.3 GI:20197177
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REFERENCE 1 (bases 1 to 82212)
Rounsley,S.D., Lin,X., Ketchum,K.A., Crosby,M.L., Brandon,R.C., Sykes,S.M., Kaul,S., Mason,T.M., Kerlavage,A.R., Adams,M.D., Somerville,C.R. and Venter,J.C.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 82212)
Lin,X.
AUTHORS Direct Submission
TITLE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr., Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 82212)
Town,C.D. and Kaul,S.
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JOURNAL Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT On Apr 18, 2002 this sequence version replaced gi:6598432.
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Query Match 34.7%; Score 1102; DB 4; Length 82212;
 Best Local Similarity 84.9%; Pred. No. 0;
 Matches 1376; Conservative 0; Mismatches 0; Indels 244; Gaps 3;

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Db 10511 CATGCTTATATAGCAGCTTGCAGCGCATTAATCCTCTCTCTTCTTGATGATCACT 10570
QY 1921 TGACAAAC----- 1928
Db 10571 TGACAAACAGGCTACTCTCCAAACACTTACGAATGTTCTTCACTCAATGTATC 10630
QY 1929 -----CAGTAACTTATTCGACACGAACTCGT 1956
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Qy	465	CATACCGTTTCGATTTTCGAAGTTGAAGCACTTGACAGCTGATCTCGAAGATTAACCA	528
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LOCUS Oryza sativa (japonica cultivar-group) transmembrane protein kinase
DEFINITION (PK3) mRNA, complete cds.
ACCESSION AY332474
VERSION AY332474.1 GI:33242912
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 3184)
Yao, Q., Peng, R. and Xiong, A.
Isolation of a transmembrane protein kinase from rice
Unpublished
2 (bases 1 to 3184)
Yao, Q., Peng, R. and Xiong, A.
Direct Submission
Submitted (30-JUN-2003) Bio-Tech Center, Shanghai Academy of
Agricultural Science, Beidi Road 2901, Shanghai 021-201106, China
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ORIGIN

Query Match 32.6%; Score 1035.2; DB 4; Length 3184;
Best Local Similarity 63.8%; Pred. No. 0;
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Qy 2814 TTCT 2817
Db 2866 TGCT 2869

RESULT 14
AX654770 2895 bp DNA linear PAT 22-MAR-2003
LOCUS AX654770
DEFINITION Sequence 4640 from Patent W003000898.
ACCESSION AX654770
VERSION AX654770.1 GI:29157584
KEYWORDS

ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Kang, I.T., F., Quan, S., Tao, Y., Whitam, S., Xie, Z., Zhu, T. and Zou, G.
Plant genes involved in defense against pathogens
Patent: WO 03000898-A 4640 03-JAN-2003;
Syngenta Participations AG (CH)
Location/Qualifiers

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1. 2895
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QY	2609	CGAAGGAAAGCCGTTGATGACGAATCCAACTCTCCACCATCTGATPATGTCAAAGACGGGG	2668
Db	2488	GCGAAGAAAGCCGCTTCGACACAAAGAACTGCAATTCATTAATTGATATCTCCAAAGCTGAT	2547
QY	2669	AACAATGAATGATGAGAAATGACAGATCCAGACATCAATGACGATGTAAGATCTCGGT	2728
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QY	2729	GTGTGAAGAAAGTTTTCACCTGGACTCTTATGACACAAAGACAGCCGATATGATCGA	2788
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Db	2668	CCGACCATGACGAGAGTTGCAAGGCTGCT	2696
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DEFINITION	Elais guineensis clone Rlk-Ofmf receptor-like protein kinase mRNA, partial cds.		
ACCESSION	AY182166		
VERSION	AY182166.1	GI:28140042	
KEYWORDS			
SOURCE	Elais guineensis (African oil palm)		
ORGANISM	Elais guineensis		
REFERENCE	See, P. T., Harikrishna, K., Ho, C. L. and Ong Abdullah, M. An examination of gene expression in somatic embryogenesis of oil palm (Elais guineensis)		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 2450)		
JOURNAL	See, P. T., Harikrishna, K., Ho, C. L. and Ong Abdullah, M. Direct Submission		
AUTHORS	Submitted (18-NOV-2002) Biotechnology, University Putra Malaysia, Serdang, Selangor 43400, Malaysia		
JOURNAL	Location/Qualifiers		
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CDS			
ORIGIN			

Query Match	25.2%	Score 800.6	DB 4	Length 2450
Best Local Similarity	64.9%	Pred. No. 2,76-256		
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				Gaps 2
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QY 887	CTCTCTGGGAAGATTCATCAGTGTATGGTCTCATGCAAGCCCTTGACAGTCTTAAGTCTA	946		
Db 61	CTCAGAGGAAAGATTCAGAGGTGATGGGCTCCATGCAACCTCTTGACAGTAATGGATTTA	120		
QY 947	AGTGGCAACTGTGAGNGATCTATTCCTCCGATTCCTGGAAATCTTACTTTCACCGAG	1006		
Db 121	AGTAAAAATGAACCTGTGGTGGACCATTCCTCCGATCTTGGCAATCTGTCTACACGGGC	180		
QY 1007	AAATTTGATTTTGACAGATAACAAGCTAGTGGTTCAATTCCACCTGAGCTTGGAAACATG	1066		
Db 181	AAGCTATACCTTACATGGAACAAGCTTACAGCAATCCCTCCAGAGTTGGGAAACATG	240		
QY 1067	TCAAACTCCATTCCTCGGAACCTCAAGTATATCATCCACGGGTCAATACCAACGAG	1126		
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QY 1127	CTTGGGAAGCTTACTGACTGTGTTGATCTGATGTGCGCAACATGATCTGGAGAAGCT	1186		
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QY 1187	ATACCTGATCATCTGAGCTCTTGACAAATCTAAACGCTTAAATGTTTCATGGACACAG	1246		
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QY 1247	TTTATGGACATATACCCCGACATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTG	1306		
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QY 1307	TCCAGCAACATATCAAAAGTCCCATCCGGTGGACTATCTGATCGTAACTTAATGAT	1366		
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QY 1487	TTTGGAAATCTAAGAAAGCATATGGAATATGATCTTTCAATATATGATATCTCGGCCCA	1546		
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QY 1547	ATTCCAGAAAGCTTAAACAATTTACAGAAACAATATTTTGTGAGACCTGSAATAATTAAC	1606		
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Db 901	GAAGATTTTCCTAGGAATATCCAAATGTTGTGTGGAAACAGTGGATGCTCTTGTGGACAA	960		
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Db 961	GATCTTACATGATGAAAGTCACTAATTTCTCGAGCTGCTGTGTTCTGCATTAACCTAGGC	1020		

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OM protein - protein search, using sw model

Run on: September 2, 2006, 06:51:05 ; Search time 48 Seconds
(without alignments)
1956.408 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5043	100.0	976	2	B84659	probable receptor
2	3059	60.7	932	2	T48489	receptor-like prot
3	1504.5	29.8	1124	2	B84742	probable receptor
4	1446	28.7	1109	2	T18536	receptor-like prot
5	1446	28.7	1232	2	T05322	hypothetical protel
6	1412.5	28.0	1133	2	B86308	hypothetical protel
7	1410.5	28.0	1003	2	T05898	hypothetical protel
8	1397	27.7	1123	2	D96756	receptor-like prot
9	1368.5	27.1	1002	2	T46033	receptor protein k
10	1367.5	27.1	982	2	T05335	hypothetical protek
11	1365.5	27.1	1192	2	T48489	receptor-like prot
12	1343	26.6	987	2	T50850	receptor protein k
13	1335.5	26.6	1088	2	B86312	FLA1.9 protein -
14	1334.5	26.5	1064	2	B86465	probable protein k
15	1331	26.4	1013	2	T10659	probable serine/tr
16	1319	26.2	996	2	B86410	protein FM18.12
17	1310	26.0	1027	2	B85089	receptor protein k
18	1301	25.8	981	2	T50851	receptor protein k
19	1296.5	25.7	978	2	B96787	protein T4012.5 (l
20	1293	25.6	999	1	S27756	receptor-like prot
21	1280	25.4	1029	2	T00712	protein kinase hom
22	1280	25.4	1143	2	B84431	probable receptor
23	1267.5	25.1	1196	2	T09356	brassinosteroid-in
24	1262	25.0	1029	2	T05050	protein kinase hom
25	1253	24.8	1120	2	B86479	hypothetical protel
26	1242	24.6	1166	2	F96598	protein F20N2.4 (l
27	1227.5	24.3	976	2	T05897	protein kinase hom
28	1216	24.1	991	2	T52400	receptor-like prot
29	1205	23.9	977	2	C96745	hypothetical prote

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31	1192.5	23.6	1134	2	T04587	hypothetical prote
32	1183	23.5	1095	2	G96746	hypothetical prote
33	1175.5	23.3	1008	2	D84434	probable receptor-
34	1149	22.8	996	2	T10725	protein kinase Xa2
35	1147.5	22.8	890	2	E84846	probable receptor-
36	1147	22.7	980	2	T03784	probable receptor
37	1144	22.7	988	2	T45717	receptor-kinase 11
38	1142	22.6	967	2	T48210	hypothetical prote
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40	1141	22.6	980	2	B84632	probable receptor-
41	1133	22.5	1025	1	A57676	protein kinase Xa2
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ALIGNMENTS

RESULT 1

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C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C/Accession: B84659
R/lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayer, C.M.; Venter, J. eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MID:20083487; PMID:10617197
A/Accession: B84659
A/Status: preliminary
A/Molecule type: DNA
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A/Gene: At2g26330
A/Map position: 2
C/Superfamily: Receptor-like protein kinase

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QY	181	PRLIYNEVLQYGLRGNLVGNI	ISPDLCQLTGLWYFDVARN	SLTSGISPEITGNCTAFQV 240
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T48489
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N/Alternate names: protein T28J14.120
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
R/Author: Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
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A/Reference: T48489
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-932 <BEV>
A/Cross-references: UNIPROT:Q9LYP7; UNIPARC:UPI0000048AE6; EMBL:AL163652
A/Experimental source: cultivar Columbia; BAC clone T28J14
C/Genetics:
A/Map position: 5
A/Intons: 43/2; 91/2; 115/2; 139/2; 163/2; 187/2; 211/2; 234/2; 258/2; 282/2; 306
A/Note: T28J14.120
C/Superfamily: Receptor-like protein kinase
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Best Local Similarity 63.1%; Pred. No. 3.4e-130;
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Qy 91 LKSLSIDLRGNRLSGQIPDEIGDCSSQLQNLDSLNFELSGDIPFSISKQLQLEQLIKNN 150
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Db 598 HMDAHTFDIMRVTEFNLEKDIYSGFVILLETGKKAVDNBNALQMLISKADDTVM 837
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Db 658 ETELEMLSSIKHRLVSLQAVSLSHLSLFPYVLENGSLMDLHGPTKKKTLMDWTRK 749
Qy 750 IAYGAOGLAYLHDCSPRIIHRDVKSSNILLDKLEARLDPFGIAKSLCVSKSHSTYV 809
Db 718 IAYGAOGLAYLHDCSPRIIHRDVKSSNILLDKLEARLDPFGIAKSLCVSKSHSTYV 809
Qy 810 MGTIGYIDPEVARTSLTEKSDVSYGIVLLELTRRAVADDESNIHLIMSKTGNNEV 869
Db 778 LGTIGYIDPEVARTSLTEKSDVSYGIVLLELTRRAVADDESNIHLIMSKTGNNEV 869
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RESULT 3
B84742
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C/Accession: B84742
R/Author: R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varakan, S.E.; Umayam, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402: 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197

Db 426 ANSSLEVLDTIRNMFTGHIPIPNLCSQKRLKLLGYNYLEGSVPSDLGCGSTLERLLIEE 485
 352 -----GKLTLD-----LFDLVANNNDLEGPDPHLSSTCTNLNVNHNKNGKSTTIPRAF 399
 Db 486 NNLRGGIPDVEKONLLFFDL--SGNNFTGFIIPSLGNLKNVTAIYISSNQLSSIPPEL 543
 400 QKLESMTYLNLSNNIKGPIPELISRIQNLDTLDSNNKINGIIPSSLDLEHLKKNLS 459
 544 GSIYKLEHLNLSHILKGIIPSELNCHKLSELDASHNLNGSIPSTLGSITELTLKSLG 603
 Db 460 RNHTITVVP-----GDF--GNLRSMEDLDGNNDISGPIPELN 496
 604 ENSESGGIPFSLFQSNKLNLIQLGNNLAGDIPVGLQLALRSLNLSNKNLNGALPDLG 663
 497 QLOHIIILRLNNNLTVGNVGLANCLSTLVNVNHNLVGDIPKQ--NNFSRFPDSPTGN 555
 664 KLMLELDVSHNLSGLTLRSLTIGSTIFINISHNLFSGVPVPSLTKFLNLSSTSSGN 723
 Db 556 PGLC-----GSMNSPCHDSRRTVRSISRALLIGIALGIVILMLVLAACRP 604
 724 SDLCINCPADGLACPESSILRPCMOSNTGKGLSTLGIAMIVGLALLFTICLFLPSA-- 781
 Db 605 HNPPFLDGLSDKVTYTPKLVILHNNMLHVIEDIMKMTENISEKTIIGHGASSTVYK 664
 782 -----FLFHCCK---SVGEIISAQEGDGLNKLVEATENLNDKXVIGKGAHGTIYK 832
 665 CVLKNCRPVAIKRL-YSHNPQSMKQFETELMELSIKHRNLVSLQAVSLHLSGLLPDY 723
 833 ATLSPDKVAVKLVFPGIKNGSVSMREITIGKVRHNLKLEEFWLKREYSLIITY 892
 Db 724 LENSGLMDLHGPTKKKTLMDVTLKIAYGAAQGLAYLHHDSPRIIHRDVKSSNILLDK 783
 893 MENSGLHDIHETPPKPLDWTSTHNIATVGAHGLAYLHFDQPAIVHARDIKPMNILLDS 952
 Db 784 DLEKRLDPLFGAKSLCS-KSHSTYVMGTGYIDPEYARTSLTEKSDVYSYIVLEL 842
 953 DLEHISDFGAKLKDLSATSIPNTVQGTGYAPENAFVTYVRSRSDYSYIVLEL 1012
 Db 843 LTRKKAVDSDSNLH-----HLMSKGNENMEMADPDTITSCKDLGVVKV---FQL 892
 1013 ITRKKAIDPEFNGETDIDVGNWRSVWTQTG--EIQKIYDPSLDELILSSVMEQVTEALSL 1070
 Db 893 ALICTKROPNDPTMHQVTRVL 914
 1071 ALRCAEKEVDKRPTRMDVVKQL 1092
 RESULT 5
 T05322
 hypothetical protein F18F4.240 - Arabidopsis thaliana
 N:Alternate names: hypothetical protein F1C12.60
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
 C/Accession: T05322; T04898
 R/Bevan, M.; Teyryn, N.; Arctiles, W.; Buyschaert, C.; Dasseville, R.; De
 ewes, H.W.; Mayer, K.F.X.; Scheller, C.
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: Z15408
 A/Accession: T05322
 A/Molecule type: DNA
 A/Residues: 1-1232 <BEV>
 A/Cross-references: UNIPROT:Q9SN91; UNIPARC:UPI0000A00ED; EMBL:AL022224
 A/Experimental source: cultivar Columbia; BAC clone F1C12
 R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, February 1998
 A/Reference number: Z15388
 A/Accession: T04898
 A/Molecule type: DNA
 A/Residues: 1-305 <BEW>
 A/Cross-references: UNIPARC:UPI0000175657; EMBL:AL021637
 A/Experimental source: cultivar Columbia; BAC clone F18F4
 C/Genetics:
 A/Map position: 4

A/Intons: 863/1; 116/1
 A/Note: F1C12.60; F18F4.240
 C/Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hom
 Query Match 28.7%; Score 1446; DB 2; Length 1232;
 Best Local Similarity 31.4%; Pred. No. 1.3e-57;
 Matches 389; Conservative 163; Mismatches 321; Indels 366; Gaps 30;
 7 IVLLGFLCFLVAT--VTSEGATLLEIKSF---KDVANNVLYDWTSSPSDYCVWRGV 61
 5 VLLILFLCFCGSGQPGIINNDQTLLEVKSLVNTPOEDPLRQW--NSDNIYCSMTGV 63
 Db 62 SCENV-TFNVAALNSDLNDEIIPAIGDKSLSDLRGNR----- 103
 64 TCNNTGFRVIALNLTLGLTGISFPWGRFDNLIHLDLSNNLVGPPIPALSNLTSLES 123
 104 ----- 103
 Db 124 LPLFNSQLTGEIIPSLQSLVNIIRSLRIGDNLVGDIPETLGNLVNLQMLALASCLRLTGP 183
 104 -----LSGOIPDEIGDCS-----SLQN 120
 Db 184 PSQGLRIVRQSLIDQNYIEGPIPAELGNSDLYFTAAEMNLNGTIPAELGRLELEI 243
 121 LDISFNEISGDIPIPSISKQLQELILKNNQLIGPIPTLSQIPNLKIIDLQNKLSGET 180
 244 LNLANNLSLGEIIPSLQSGEMSQLQYLSIMANQLGLIPKSLADLGNLQTLDSLANNLTGEI 303
 181 PRLIYW-----NEWQYLGRNNLVGNISPLQLQTL 214
 304 PE-EFNMNSQLDLVLANNHLSGLPKSICSNNTNLEQLVLSQTLGSELPELSKQSL 362
 215 WYFDVRNNSLTGSIPT----- 231
 363 KQDLDSNLSLAGSIPALFELVELTDLYLNNLTLEGLSPSISNLNLQMLVLYHNNLEG 422
 232 -----IGCTAFOVLDLSLNQLTGEIPFPIGL- 261
 423 KLPEKISALRKLVELFLYENRFGEIPEQIEGCTTSKMIIMFNHGEGLIPISIGRKL 482
 262 ATLSLQGNLSGKIPISVIGMQALAVLDLSGNLSGSPILGNLFTBEKLYHNSKLTG 321
 483 NLHLRQNELVGGIPASLGNCHQNLNIDLADNQLSGSIPSPFGLKGLDEMLYNSLQ 542
 322 S-----IPPELGNMSKHL 334
 543 NLDPDSLILRNLRINLSHRNLNGTIHPLCGSSSYLSFDVTNNGFDEIPELGNQND 602
 335 YLELNDNLTHGIIPEELGKLTDLFDLVANNNDLEGPDPHLSSTCTNLNVNHNKNGKFSGT 394
 603 RLRLGKNQLTGKIPWLTGKIRELSLDMSSNALTGITPIQLVCKLTHIDLNNNPLSGP 662
 395 IPRAFQLEEMTYLNLS-----NNIKGPIPELISRIQNL 430
 663 IPPWGLSGLQGBEIKSSNQFVSLPELEFNCTKLVLSDGNSLMSIPEQIEGNIGALN 722
 431 TLDSNNKINGIIPSSLDLEHLKKNLSRNHTITGVVPGDFGNLRIME-IDLSNNDISG 489
 723 VLNLDKQFSGSLPQAMGKLSKLYELRLSNLSLTGEIPVEIGQLQDLSALDLSYNNFTG 782
 490 PIPELNQNLNILLRLNNNLTVGNV-GSLANCLSTLVNVNHNLVGDIPKNNNSRFS 548
 783 DISSITGTLKLETLDSHQLTGEVPGSDMKSLGYLVNFSNNLGGKTKK--QFSRP 840
 549 PDSFIGNPGCGSMNSPCHDSRRTVRSISRALLIGIALGIVILMLVLAACR----- 603
 841 ADSFLGNTGLCGSPL-SRCN-----RVATTIATLRI-----GLMILVIALFFQORHDFK 889
 604 --PHNPPFLDGLSDKVTYTPKLVILHNNMLHV---YEDIMKMTENISEKTIIGHGA 658
 890 KVGHGSAIYSSSSSSGATHKP-----LFRNGASKSDIRMEDIMETHNLSSEPMIGSGG 944
 659 SSTYKCVLKNCKRPAIKR-LYSHNPQSMKQFETELMELSIKHRNLVSLQAV--SLSHL 715

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Db      945 SGKYYKALENGEFTAVAKKILMKDLMNSKFSREVKTLGRIRRHRLVVKLMGYCSSSEG 1004
Qy      716 GSLFLPYDLNGSLMDLHG-----PRKKTLMDMTLKLAYGAAGLAVLHDCSRIT 770
Db      1005 LNLILYEYMGKSTWDLHEDKPYLERKKLLDMEALRIAVGAQVEYLHDCVPIV 1064
Qy      771 HRVKSNNILDDKLEARTDQFIKSL---CVSKSTSTYVMGTIGYIDPEYARTSRLT 827
Db      1065 HRDIKSNVLDLDSNMEHLGDFGLAKVLTENCNTNTSNWTFACSYGIAPETAYSLKAT 1124
Qy      828 EKSDVYSYGIIVLELLTRRAVD---ESNL-----HHLIMSKTGNNEVEMADPDI-- 876
Db      1125 EKSDVYSYGIIVLEIVTGKPTDSVFGAEMDVWRVETHLEVAGSARDKLI---DPLKRP 1181
Qy      877 -----TSTCKDGVKKVYFQALALCTKROPNDPRTMHQ 909
Db      1182 LILFEEDAC-----QVLEIALQCTKTSPQERPSRQ 1213

RESULT 6
E86308
hypothetical protein F20D23.7 - Arabidopsis thaliana
C:/Species: Arabidopsis thaliana (mouse-ear cress)
C:/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C:/Accession: E86308
R:/theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Comu, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
aneen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, J.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltz, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:/Reference number: A86141; MUID:21016719; PMID:11130712
A:/Accession: E86308
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-1133 <STO>
A:/Cross-references: UNIPROT:Q9SH12; UNIPARC:UP10000048275; GB:AE005172; NID:95734762; PM
C:/Genetics:
A:/Map position: 1
C:/Superfamily: Receptor-like protein kinase

Query Match      28.0%; Score 1412.5; DB 2; Length 1133;
Best Local Similarity 32.6%; Pred. No. 3,7e-56;
Matches 371; Conservative 169; Mismatches 392; Indels 207; Gaps 23;

Qy      7 IVVLGFLCLSLVAVTTSSEGAFLLEIKSKFDVNNVLYPWTTSPSSDYCVWGVGSCENV 66
Db      11 VILCSSSF---ILVRSINEGRVLEFKAFPLANDSNGYLAWSNOLDNPN-CNMWGIACTHL 66
Qy      67 TENVALNLTSDLNIDGEISPAIGD-----KSLISDLRGN 102
Db      67 R-TVTSVDLNGMNLSETLSPLICKLHGLKLANSTNFISPIQDLSLCSLEVLDTCTN 125
Qy      103 R-----LSGQIDPEIGDCSSLOMLDLSPNELSGDIPPSISK 138
Db      126 RFHGVPIPIQITMTITLKLKLYLCENVLFSGSIPROIGNLSIQELVIYSNNLTGVIIPSMAX 185
Qy      139 LKQLEDLILKNNOLIGIPSTLSQIPRLKTLDLAONKLTSEIRRLIYMWENVLOYLGKGN 198
Db      186 LKRLRIIRGRNFGSVGIPSEISGCSLKVLAENLLESLSPKOLEKQNTLDLILMON 245
Qy      199 NLVGNISPDLCQTLGLWYFVRNNSLTGSIPTIGNTAFQVLDLSTNOLTGEPIDPDI-- 257
Db      246 RLSGEIPSPVGNISRLLEVALAHENYFTGSIIPREIGLTKKRLVLYTNOLTGEPREIGN 305
Qy      258 FLQVATLSLOGNOLSGKIPSVIGLMOALAVLDLSGNLSSGSPPIIGLNTFEKLYLHNS 317
Db      306 LIDAAIDISENQTLGFIPEKFGHILNLKLHLFENILGPIPREIGELTLLLEKLDLSIN 365

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Qy      318 KLNGSIPEELGNMSKLYLELNDNHLTGHTPEELGKLTDLFDLVANNNDLEGP1PDLSS 377
Db      366 KLNGTIPQELQIPLYVDLQLPDNLQEGKIPLPIGYSNFSLDMSKNSLSGPIPAHFCR 425
Qy      378 CTNLSNLNVGNKFSGTIPRAPQKLESMTYLNLSNNIKGPIPEL----- 423
Db      426 FQTLILSLGSNNLSNIPIDLTCTKSLTKMLGDNLQGLSLTELFLNLQNLALBELHON 485
Qy      424 -----SRIGNL----- 429
Db      486 WLSGNISADLGLKLNLERLANNNEFTGEIPEIGNLTKIVGNISSNQTLGHIPELGS 545
Qy      430 -----DILDISNNKINGIIPSSIGDLEHLKMLNSRHRTIGVVGDDGNLSINEIDL--- 482
Db      546 CVTIQRLDLSGNKFSFGYIAOELQOLVLELTRLSDRLTGEIPIHSPSFDLTRLNELQGN 605
Qy      483 -----SNNDISGPIPEELNOLQNIILRLNNNLGTNV-GSLA 519
Db      606 LLSENIPVELGKLTSLQISLNLISNNLSGTIPSLGNLQMLELTYLNDNLTSGEIPASIG 665
Qy      520 NCLSLTLVNLVSHNLVGDIPKNNFSRFPDSFTGNPGLCGSWLNG-----PCHDSRTV 574
Db      666 NLMSLICNISNNNLVGTVPDIAVFORMDSNFGNMGHGLCNSORSHCOPLVPHSDSKLW 725
Qy      575 RVGIS-RAAILGIA--IGGLVILMLV-----IAACRPNPPFLDGLDKPV 619
Db      726 LINGSQOKLITTCIVIGSVFLITGLCWTIKRREPFAVALEDOTKEDVMD----- 778
Qy      620 TVSTPKVLVILHMMALHVEDIMRMTENSEKYLIGHGASSTVYKCVLKNCKKPAIKRLY 679
Db      779 SYVFPKKGK-----TGGLVDARINSEVDVLRGACGTYYAKMGSGEYIAVKLN 830
Qy      680 S--HNPQMKQFTELEMLSTIHRNLVLSIQAVSLHLSLFLFYDLNGSLMDLHGPT 737
Db      831 SRGEGASDNSFPAELISTGKIRHRNIVKLYGFCYHQNSNLLEYEYMSKSLGEOLQGE 890
Qy      738 KKKTLMDRLKLAAGAAGLALHHDSPRIIHRVKSNNILDDLEARLDPGIAX 797
Db      891 KNCLLDMNARYRALDAAGSLCYLHHDCKPQIVHRDIKSNLILDRFQHLVHVDGIAX 950
Qy      798 LCVSKSTSTYVMGTIGYIDPEYARTSRLTEKSDVSYGIVLELLTRKAV---DDESN 854
Db      951 IDLSYKSKSAVAGSYGIAPETAYTMKTEKCDIYSPGVILLELTKGPPVQPLDGGD 1010
Qy      855 LHHLMSTKGN--EVNEMADPDI-TSTCKDGVKKVYFQALALCTKROPNDPRTMHQVTR 912
Db      1011 LVWVVRISIRNMIPRIEMFDARLDNDKRTVHMSLVLKIALFCTSNSPASRPTREVA 1070
Qy      913 VLGSFMLSQPPAATTSATLQSCVDE-----YANLKT--PHSVNCSMSASDAQ 963
Db      1071 ----MTEARSSSLSSSSITSETPLEANSSKGMVLIHITHHTLTLCCNFRTECDSHM 1124

RESULT 7
T05898
hypothetical protein F6H11.170 - Arabidopsis thaliana
C:/Species: Arabidopsis thaliana (mouse-ear cress)
C:/Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 31-Dec-2004
C:/Accession: T05898
R:/Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewes
submitted to the Protein Sequence Database, April 1998
A:/Reference number: Z15456
A:/Accession: T05898
A:/Molecule type: DNA
A:/Residues: 1-1003 <BEV>
A:/Cross-references: UNIPROT:Q49545; UNIPARC:UP10000042341; EMBL:AL021684; GSPDB:GN00063;
A:/Experimental source: cultivar Columbia; BAC clone F6H11
C:/Genetics:
A:/Gene: ATSP:F6H11.170
A:/Map position: 5
A:/Intons: 867/1
C:/Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hom

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Db      542 FTQGIPEQLNQLNQLGTMNLSRNLEBSLEPAQLSNCSLSEFVDGFRSLNGSVPSNSNM 601
Qy      447 -----LGDLEHLKRNLSRNHITGVVPGDFGRLR-IMEIDUSNN 485
Db      602 KGLTTLVLSERNRSGGIPQFLPELKKLSTQIARNAGGEPSSIGLEIDLYDLDSGN 661
Qy      486 DISGPIPEELNQLNQLLENNNLGNVGSGLANCLSLVYLVNSHNVLDIPKNNNFS 545
Db      662 GLTGEIPAKGLDKLTRLNLSNNLTGSLSVLKGLTSLHVDVSNQFTGPIDNLEGO 721
Qy      546 RFS-PSDFIGNPGLC-----GSWLNSE-----CHDSRTVRVSIIRAIIGIAGLVIL 594
Db      722 LLEPSEFSGNPNLCIPHSFSASNNRSALKYCDQSKRSKSGISTQIYLVANLSSLLV 781
Qy      595 LNVLIACRHPNPPPL-----DGLDKPVYTSY-----PKLVILHNMALHVEDIMRT 645
Db      782 LVVVLALV-----FICLRKRKRPEKDAYVFTQEBGPSILL-----NKVLAAT 824
Qy      646 ENISEKXIIIGHGASSTYKCVLKNCKFPVAKRL-YSHNPQSMQFETELMSSIKRNL 704
Db      825 DNLEKTTTGRGAHGIYRRASLSGKYYAVKRLVFASHIRANQSMREIDTIGKVRHNL 884
Qy      705 VSLQAVSLSHGSLFYDYLENGSLMDLHGPT-KKTLTMDTFLKIAVGAQGLAYLH 763
Db      885 IKLGEFRLKDDGLMRLVMPKSLYDLHGVSPKENVLDMSARVNVALGVAHGLAYLH 944
Qy      764 DCSBRIITHRVKSNILLDKDLRLTDFGIANSCLVSKSHSTTYMGTTGYIDPEYAT 823
Db      945 DCHPPIVHRDIKEENIMLMDLEPHICDFGLARLLDSTVSTAT-VYGTGYIAFENAFK 1003
Qy      824 SRLTEKSDVSYGVILLELTRRAVD-----DESNLHLIMS-KTCNNNEVME-AD 873
Db      1004 TVRGRESDVSYGVILLELTRRAVDKSPPESTDIYSWRSALSSNNVDEMTTIVD 1063
Qy      874 PDITSTCKDLGV--VKVFOALALCTKROPNDPRPTMHQVTRVGSFMLEQPPATDTS 930
Db      1064 PIVDELDSLSLEQWQVIELALSTCTQODPARMPTMRDAVKL-----EDV 1110
Qy      931 ATLAGSCYVD 940
Db      1111 KHLARSCSSD 1120

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RESULT 9
T46033
receptor protein kinase-like protein - Arabidopsis thaliana
N:Alternate names: protein T16K5.20
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C:Accession: T46033
R:Reger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223015
A:Accession: T46033
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1002 <RIE>
A:Cross-references: UNIPROT:Q9M221; UNIPARC:UP1000000C70C; EMBL:AL132965
A:Experimental source: cultivar Columbia; BAC clone T16K5
C:Genetics:
A:Map position: 3
A:Intons: 863/1
A:Note: T16K5.20
C:Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hc

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Query Match      27.1%; Score 1368.5; DB 2; Length 1002;
Best local Similarity 35.1%; Pred. No. 3e-54;
Matches 351; Conservative 179; Mismatches 365; Indels 105; Gaps 24;
Qy      7 IVLLGFLCFLSVATVTSSEGATLLLEIKSF--KDVNNVLVDWTSPSSDYCVWRGVSC 64
Db      10 ILLIHSHSFTVAKPT--ELHALLSLKSSFTIDEHSPILTSMVL--STTFCGWTGVTC 65

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Qy      65 NTFNVVALNLSLNDGEISPAIGDKSLSTDLRGNRLSGQIPPEIGDCSSLOMLDS 124
Db      66 VSLRHVTSLDLSLNLSTGLSVDAHPLPLQNLISLANQSGPIPPQISNLVELRHLNLS 125
Qy      125 FNEISGDIPEPSISK-LKOLEQLIKNNOLGPIPTSTQIPNLKIIDLAQNKLSGEIPRL 183
Db      126 NNFNFGSFPPELSSGLVNLRLVDLVNNNLTGDPVSLTNTQRLHLLGNNYSFGKIPAT 185
Qy      184 IYNEVLQYIGLRGNLVGNISPDLCQLTGL-----WYDVRNNSLTGSIPEITGNCTAF 238
Db      186 YGTMPVLEVLAVSGNEITGKIPEIENLTLTRELTYGY-----NAPENGILPEIENLSEL 241
Qy      239 QVLDLSVNLQTLGEPIDIGLQ-VATLSLQGNLQSKIPISVIGLMALAVLDLSGNLSG 297
Db      242 VRFDAANCGLTGEPIDIGLQVLDLVQVNAFTGTTIOELDLSLSMDSNNFTGT 301
Qy      298 SIPIILGNLTFTFKLYLHNSKLTGSIPPELGNNSKLHYELANDNHLGHIPELGLTDL 357
Db      302 EIFTSPQLKNLNLNLFRNKLVGALPEFIGNPELEVLQLMENNFTGSIPOKLGENGR 361
Qy      358 FDLNVANDLEGPIPHLSSCTNLNSLVHNGKFSGTTPRAFQKLESMYTLNLSNNIK 417
Db      362 VIIDLSSNKLTLGTLPPNMGSGNRLMTLITLGNLFGSIPDSLGKCSLTIRIRGENFLNG 421
Qy      418 PLEVE-----LSRI-----GNLDTLDSNNKNGIIPESIGPLEH 452
Db      422 SIKELEFGLPKLSQVELQDNVLTGELPISGGVSGDLQGISLNNQSLSPALATGLSG 481
Qy      453 ILKRNLSRNHITGVVPGDFGNLSRIME-----IDLSSNNDIS 488
Db      482 VQKLILDNKNGFSSIPPEIGRLQQLSKDPFHNLPFGRIAPEISRCKLTFVDSLNEBS 541
Qy      489 GPIPEELNQLNQLLENNNLGNVGSGLANCLSLVYLVNSHNVLDIPKNNNFSR 547
Db      542 GDIPNEITGMKILNYLNSRNHLVGSIPVTIASMQSLTSDVFYNNLISGLVPSGTQFSYF 601
Qy      548 SPDSFGNPELQGSWLNSE-----HDSR-RTVAVSISRAIIGIAGLVILMVLIAC 602
Db      602 NYTSPVGNSHLCCPYL-GPCGKGTQSHVAPLSATTKLLVLGLDFCSWVFAVAIILKAR 660
Qy      603 RPHNPPFLDGLDKVTVSTPKLVILHNMML-HYVEDIMRTENLSEKYIIIGHGASST 661
Db      661 SLRNA-----SEAKAMRLTAFQRLDFTCDDVL--DSLKERNIIIGKGGAGI 703
Qy      662 VYKCVLKNCKPVAIKRL-YSHNPQSMQFETELMSSIKRNLVSLQAVSLSHGSL 719
Db      704 VYKGTMPKGLVAVKRLATWSSHSHDHGFNAEIQTLGRIRRHIVRLLGFCSNHETNLL 763
Qy      720 FVYDLENGSLMDLHGPPTKKTLTMDTFLKIAVGAQGLAYLHSDSPRIIHHDVSSNI 729
Db      764 VVEYMPNGSLGEVLH-KKGGHLMWTRKYLAEAKGCYLLHDDSPILVHSDVSSNI 822
Qy      780 LLDKDLRLTDFGIANSCLVSKSHSTTYMGTTGYIDPEYARTSRLTEKSDVSYGV 838
Db      823 LLDNSFEAHVADPGLAKFLQDSTGSCMSAIAAGSYGIAPRYATLKDVBKSNVYFSGV 882
Qy      839 LLELLTRRAV--DDESNLHLIMSKTGNN--VEMADPDITSTCKDLGVVKKVFOQLA 893
Db      883 LLELLTGKPVGFSGVDIVQVRSMTDSNKDCVLKIDLRLSSV--PVHEVTHTVFYVA 940
Qy      894 LLCTKROPNDPRPTMHQVTRV--GSFMLEQPPATDTS 930
Db      941 LLCVEQAVERPMPREVVOILTEIPKIPUSKQQAESDVT 980

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RESULT 10
T05335
hypothetical protein FIC12.190 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C:Accession: T05335
R:Bevan, M.; Ardiles, W.; Buyschaert, C.; Daseville, R.; De Clerck, R.; De

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ewes, H.W.; Mayer, K.F.X.; Schueller, C.

submitted to the Protein Sequence Database, April 1998

A:Reference number: 215408

A:Accession: T05335

A:Molecule type: DNA

A:Residues: 1-992 <BEV>

A:Cross-references: UNIPROT:O65440; UNIPARC:UPI0000048993; EMBL:AL022224

A:Experimental source: cultivar Columbia; BAC clone F1C12

C:Genetics:

A:Map position: 4

A:Intons: 884/1

A:Note: F1C12.190

C:Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hc

Query Match 27.1%; Score 1367.5; DB 2; Length 992;

Best Local Similarity 34.1%; Pred. No. 3.3e-54; Indels 161; Gaps 25;

Matches 349; Conservative 170; Mismatches 342; Indels 161; Gaps 25;

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QY 13 LFCISLVATVT---SEEGATLLEIKKSPKDVNNVLYDMTTPSSSDYCVWRGVSCENTFN 69
DB 18 LDCSSLSPLNLSIRQANVLISLKQSPDSYDPSLDSMNIPNFSLSGWTGVCSDNLNQS 77
QY 70 VVALNLSDLNDEISPAIGDK-SLISIDIRNLSGQIPDEIGDCSSLONLDSFNEI 128
DB 78 ITRLDLSNLSISGTSPEISRLSPSLVFLDSSNSFSGELPKETVELSGLEVLNISSNVF 137
QY 129 SGDIPLF-SISKQLEDTLKNQDLPPESTLSQINLKLIDLAOKKLSGEIPRLIYWN 187
DB 138 EGELETRGFSOMTQVLTLDAYNSPNSLPLSTTLRLLEHLDGNYFPDEIRSYGSF 197
QY 188 EVLQYLGRLGNLVGNISPDLCQLT-----GLWYFDVRNN 222
DB 198 LSLKFLSLSGNDLRGRIPNELANITTLVOLYLYNDYRGISPADPGRILNLVHLDLANC 257
QY 223 SLTGSIPETTGNTAFOVLDLSYNQLTGEIPEDIG-FLQVATLSLQGNQSGKIPSVIGL 281
DB 258 SLKSIIPAEIGNLKNLEVLFLQTNELTGSVPREIGNNTSLKTTLDLSNNFLEGEIPELISG 317
QY 282 MQMLAVLDLSGNLSGSIPIPLGNLTFTKLYLHNSKLTGSIPELANSMSLHYLENDN 341
DB 318 LQKQLNLPNLPNRRHGEIPEFVSELPLDQLIKLWHNNFTGKIPKSLDSNGNLIEIDLSIN 377
QY 342 HLNGHIPPETGLKLDLPDLVANNDESGIPDLHSSC----- 378
DB 378 KLTGTLPESLCFGRRLKILIFNNFLFGPLPELDCGCEPLMRPRLGNPLTSKLPKGLY 437
QY 379 -TNLSLNVHGNKSGSTIPR---AFQKLESMTYLNSSNNIKGPIPELBSRIGLDTL 434
DB 438 LPLNLSLELQNNPLTGEIPEEEAGNAQFSSLTQINLSNNRSLGPIPSIRNLRSLSQIILL 497
QY 435 SNNKINGIIPSSIGDLDEHLKMNLSRNHITGVPGDFGNLSIMEIPLDSNNIDISGPIPEE 494
DB 498 GANRLSQIPEISLSKSLKIDMSRNNSFGSKPPEEGDCMSLTLYLDLSHQISGQIPVQ 557
QY 495 LNLQNLITLRLR---NNNLTVGNVSLANCLSLTVLVSHNNLVGDI PKXNNFSRSPD 550
DB 558 ISQRLINLVNVSNNSFNQSLPNEIYWK---SLTSADFSHNNFSGVSPTSQGSYFNNT 614
QY 551 SFIGNPGLCGSMNSPCHDS-----RRIVRVSISQAALLGIAIGLVLLM 596
DB 615 SFLNPLPLCG-FSSNPFCGSONOSQOLNQNNAARSGEISAKFKLFFGGLGGLFFFLV 673
QY 597 VLIATA-----GRHPPPFLDGLSLDKPVTYSPKLVLIHMMNALHYEDIDMMNTNLSSEKY 652
DB 674 VLAIVKRRKRRKKNP-----NLKMLIGFO--KLGF---RSEHILECV-----KENH 714
QY 653 IIGHAASIVYKCVLKQCKPVAIKRLY-----SHNPQSMKQFTELEMLSSIRGNLVS 706
DB 715 VIGKGGGIYKGVMPNGEEVAIVAKKLLITKSSHD---NGLAAEIQTLGRIRHRIVR 770
QY 707 LQAVSLHSLGSLFVYDLENGSLMDLHGPTKKTLDMDTPLKAYGAAGCALVTLHDDCS 766
DB 771 LLAFCSKNDVNLVLEYEMPNGSLGEVLHGKA-GVFLKWTETRLQIALLEAAKGLCYLHDDCS 829

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RESULT 11

T48499

receptor-like protein kinase-like protein - Arabidopsis thaliana

N:Alternate names: protein T28J14.220

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004

C:Accession: T48499

R:Bayan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Len

submitted to the Protein Sequence Database, April 2000

A:Reference number: 224493

A:Accession: T48499

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1192 <BEV>

A:Cross-references: UNIPROT:Q9LYN8; UNIPARC:UPI0000048AE7; EMBL:AL163652

A:Experimental source: cultivar Columbia; BAC clone T28J14

C:Genetics:

A:Map position: 5

A:Note: T28J14.220

C:Superfamily: Receptor-like protein kinase

Query Match 27.1%; Score 1365.5; DB 2; Length 1192;

Best Local Similarity 31.1%; Pred. No. 5e-54; Indels 315; Gaps 28;

Matches 375; Conservative 160; Mismatches 356; Indels 315; Gaps 28;

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QY 2 ALPFDVILGFLFCLSLVATVTSEEGATLLEIKKSPKDVNNVLYDMTTPSSSDYCVWRGV 61
DB 6 ALF---LFLFFSSSSAIVDLSET--TSLSFRRSLN-PSLLSMWNVSASACHDWGV 60
QY 62 SCENVTFNVVALNLSDLNDEISPAIGDKSLISIDIRNLSGQIPDEIGDCSSLONL 121
DB 61 TC--LLGRVNSLSLPSLSLQGIPEKISSLKNRELCLAGNQSCKIPPEIWNLKHQLTL 118
QY 122 DLSFNEISGDIPIPSISKQLEDTLKNQDLPPESTLSQINLKLIDLAOKKLSGEIPEL 180
DB 119 DLSGNSLTGLLPLPLSLPELPLVLDLSDNHFSSLPSPFISLPALSSLDVSNNSLSGEI 178
QY 181 PRLI--YMNVEVLYGLRG---NNLVGNIS-----PDLQLTGLWY 216
DB 179 PREIGKLSNLSNLYMGLNSPFGQIPSEIGNISLTKNPAAPSCFPNGPLPREISKLGHIAK 238
QY 217 FVVRNN-----SLTGSIPETTGNTAFOVLDLSYNQLTGEI 252
DB 239 LDLSYNPLKCSIPKSPGELNLSILNLVSAELGLIPPELGNCKSLKSLMNSLSGPL 298
QY 253 PFDIGFLOVATLSLQGNQSGKIPSVIGLMO-----LGNLFTFK----- 311
DB 299 PLEISEIPLTFAERNQSLGSLPSMWKGVKVDLSLLANNRPSGEIPHEIEDCPMLKHL 358
QY 284 -----ALAVLDLSGNLSGSIPI-----LGNLFTFK----- 311
DB 359 SLASNLSGSIPELSCGSSGLBAIDLSGNLSLSTIEVDFGCGSLGELLTNNQINSIP 418
QY 312 -----LYHNSKLTLSI-----PPELGNNSKLHYLE 337

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Db 419 EDLWKLPLMALDLDSDNNFTGEIPKSLWKSNTIMEFTASVNRLEGYLPAEIGNASLRLV 478
Qy 338 LNDNHLTGHTPEELGKLTDLFDLVANNDEGPIPDHLSSTNINSLNV----- 386
Db 479 LSDNQLTGELPREIGKLTSLVSLNLANMFQGIPELGDCTSLTTLTDLGNNLQGIIPD 538
Qy 387 -----HG-----NKPSGTIPR 397
Db 539 KITAAALQCLVLSYNNLSGSIPEKPSAYFHQIEMPDLSFLQHIGIPDLSTNRLSGPIPE 598
Qy 398 AFQKLESMTYLNNSSNIKGPPIVELSRIGNLTDLIS----- 435
Db 599 ELGECVLVYSLSNHLSGEIPASLSRLTNLTLLDSNALTSGIPKEMGNLSKLQGLN 658
Qy 436 --NNKINGIIPSSIGDLEHLKNNLSRNHTGVPGPGNRLSRIMEIDLSNNDISGPIPE 493
Db 659 LANNQGLHGPESGGLGSLVKLNLTNKKLDGVPASLGNLKELTNHDLSFNLSGELS 718
Qy 494 ELNQLQNIILRLNENNLTVGNVGS-LANCLSLTVLNTSHNNLVGDIP----- 539
Db 719 ELSTMEKLVGLYIEQKFTGEIPBELGNLTQLETLVDSENLISGEITPKICGLPNEFLN 778
Qy 540 --KNNFSRSPDS-----FIGNPGCGSWLNSPCHDSRRTVVSIISRAILQIAI 588
Db 779 LAKNNLRGEVPSDGVCDPSPKALLSGNKELCGRVVGSDCKIEGFKLR---SAMGIAGLML 835
Qy 589 GGVILMLVLAACR-----PHNPP-----FLDGLSDKVTYSTR 624
Db 836 GFTIIVFVFSLRMMATKRVKQDDPERMESRLGFVDNLVFLSGSRSPR----- 890
Qy 625 KLVILHNNMLHYE-----DIMRMTENLSEKTIIGHGASSTYKCVLKCKEPAVI 675
Db 891 ----LSINIM--FEQPLKVRGLDYEATDHSKNNIIGDGGGTYKACLPBEKVAV 944
Qy 676 KRLVSHNPQSMKQFETELMLSSIKHNNVSLQVSLSHSGSLFYDLNGSLMDLHG 735
Db 945 KKLSEAKTQGNREPMAMETLGVKHPNLVSLGYSFSEKLLVYEVNNGSLDHMLRN 1004
Qy 736 PT-KKKTLDMDTRKIVGAAGLAIYHDCSPRIHRDYKSSNILLDKLEARLTDFGI 794
Db 1005 QTGMLEVLDMSKRLKIVAGARGLAFHGHGFIPIHRIKASNILLDGGFEPEVADFG 1064
Qy 795 AKSLCVSKSHSTFVMGTIGYIDPEYARTSRLTEKSDVSYGIVLELLTRKAV----- 849
Db 1065 ARLISACESVSTYIAGTFGIIPPEYQASARATTKGVISFVGLLVLGKEGTGDFK 1124
Qy 850 -DDESNIHLHIMSKTGNNEVEMADPITSTCKDLGVVKKVFOQLALCTKROPNDREPTM 908
Db 1125 ESEGNLVGMAIQINGKKAVDVIDPLVSVALKNSQL-RLDQIAMLCLAETPAKRNML 1183
Qy 909 QVTRVL 914
Db 1184 DVLKAL 1189

RESULT 12
receptor protein kinase homolog [imported] - soybean
C/Species: Glycine max (soybean)
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004
C/Accession: T50850
R/Yamamoto, E.; Karakaya, H.C.; Knad, H.T.
Biochim. Biophys. Acta 1491, 333-340, 2000
A/Title: Molecular characterization of two soybean homologs of Arabidopsis thaliana CLAV
A/Reference number: Z25262
A/Accession: T50850
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-987 <YAM>
A/Cross-references: UNIPROT:Q9M6A7, UNIPARC:UPI00000AC3C7, EMBL:AF197947, PIDN:AAF5906,
C/Genetics:
A/Gene: CLV1B
C/Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hd

Query Match 26.6%; Score 1343; DB 2; Length 987;
Best Local Similarity 34.1%; Pred. No. 4.1e-53;
Matches 346; Conservative 175; Mismatches 358; Indels 136; Gaps 24;
Qy 9 LAGFLFCLSL-VATVTS-BEGATLLEIKKSPKD---VNNVLYDMTSPS-SDYCVWRGVS 62
Db 9 LLEFPIFMIRVATCSFTDMESLKLKOSMKDDKADALHDMKFFPSLSAHCFFSG 68
Qy 63 CENVTFVVALNLSDLNDEISPAIGDKSLSIDRGRSLSGQIPDEIGDCSSLQND 122
Db 69 CDR-ELRVAINVSFVPLFCHLPEPEIGQLDKENLTVSQNNLTGVLPKELAALTSLKLN 127
Qy 123 LSFNELS-----GDIPFSIKLKQLEBOLIKNNOLGPIR 157
Db 128 ISHWVSGHPFGQIILPMTKLEVLVDYDNNFTPLPELVKLEKTKLKLDGNYFSGSIP 187
Qy 158 STLQIPIMLKIIDLAKNKLSEIPRLIYWNVEVLQYGLRGNNLV-GNISPDLCQLTGLMY 216
Db 188 ESYSEPKSLFSLSTNSLSGKIPKSLSKTKTRYKLGYNNAYEGGIPPEFGSMKSLRY 247
Qy 217 FVVRNNSLTGSIPEETGCTAFQVLDLSTYNQLTGEIPFDI-GFLQVATSLQGNQSGKI 275
Db 248 LDISSCNLSGEIPPSLANLTNLTDLFLQINNLGTIIPSELAMVWSLMSIDLSTINDLTGEI 307
Qy 276 PSVIGLMQALAVDLGNNLSGSIPTLIGNLTTEKLYHSNKLTSIPBELNMSKLYH 335
Db 308 PMGFSQLRNLTLNPFQNNLRGVSFVSGELPNLETLQMDNNPFSVLPNQLONGKLF 367
Qy 336 LEINDNHLTGHTPEELGKLTDLFDLVANNDEGPIPDHLSSTNINSLNVHNNKSGTII 395
Db 368 FDIYKHHFTGLIRDLCKSGRLDTIMTDNFPFGPIPELNGKSLTKIRASNNVYNGV 427
Qy 396 PRAPQKLESMTYLNNSSNIKGPPIVELSRIGNLTDLSDNNKINGIIPSSIGDLEHLK 455
Db 428 PSGIFKLPSVTIIEILANNRFGELPPEISG-ESLGLITLSSNNLFGSGKIPALNKLRLAQ 486
Qy 456 MNLNRNHTGVPGDGNLRSIMEIDLSNNDISGPIPELNOQLNIILRLNENNLTVGN 515
Db 487 LSLDANFVGEITGEVFDLPMLTIVNLSGNLTLGPITTLTRCVSLAVDLSSNMLEGKI 546
Qy 516 G-----SLAN-----CLSLTVLNVSHNNLVGDIPKNNNFSRSPD 550
Db 547 PKGIKULTDLSINVSINOQSPVPEIRFMLSITLTDLSNNNFIKGVPPGQFAVSEK 606
Qy 551 SFTGNPGLCGSWLNSPCHDS-----RRTVVISIRAAIIGIAGLVLMLVLI 599
Db 607 SFGNPNLCTS--HSCPNSSLYPDALKKRGPMSLKSTRVIVIAIAGTAAALVAVTV 663
Qy 600 AACRPHNPPFLDGSIDKPVYTSYTPKLVILHNNMA-----LHYV-----EDIMRMTENL 648
Db 664 YMMRRRK-----MMLAKTWKLTAFORLNFKAEDVV---ECL 696
Qy 649 SEKYIIGHGASSTYKCVLKNCKPVAIKRLY-SHNQSMKQFETELMLSSIKHNNVSL 707
Db 697 KENNIITGKGAGIVYGSMNGTDVAIKRLVAGSGGRNDYGFALLETLOKIHNNIMRL 756
Qy 708 QAVSLSHLSGLFYDYLENGSLMDLHGPTKKKTLDMTRLKTIAYGAAGLAIYHDCSP 767
Db 757 LGVSNKETVILLIYEVMPNGSLGEMLHG-AKGHGLKWMKMYKIAVBAKGLCYLHDCSP 845
Qy 768 RIHRPVKSNILLDDLEARLTPDGLASLC-VSKSHNSTYVMGTIGYIDPEYARTSRL 826
Db 816 LIHRDVKSNILLDDLEAHVADFGIAKFLVDPGASQSSSTAGSIVTAPEYATYTLKV 875
Qy 827 TEKSDVSYGIVLELLETRKAVDDESNIHLI--MSKTGNNEVEMADP----- 874
Db 876 DEKSDVYSRGVVLLEILIGRKPVGEGDGDVIGWNNKR---LELAQPSDAALVLAVY 931
Qy 875 DITSCKDLGVVKKVFOQLALCTKROPNDREPTMHQVTRVLGSMVSEQPPAATDT 929
Db 932 DPLSGVPLTSTVIMENIAMCVKEMGPARPTWREVVH-----MSEPPHSATHT 981

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QY 779 ILDDDLKRLDIFGLAKSLCVSKHITSYVWGITIGYIDPEVARTSLRLKSNVSGYV 838
D 837 ILLDNLRLARIDFGLAR--MMARKKETVWASYSYIAPEYXTLKVBEKIDISYGV 895
QY 839 LLELLTRRAVDE-----SNLHLLIMSKTGNNEVSMMA--DPDITSTCKDLGYVK-----V 889
D 896 LLELLTGRPPLEPEGESVDIVIEWARRKIRDNISLEALDPNV--GNCR---VYQEEMLTV 951
QY 890 FQALICTKROENDRPTMHQVTRVLG 915
D 952 LQIALCTTKLEPKDRPSMRDIVISMIG 977

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Job time : 56 secs